

R-NT2RP3004262//Mus musculus heat shock protein hsp40-3 gene, complete cds.//2.7e-43:528:73//AF092536

R-NT2RP3004334//Homo sapiens chromosome 17, clone hRPC.1110_E_20, complete sequence.//1.4e-06:435:62//AC004231

R-NT2RP3004341//CITBI-E1-2503F11.TR CITBI-E1 Homo sapiens genomic clone 2503F11, genomic survey sequence.//0.0018:210:65//AQ263365

R-NT2RP3004348//Homo sapiens chromosome 17, clone hRPK.85_B_7, complete sequence.//7.1e-46:340:83//AC005695

R-NT2RP3004349//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 11703, WORKING DRAFT SEQUENCE.//9.4e-29:263:79//AL020995

R-NT2RP3004378//Human DNA sequence from PAC 27K14 on chromosome Xp11.3-Xp11.4. Contains monoamine oxidase B (MAOB), ESTs and polymorphic CA repeats.//2.0e-67:422:90//Z95125

R-NT2RP3004399//HS_3046_A1_E02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3046 Col=3 Row=I, genomic survey sequence.//0.00014:186:67//AQ137619

R-NT2RP3004424//RPCI11-59I14.TJ RPCI11 Homo sapiens genomic clone R-59I14, genomic survey sequence.//7.4e-71:370:95//AQ201461

R-NT2RP3004428//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS ** * from clone Y66A7, WORKING DRAFT SEQUENCE.//0.096:205:64//AL022282

R-NT2RP3004451//Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence.//0.0029:396:60//AC005824

R-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds.//2.9e-106:526:98//AB007917

R-NT2RP3004466

R-NT2RP3004470//Homo sapiens chromosome 5, Bac clone 5m9 (LBNL H220), complete sequence.//8.3e-06:229:64//AC005895

R-NT2RP3004472//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.87:442:59//AC

005504

R-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds.//1.6e-105:521:97//AB007925

R-NT2RP3004480//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds.//3.9e-38:322:81//U47024

R-NT2RP3004490//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//4.2e-96:527:92//AC003982

R-NT2RP3004498//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//2.3e-43:342:82//AC006023

R-NT2RP3004503//Human cosmid g1572c101, complete sequence.//2.3e-25:392:68//AC000357

R-NT2RP3004504//M.musculus mRNA for CPEB protein.//1.8e-28:387:70//Y0826
0

R-NT2RP3004507

R-NT2RP3004527//Homo sapiens chromosome 14, BAC CITB-135H17 containing the RAD51L1 gene, complete sequence.//0.68:244:62//AC004518

R-NT2RP3004534//Mouse oncogene (ect2) mRNA, complete cds.//2.6e-79:525:84//L11316

R-NT2RP3004544

R-NT2RP3004566

R-NT2RP3004569//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.96:296:58//AC004709

R-NT2RP3004572//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//8.2e-12:457:63//AC005083

R-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//2.4e-97:488:96//AB007946

R-NT2RP3004594//Homo sapiens BAC clone NH0436H22 from 2, complete sequence.//1.7e-10:368:61//AC005234

R-NT2RP3004617

R-NT2RP3004618//F2H16TF IGF Arabidopsis thaliana genomic clone F2H16, genomic survey sequence.//0.96:212:64//B26414

R-NT2RP3004670//Homo sapiens GN6ST mRNA for N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST), complete cds.//2.2e-55:291:95//AB014679

R-NT2RP4000008//H.sapiens polyA site DNA sequence.//2.5e-25:202:85//Z24749

R-NT2RP4000023//CIT-HSP-2372A9.TF CIT-HSP Homo sapiens genomic clone 2372A9, genomic survey sequence.//3.6e-51:313:89//AQ112388

R-NT2RP4000035//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.3e-69:536:81//AC005015

R-NT2RP4000049//Homo sapiens TRAIL receptor 2 mRNA, complete cds.//2.1e-58:289:82//AF016266

R-NT2RP4000051//Homo sapiens Chromosome 22q11.2 Cosmid Clone 20b In DGCR Region, complete sequence.//0.56:462:58//AC000074

R-NT2RP4000078//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00021:460:60//AC005506

R-NT2RP4000102//Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence.//1.6e-08:518:58//AC004648

R-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//3.5e-106:536:96//AB011538

R-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds.//1.1e-110:554:97//AB007952

R-NT2RP4000147

R-NT2RP4000150//Rat proto-oncogene (Ets-1) mRNA, complete cds.//3.5e-46:395:83//L20681

R-NT2RP4000151

R-NT2RP4000159//Caenorhabditis elegans cosmid R02F11.//0.00011:261:63//A

F016439

R-NT2RP4000167//RPCI11-59L8.TK RPCI11 Homo sapiens genomic clone R-59L8,
genomic survey sequence.//6.2e-26:163:93//AQ200049

R-NT2RP4000185

R-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.//4.
6e-99:505:96//AB014600

R-NT2RP4000212//, complete sequence.//1.0e-106:538:96//AC005300

R-NT2RP4000214//Homo sapiens chromosome 19, CIT-HSP-444n24, complete seq
uence.//1.2e-39:272:88//AC005261

R-NT2RP4000218//Homo sapiens PAC clone DJ0320J15 from Xq23, complete seq
uence.//1.6e-09:457:60//AC004081

R-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP
).//9.0e-69:354:96//AJ006470

R-NT2RP4000246//Mus musculus mRNA for NDPP-1 protein, complete cds.//2.0
e-27:344:73//D10727

R-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence./
/9.7e-78:381:99//AF091092

R-NT2RP4000263//CIT-HSP-2336N24.TF CIT-HSP Homo sapiens genomic clone 23
36N24, genomic survey sequence.//0.26:124:69//AQ043515

R-NT2RP4000290//ORF 5' of ECLF2...ECRF3=G protein-coupled receptor homol
og [herpesvirus saimiri HVS, host-squirrel monkey, Genomic, 4 genes, 372
0 nt].//0.12:326:61//S76368

R-NT2RP4000312//Human DNA sequence from clone 523E19 on chromosome 6p11.
2-12.3 Contains ESTs STS and GSSs, complete sequence.//2.2e-111:538:98//
AL033384

R-NT2RP4000321//Homo sapiens clone 24453 mRNA sequence.//1.4e-108:515:99
//AF070524

R-NT2RP4000323//S.cerevisiae telomeric sequence DNA, clone YLP108CA-2-i.
//0.048:107:69//M34311

R-NT2RP4000355//Homo sapiens clone DJ1136A10, WORKING DRAFT SEQUENCE, 4 unordered pieces.//4.3e-39:350:79//AC004972

R-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//2.4e-109:520:99//AB018281

R-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//8.7e-109:527:98//AF044195

R-NT2RP4000370//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//9.9e-25:348:72//AC005154

R-NT2RP4000376//Rattus norvegicus phospholipase A-2-activating protein (plap) mRNA, complete cds.//2.2e-69:391:89//U17901

R-NT2RP4000381//Homo sapiens chromosome 17, clone hRPK.394_K_10, complete sequence.//0.066:197:63//AC006080

R-NT2RP4000415//345F19.TV CIT978SKA1 Homo sapiens genomic clone A-345F19, genomic survey sequence.//0.10:79:75//B15527

R-NT2RP4000417//Homo sapiens full length insert cDNA clone ZD52B10.//9.6e-96:468:97//AF086313

R-NT2RP4000424//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1 q23-25. Contains FM02 and FM03 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete sequence.//1.8e-08:489:59//AL021026

R-NT2RP4000448//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//3.3e-07:510:60//AC005505

R-NT2RP4000449//HS_2037_B2_A09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037 Col=18 Row=B, genomic survey sequence.//1.3e-58:375:88//AQ243047

R-NT2RP4000455//Phocine herpesvirus type 1 glycoprotein D (gD) gene, partial cds.//0.62:133:63//U92271

R-NT2RP4000457

R-NT2RP4000480//cSRL-54b11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-54b11, genomic survey sequence.//2.1e-19:145:88//B05082

R-NT2RP4000481

R-NT2RP4000500

R-NT2RP4000515//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//1.4e-05:411:59//AC005140

R-NT2RP4000517//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence.//2.7e-21:230:77//AC003007

R-NT2RP4000518//Homo sapiens DNA sequence from PAC 206D15 on chromosome 1q24. Contains a Reduced Folate Carrier protein (RFC) LIKE gene, a mitochondrial ATP Synthetase protein 8 (ATP8, MTATP8) LIKE pseudogene, an unknown gene and the last exon of the JEM1 gene coding for the Basic-Leucine Zipper nuclear factor JEM-1. Contains ESTs, an STS and a BAC end sequence (GSS), complete sequence.//0.0080:461:59//AL021068

R-NT2RP4000519

R-NT2RP4000524

R-NT2RP4000528//Homo sapiens chromosome 17, clone hRPK.138_P_22, complete sequence.//0.99:158:66//AC005697

R-NT2RP4000541//Homo sapiens Chromosome 22q11.2 Cosmid Clone 33e In DGCR Region, complete sequence.//1.0:309:59//AC000078

R-NT2RP4000556//Rattus norvegicus cell cycle protein p55CDC gene, complete cds.//0.0031:126:72//AF052695

R-NT2RP4000588//Homo sapiens BAC clone RG208K23 from 7q31, complete sequence.//1.0:186:64//AC004161

R-NT2RP4000614//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***
from contig 3-62, complete sequence.//1.4e-06:526:58//AL009013

R-NT2RP4000638//Homo sapiens chromosome 17, clone hCIT.468_F_23, WORKING
DRAFT SEQUENCE, 3 unordered pieces.//6.9e-48:497:75//AC004666

R-NT2RP4000648//CIT-HSP-230017.TR CIT-HSP Homo sapiens genomic clone 230
017, genomic survey sequence.//0.22:110:68//AQ012747

R-NT2RP4000657//Lycodichthys dearborni type III antifreeze peptide gene,
clone 5' LD-1/NotI-EcoRI subclone SphI-XbaI, partial cds.//0.0065:189:63
//U20443

R-NT2RP4000704//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 409J21, WORKING DRAFT SEQUENCE.//0.22:334:60//Z83824

R-NT2RP4000724//Homo sapiens Chromosome 22q11.2 Cosmid Clone 56c In DGCR
Region, complete sequence.//2.2e-70:448:88//AC000080

R-NT2RP4000728//CIT-HSP-2310K14.TF CIT-HSP Homo sapiens genomic clone 23
10K14, genomic survey sequence.//0.00013:289:61//AQ019669

R-NT2RP4000739//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE,
21 unordered pieces.//0.53:254:61//AC004765

R-NT2RP4000781//P.cepacia fusaric acid-resistance genes encoding 5 prote
ins, complete cds.//1.0:392:59//D12503

R-NT2RP4000817//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human
BAC library) complete sequence.//0.59:378:58//AC003037

R-NT2RP4000833//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone Y313F4, WORKING DRAFT SEQUENCE.//3.4e-53:307:85//AL023808

R-NT2RP4000837//Homo sapiens T-cell receptor alpha delta locus from base
s 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence.
//7.0e-50:367:77//AE000660

R-NT2RP4000855

R-NT2RP4000865//Homo sapiens chromosome 17, clone HRPC905N1, complete se
quence.//1.5e-78:479:88//AC003098

R-NT2RP4000878//Mus musculus mRNA for myeloid associated differentiation protein.//4.5e-09:186:69//AJ001616

R-NT2RP4000879//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.8e-08:364:60//AC004153

R-NT2RP4000907//Human S-adenosylmethionine decarboxylase (AMD1) gene, exons 5-9.//3.5e-90:459:96//M88006

R-NT2RP4000915//H.sapiens ung gene for uracil DNA-glycosylase.//7.6e-09:392:61//X89398

R-NT2RP4000925//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//5.8e-45:264:92//U42975

R-NT2RP4000927//epstein-barr virus simple repeat array (ir3).//0.00012:367:61//J02079

R-NT2RP4000928//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone : MCL19, complete sequence.//1.0:138:68//AB006698

R-NT2RP4000929//Human DNA sequence from PAC 293L6 on chromosome 22, complete sequence.//0.45:288:62//Z82197

R-NT2RP4000955//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 633019, WORKING DRAFT SEQUENCE.//1.1e-09:322:62//AL022302

R-NT2RP4000973//Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions.//2.3e-06:326:62//AF003528

R-NT2RP4000975

R-NT2RP4000979//HS_3009_B1_F08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3009 Col=15 Row=L, genomic survey sequence.//2.3e-14:117:89//AQ090957

R-NT2RP4000984//Human immunodeficiency virus type 1 envelope glycoprotein (env) gene, C2-V3 region, isolate HIV194UG011INT.01_dilPD, partial cds.//0.11:219:62//U44882

R-NT2RP4000989//Sequence 30 from patent US 5552281.//3.5e-25:154:97//I25
669

R-NT2RP4000996//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//3.8e-07:421:59//AF030694

R-NT2RP4000997//Homo sapiens chromosome 17, clone 104H12, complete sequence.//4.2e-37:499:72//AC000003

R-NT2RP4001004//HS_3163_A2_H02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3163 Col=4 Row=0, genomic survey sequence.//2.8e-38:241:90//AQ168515

R-NT2RP4001006//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//7.1e-55:372:73//AC006023

R-NT2RP4001010//Homo sapiens full length insert cDNA clone ZD38E12.//3.3e-09:153:74//AF086247

R-NT2RP4001029//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//2.1e-34:361:78//U20086

R-NT2RP4001041//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//9.9e-84:435:96//AC005216

R-NT2RP4001057//Homo sapiens KIAA0399 mRNA, partial cds.//6.2e-50:282:94//AB007859

R-NT2RP4001064//H.sapiens NOS2 gene, exon 15.//0.71:183:61//X85771

R-NT2RP4001078//Human D-site binding protein gene, exon 4 and complete cds.//1.9e-114:569:97//U48213

R-NT2RP4001079//Homo sapiens mRNA for putative Ca²⁺-transporting ATPase, partial.//2.4e-118:574:98//AJ010953

R-NT2RP4001080//Plasmodium falciparum chromosome 2, section 66 of 73 of the complete sequence.//0.013:430:58//AE001429

R-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds.//1.

8e-119:548:95//AB011164

R-NT2RP4001095//Homo sapiens cosmids IM0525, LC1233, Qc3C1, LB1439, Qc12 C11 and 220B3 from Xq28, complete sequence.//2.8e-39:312:81//AF003626

R-NT2RP4001100//Human DNA sequence from cosmid U85A3, between markers DX S366 and DXS87 on chromosome X contains rad21 and T-cell cyclophorin pseudogenes, STS.//8.7e-41:389:78//Z78021

R-NT2RP4001117//Canis familiaris sec61 homologue mRNA, complete cds.//2.8e-12:292:68//M96629

R-NT2RP4001122//Caenorhabditis elegans cosmid F44D12, complete sequence.//0.97:129:66//Z68298

R-NT2RP4001126//HS_3146_A1_B05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3146 Col=9 Row=C, genomic survey sequence.//0.013:268:63//AQ141093

R-NT2RP4001138

R-NT2RP4001143//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 64K7, WORKING DRAFT SEQUENCE.//1.8e-31:380:68//AL031668

R-NT2RP4001148//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.2e-83:325:92//AC005095

R-NT2RP4001149//Mouse mRNA for thymic epithelial cell surface antigen, complete cds.//8.1e-32:553:67//D67067

R-NT2RP4001150//AK011 Genomic DNA Hordeum vulgare genomic clone tel44a similar to barley TAS, genomic survey sequence.//0.91:132:63//AQ248412

R-NT2RP4001159//Cloning vector pAP3neo DNA, complete sequence.//4.0e-118:437:97//AB003468

R-NT2RP4001174//Homo sapiens 12q24 BAC RPC111-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//1.7e-33:289:82//AC002996

R-NT2RP4001206//P.falciparum mRNA for AARP2 protein.//0.93:187:64//Y0892

R-NT2RP4001207

R-NT2RP4001210//CIT-HSP-2042D13.TF CIT-HSP Homo sapiens genomic clone 2042D13, genomic survey sequence.//3.8e-06:268:63//B74772

R-NT2RP4001213//Human zinc finger protein 20.(ZNF20) pentanucleotide repeat polymorphism.//4.7e-16:371:66//M99593

R-NT2RP4001219//HS_2190_A1_A06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2190 Col=11 Row=A, genomic survey sequence.//2.4e-06:288:61//AQ216635

R-NT2RP4001228//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P2, WORKING DRAFT SEQUENCE.//0.024:357:58//AL031745

R-NT2RP4001235//HS_3047_A1_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=13 Row=I, genomic survey sequence.//0.0033:301:63//AQ126918

R-NT2RP4001256//HS_3007_A2_B06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=12 Row=C, genomic survey sequence.//1.5e-11:140:80//AQ118389

R-NT2RP4001260//Plasmodium falciparum chromosome 2, section 63 of 73 of the complete sequence.//0.0013:486:59//AE001426

R-NT2RP4001274//RPCI11-24021.TKBF RPCI-11 Homo sapiens genomic clone RPCI-11-24021, genomic survey sequence.//3.9e-25:142:99//AQ013887

R-NT2RP4001276//Homo sapiens full length insert cDNA clone ZD55D10.//1.2e-10:90:92//AF086334

R-NT2RP4001313//Mus musculus orphan nuclear hormone receptor (CAR) gene, complete sequence.//7.7e-23:466:66//AF009326

R-NT2RP4001315//CIT-HSP-2312C6.TR CIT-HSP Homo sapiens genomic clone 2312C6, genomic survey sequence.//0.98:305:62//AQ018036

R-NT2RP4001339

R-NT2RP4001345

R-NT2RP4001351//Fruitfly strain g20 mitochondrial DNA, A+T-rich region,

partial sequence.//0.00082:260:59//AB003097

R-NT2RP4001353//RPCI11-55N17.TJ RPCI11 Homo sapiens genomic clone R-55N17, genomic survey sequence.//0.74:106:66//AQ081821

R-NT2RP4001372

R-NT2RP4001373//Homo sapiens chromosome 17, clone hRPK.394_K_10, complete sequence.//1.5e-09:473:60//AC006080

R-NT2RP4001375

R-NT2RP4001379//CIT-HSP-2335A10.TF CIT-HSP Homo sapiens genomic clone 2335A10, genomic survey sequence.//9.4e-41:441:75//AQ040083

R-NT2RP4001389//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//2.4e-22:276:73//AC004691

R-NT2RP4001407//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.49:254:61//AC005140

R-NT2RP4001414

R-NT2RP4001433//Human prohibitin (PHB) gene, exons 1-7.//6.6e-66:357:90//L14272

R-NT2RP4001442//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.11:307:59//AC005308

R-NT2RP4001447//cSRL-58d2-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-58d2, genomic survey sequence.//0.0039:112:71//B05220

R-NT2RP4001474

R-NT2RP4001483

R-NT2RP4001498//Plasmodium falciparum (clone Dd2) heat shock protein 86 gene, complete cds.//1.2e-07:339:61//L34027

R-NT2RP4001502//HS_2187_B1_C10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2187 Col=19 Row=F, genomic survey

sequence.//1.3e-20:183:81//AQ214108

R-NT2RP4001507//Arabidopsis thaliana chromosome 1 BAC T17H3 sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.15:333:62//AC005916

R-NT2RP4001524//Genomic sequence from Human 13, complete sequence.//0.96:159:65//AC001226

R-NT2RP4001529//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//9.5e-34:337:80//U20086

R-NT2RP4001547//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.00027:336:63//AC004710

R-NT2RP4001551//Arabidopsis thaliana BAC T12H20.//1.5e-11:517:60//AF080119

R-NT2RP4001555//Human DNA sequence from PAC 481A17 on chromosome X contains ESTs.//0.0069:305:62//Z82212

R-NT2RP4001567//RPCI11-61A2.TJ RPCI11 Homo sapiens genomic clone R-61A2, genomic survey sequence.//0.0072:180:60//AQ200771

R-NT2RP4001568

R-NT2RP4001571//Trypanoplasma borreli kinetoplast ribosomal protein S12 (RPS12), putative cryptogene (GR11), 12S ribosomal RNA, and apocytochrome b (CYb) genes, primary transcripts, and cytochrome c oxidase subunit I II (COIII) gene, complete cds.//1.6e-09:555:58//U14181

R-NT2RP4001574//HS_2247_B1_B05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2247 Col=9 Row=D, genomic survey sequence.//1.1e-41:254:90//AQ182345

R-NT2RP4001575//Human DNA sequence from clone 1033B10 on chromosome 6p21.2-21.31. Contains the BING5 gene, exons 11 to 15 of the BING4 gene, the gene for GALT3 (beta3-Galactosyltransferase), the RPS18 (40S ribosomal protein S18) gene, the SACM2L (suppressor of actin mutation 2, yeast, homolog) gene, a pseudogene similar to TAT-SF1, a Pseudogene similar to zi

nc finger genes, the RING1 gene, the gene for HKE6 (RING2), the gene for HKE4 (RING5), the RXRB (Retinoid X receptor beta) gene, the COL11A2 (collagen, type XI, alpha 2) gene, the HLA-DPB2 pseudogene and part of the HLA-DPA3 pseudogene. Contains predicted CpG islands, ESTs, STSS, and GSSs, complete sequence.//1.1e-118:567:98//AL031228

R-NT2RP4001592//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE.//2.5e-09:370:61//AL031650

R-NT2RP4001610//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence.//0.99:73:75//AC002364

R-NT2RP4001614

R-NT2RP4001634//Homo sapiens full length insert cDNA clone YU73B11.//5.8e-101:526:94//AF087969

R-NT2RP4001638//Homo sapiens clone 23967 unknown mRNA, partial cds.//5.4e-115:559:97//AF007151

R-NT2RP4001644//M.musculus mRNA for map kinase interacting kinase, Mnk2.//6.8e-33:286:79//Y11092

R-NT2RP4001656//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//2.2e-109:515:99//AC000384

R-NT2RP4001677//Genomic sequence from Human 9q34, complete sequence.//0.19:504:58//AC000397

R-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//4.5e-115:583:96//U96629

R-NT2RP4001725//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.98:301:60//AC000380

R-NT2RP4001730//Caenorhabditis elegans cosmid F48E3.//2.2e-17:328:64//U28735

R-NT2RP4001739//RPCI11-74E7.TJ RPCI11 Homo sapiens genomic clone R-74E7, genomic survey sequence.//1.1e-08:141:65//AQ268408

R-NT2RP4001753//H.sapiens HZF3 mRNA for zinc finger protein.//1.7e-111:552:96//X78926

R-NT2RP4001760//Mouse oncogene (ect2) mRNA, complete cds.//9.3e-27:358:72//L11316

R-NT2RP4001790//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.7e-99:484:98//AC005020

R-NT2RP4001803//HS_3087_B2_B05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3087 Col=10 Row=D, genomic survey sequence.//2.7e-96:471:97//AQ121405

R-NT2RP4001822

R-NT2RP4001823

R-NT2RP4001828//Human DNA sequence from PAC 179I15, BRCA2 gene region chromosome 13q12-q13 contains Klotho ESTs and CpG island.//4.1e-14:136:83/Z92540

R-NT2RP4001838//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//2.5e-06:418:60//AE001372

R-NT2RP4001849//P.falciparum serine rich protein (SERP I) gene.//0.64:135:67//J03983

R-NT2RP4001889//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//4.3e-26:212:82//AC004548

R-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.8e-111:570:96//AC005014

R-NT2RP4001896

R-NT2RP4001901

R-NT2RP4001927//Borrelia burgdorferi (section 32 of 70) of the complete genome.//1.0:242:60//AE001146

R-NT2RP4001938//Human aminopeptidase N gene, exon 1.//3.3e-42:195:85//M55523

R-NT2RP4001946//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic

sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.97:371:57//ACO
04157

R-NT2RP4001950//RPCI11-69C18.TJ RPCI11 Homo sapiens genomic clone R-69C1
8, genomic survey sequence.//4.7e-91:552:89//AQ236641

R-NT2RP4001953//Homo sapiens DNA sequence from PAC 958B3 on chromosome X
p22.11-Xp22.22. Contains ESTs STS and CpG island.//6.6e-70:325:84//Z9302
3

R-NT2RP4001966//Rat mRNA for growth potentiating factor, complete cds.//
5.5e-37:141:86//D42148

R-NT2RP4001975//Human Newcastle disease virus inducible protein mRNA, pa
rtial 3' UTR region.//1.0e-46:242:98//U25276

R-NT2RP4002018//RPCI11-76I23.TV RPCI11 Homo sapiens genomic clone R-76I2
3, genomic survey sequence.//7.9e-89:438:97//AQ268536

R-NT2RP4002047//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 97P20, WORKING DRAFT SEQUENCE.//4.1e-07:325:62//AL031297

R-NT2RP4002052//Human DNA sequence from clone 352E11 on chromosome 22q13
.1-13.31. Contains GSSs, complete sequence.//0.31:452:57//AL022353

R-NT2RP4002058//RPCI11-69O1.TJ RPCI11 Homo sapiens genomic clone R-69O1,
genomic survey sequence.//0.23:163:64//AQ268418

R-NT2RP4002071//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 1172A22, WORKING DRAFT SEQUENCE.//1.1e-11:407:62//AL034386

R-NT2RP4002075//Human DNA sequence from clone 21F7 on chromosome 6q16.1-
21. Contains part of an exon of a putative new gene and STSs and GSSs, c
omplete sequence.//0.085:350:61//AL033375

R-NT2RP4002078//RPCI11-79I16.TV RPCI11 Homo sapiens genomic clone R-79I1
6, genomic survey sequence.//3.3e-87:452:95//AQ283131

R-NT2RP4002081

R-NT2RP4002083//Homo sapiens mineralocorticoid receptor (MLR), exon 5.//
0.50:256:61//AF068619

R-NT2RP4002408//CIT-HSP-2376023.TF CIT-HSP Homo sapiens genomic clone 2376023, genomic survey sequence.//6.8e-62:320:96//AQ111163

R-NT2RP4002791//Human PAC clone DJ318C15 from Xq23, complete sequence.//0.022:435:61//AC002476

R-NT2RP4002888//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//6.0e-56:660:71//AC002383

R-NT2RP4002905//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-20, complete sequence.//0.0017:533:57//AL008972

R-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds.//8.7e-114:605:94//AB007934

R-OVARC1000004//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//2.1e-43:326:74//AC005510

R-OVARC1000006//HS_2253_B1_F01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=1 Row=L, genomic survey sequence.//3.7e-35:191:98//AQ069124

R-OVARC1000013//HS_2212_A2_G06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2212 Col=12 Row=M, genomic survey sequence.//0.14:212:63//AQ210584

R-OVARC1000014//Human DNA sequence from PAC 463A9, on chromosome Xq25 contains STS.//0.0053:356:62//Z80232

R-OVARC1000017

R-OVARC1000035//RPCI11-65E1.TJ RPCI11 Homo sapiens genomic clone R-65E1, genomic survey sequence.//3.3e-05:236:63//AQ237194

R-OVARC1000058//Homo sapiens DNA sequence from BAC 390C10 on chromosome 22q11.21-12.1. Contains an Immunoglobulin LIKE gene and a pseudogene similar to Beta Crystallin. Contains ESTs, STSS, GSSs and taga and tat repeat polymorphisms, complete sequence.//2.7e-48:325:82//AL008721

R-OVARC1000060//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27K12, WORKING DRAFT SEQUENCE.//5.0e-21:297:70//AL033397

R-OVARC1000068//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.00038:553:58//X95276

R-OVARC1000071//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 596C15, WORKING DRAFT SEQUENCE.//5.1e-110:599:93//AL031387

R-OVARC1000085//DNA encoding component HC5 of human proteasome.//2.7e-65:366:92//E03413

R-OVARC1000087//CIT-HSP-2172N17.TF CIT-HSP Homo sapiens genomic clone 2172N17, genomic survey sequence.//0.80:285:59//B94391

R-OVARC1000091

R-OVARC1000092//CIT-HSP-2373J20.TR CIT-HSP Homo sapiens genomic clone 2373J20, genomic survey sequence.//1.4e-17:141:85//AQ111520

R-OVARC1000106

R-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//2.6e-100:495:97//AF069250

R-OVARC1000114//Homo sapiens partial XPGC gene, exon 2.//9.5e-49:392:80//X71342

R-OVARC1000133//Human Chromosome 16 BAC clone CIT987SK-A-362G6, complete sequence.//0.00020:243:65//U95740

R-OVARC1000145//Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q25, complete sequence.//1.8e-16:370:67//AC005385

R-OVARC1000148//CIT-HSP-2386P14.TF.1 CIT-HSP Homo sapiens genomic clone 2386P14, genomic survey sequence.//1.1e-05:55:98//AQ240492

R-OVARC1000151//M.musculus GEG-154 mRNA.//9.8e-21:192:81//X71642

R-OVARC1000168//CIT-HSP-2336F6.TR CIT-HSP Homo sapiens genomic clone 2336F6, genomic survey sequence.//0.050:176:62//AQ042932

R-OVARC1000191//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.7e-08:534:58//AC005506

R-OVARC1000198//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4

, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//5.2e-111:556:96//AC004604

R-OVARC1000209//Blacus sp. 16S ribosomal RNA gene, partial sequence.//0.55:165:67//AF003501

R-OVARC1000212//Mouse DNA for beta-casein.//0.56:225:63//X13484

R-OVARC1000240//Homo sapiens chromosome 17, clone hRPK.63_A_1, complete sequence.//6.2e-38:193:82//AC005670

R-OVARC1000241//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//1.1e-25:312:73//AF060194

R-OVARC1000288//Human HepG2 3' region MboI cDNA, clone hmd1d01m3.//5.4e-07:128:70//D17131

R-OVARC1000302//Homo sapiens chromosome 17, clone hRPK.651_L_9, complete sequence.//1.7e-10:100:88//AC005971

R-OVARC1000304//Mouse mRNA from Mov10 locus.//7.9e-66:379:81//X52574

R-OVARC1000309

R-OVARC1000321//Homo sapiens clone NH0479C13; WORKING DRAFT SEQUENCE, 12 unordered pieces.//6.5e-83:453:94//AC005236

R-OVARC1000326//Rattus norvegicus lamina-associated polypeptide 1C (LAP1 C) mRNA, complete cds.//5.0e-58:455:81//U19614

R-OVARC1000335//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0483I23; HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.034:429:60//AC005690

R-OVARC1000347//Mus musculus HRS gene, complete cds.//4.6e-06:339:61//AF020308

R-OVARC1000384//D.discoideum glycoprotein 24 A and B (GP24A and GP24B) genes, complete cds.//0.48:296:62//M27588

R-OVARC1000408//Homo sapiens DNA from chromosome 19-cosmid R27740 containing MEF2B and RSRFR2 genes, genomic sequence.//9.4e-39:286:87//AD00081

R-OVARC1000411//CIT-HSP-2303H10.TF CIT-HSP Homo sapiens genomic clone 2303H10, genomic survey sequence.//1.5e-07:94:84//AQ016720

R-OVARC1000414//Homo sapiens genomic DNA, 21q region, clone: 149C3X10, genomic survey sequence.//1.8e-32:296:75//AG002388

R-OVARC1000420//Homo sapiens clone DJ1137M13, complete sequence.//2.0e-48:354:77//AC005378

R-OVARC1000427//D.discoideum vegetative specific gene V18 gene for ribosomal protein.//2.5e-09:370:59//X15382

R-OVARC1000431//HS_2199_A2_E02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2199 Col=4 Row=I, genomic survey sequence.//1.3e-34:186:98//AQ093722

R-OVARC1000437//Gallus gallus tensin mRNA, 3' end.//1.3e-15:160:80//L06662

R-OVARC1000440//Homo sapiens BAC clone NH0538D15 from 7q11.23-q21.1, complete sequence.//0.0054:337:61//AC006043

R-OVARC1000442//CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey sequence.//1.0e-45:322:86//AQ037381

R-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds.//1.1e-77:418:94//AB014583

R-OVARC1000461//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 215D11, WORKING DRAFT SEQUENCE.//0.62:333:59//AL034417

R-OVARC1000465//Bos taurus guanine nucleotide-exchange protein (ARF-GEPI) mRNA, complete cds.//1.1e-81:489:91//AF023451

R-OVARC1000466//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//0.0088:98:72//AC004526

R-OVARC1000473//Homo sapiens full length insert cDNA clone YI53C10.//3.2e-92:317:100//AF085851

R-OVARC1000479//Rattus norvegicus mRNA for TIP120, complete cds.//2.7e-70:502:84//D87671

R-OVARC1000486//Dictyostelium discoideum FusC (fusC) gene, partial cds./
/0.52:411:58//AF019984

R-OVARC1000496

R-OVARC1000520//Homo sapiens PAC clone DJ412A9 from 22, complete sequenc
e.//3.8e-17:294:71//AC005005

R-OVARC1000526//Homo sapiens clone GS438P06, WORKING DRAFT SEQUENCE, 17
unordered pieces.//4.5e-109:547:96//AC005024

R-OVARC1000533//Homo sapiens chromosome 19, cosmid R30385, complete sequ
ence.//3.0e-46:264:93//AC004510

R-OVARC1000543//Caenorhabditis elegans cosmid F10C1.//0.00063:417:59//U4
9831

R-OVARC1000556//Homo sapiens DNA sequence from PAC 168L15 on chromosome
6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS.
CpG island, complete sequence.//1.5e-39:144:92//AL022069

R-OVARC1000557//Homo sapiens chromosome 19, cosmid R32469, complete sequ
ence.//1.5e-81:429:96//AC005197

R-OVARC1000564//Homo sapiens chromosome 17, clone HRPC837J1, complete se
quence.//0.83:301:58//AC004223

R-OVARC1000573//Homo sapiens Xq28 genomic DNA in the region of the ALD l
ocus containing the genes for creatine transporter (SLC6A8), CDM, adreno
leukodystrophy (ALD), Na+-isocitrate dehydrogenase gamma subunit (IDH),
and translocon-associated protein delta (TRAP) genes, complete cds, plex
in related protein (PLEXR) and serine kinase (SK) genes, partial cds, Xq
28lul gene and cytochrome C (CCp) pseudogene.//2.4e-44:300:88//U52111

R-OVARC1000578//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete
sequence.//6.4e-48:436:78//AF001549

R-OVARC1000588//Homo sapiens chromosome 19, cosmid F19847, complete sequ
ence.//2.7e-32:313:78//AC005952

R-OVARC1000605

R-OVARC1000622//Homo sapiens PAC clone DJ0942116 from 7q11, complete sequence.//6.2e-43:328:83//AC006012

R-OVARC1000640//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.9e-47:514:73//AC005840

R-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds.//1.6e-29:162:100//AB011162

R-OVARC1000678//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.50:270:60//AC005140

R-OVARC1000679//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7.//1.4e-83:549:86//AJ001713

R-OVARC1000681//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 257E24, WORKING DRAFT SEQUENCE.//3.2e-13:160:76//AL034424

R-OVARC1000689//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds.//0.90:230:61//U32943

R-OVARC1000700//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//5.1e-15:133:85//AC005754

R-OVARC1000703//Homo sapiens chromosome 22, clone hRPC.130_H_16, complete sequence.//6.9e-48:525:73//AC005585

R-OVARC1000730//HS_3018_B1_H10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=19 Row=P, genomic survey sequence.//0.00019:198:63//AQ093513

R-OVARC1000746//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.98:154:65//X95276

R-OVARC1000769//Human coagulation factor XI gene, intron 2, partial, clone pTZ18R.//2.0e-30:187:78//M21185

R-OVARC1000771

R-OVARC1000781//Sequence 5 from Patent W09722695.//8.4e-47:401:77//A6355

R-OVARC1000787//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence.//7.8e-111:567:96//AC004542

R-OVARC1000800//Homo sapiens mitochondrial HSP75 mRNA, complete cds.//1.3e-17:119:95//L15189

R-OVARC1000802//Homo sapiens chromosome 5, BAC clone 120c13 (LBNL H171), complete sequence.//2.3e-51:482:78//AC005574

R-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC.//3.6e-105:536:95//Y17711

R-OVARC1000846//Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence.//2.7e-107:538:96//AC004494

R-OVARC1000850//Homo sapiens PB39 mRNA, complete cds.//3.6e-114:579:96//AF045584

R-OVARC1000862//M.musculus Fif mRNA.//2.3e-20:346:73//X71978

R-OVARC1000876//Plasmodium falciparum chromosome 2, section 53 of 73 of the complete sequence.//9.1e-08:427:58//AE001416

R-OVARC1000883//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//5.6e-34:357:78//U20086

R-OVARC1000885//Lycopersicon esculentum alcohol dehydrogenase homolog (GAD3) mRNA, partial cds.//0.47:305:60//U21801

R-OVARC1000886

R-OVARC1000891//HS_3082_A2_F04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3082 Col=8 Row=K, genomic survey sequence.//1.1e-16:187:79//AQ122500

R-OVARC1000897//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//7.2e-07:476:60//AL020989

R-OVARC1000912

R-OVARC1000915//Homo sapiens chromosome 17, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000924//Homo sapiens Chromosome 22q11.2 Cosmid Clone cosk In NF1 Region, complete sequence.//1.6e-77:465:90//AC002471

R-OVARC1000936//HS_2195_A2_C12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=24 Row=E, genomic survey sequence.//2.4e-76:463:90//AQ191108

R-OVARC1000937//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 250D10, WORKING DRAFT SEQUENCE.//0.0028:161:65//Z99716

R-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//3.5e-62:526:78//AB005549

R-OVARC1000948//Hypera postica NADH dehydrogenase subunit 1 (ND1) gene, partial cds, tRNA-Leu gene, complete sequence, and 16S ribosomal gene, partial sequence, mitochondrial genes encoding mitochondrial products.//0.018:212:61//U61169

R-OVARC1000959//CIT-HSP-2371K16.TR CIT-HSP Homo sapiens genomic clone 2371K16, genomic survey sequence.//1.1e-45:303:87//AQ111323

R-OVARC1000960//Homo sapiens BAC clone GS293C05 from 7q21-q22, complete sequence.//7.5e-44:353:81//AC005021

R-OVARC1000971//H.sapiens DNA for repeat unit locus D18S51 (285 bp).//2.2e-07:223:70//X91255

R-OVARC1000984

R-OVARC1000996//Human DNA sequence from clone 272L16 on chromosome 1q32.1-32.3. Contains the 3' end of the LAMB3 gene for Laminin, Beta 3 (Nicein, Kalinin, BM600) and a novel Rat Ca²⁺/Calmodulin dependent Protein Kinase LIKE gene. Contains ESTs, STSSs, GSSs, genomic marker D1S491 and a ca repeat polymorphism, complete sequence.//1.3e-06:179:70//AL023754

R-OVARC1000999//Homo sapiens chromosome 17, clone hCIT.457_L_16, complete sequence.//5.8e-71:332:87//AC003957

R-OVARC1001000//HS_3032_B1_G11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=21 Row=N, genomic survey

sequence.//5.1e-51:257:99//AQ096695
R-OVARC1001004//Homo. sapiens from UWGC:y18c282 from 6p21, complete sequence.//5.6e-92:473:96//AC004190
R-OVARC1001010//RPCI11-10P1.TV RPCI-11 Homo sapiens genomic clone RPCI-11-10P1, genomic survey sequence.//4.1e-05:201:65//B71813
R-OVARC1001011//Homo sapiens clone DJ1021I20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.9e-18:219:69//AC005520
R-OVARC1001032//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE.//2.7e-89:464:86//AL022345
R-OVARC1001034//Homo sapiens chromosome 20, BAC clone 99 (LBNL H80), complete sequence.//1.4e-18:451:64//AC005220
R-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds.//1.3e-99:501:96//AF099149
R-OVARC1001040//Homo sapiens chromosome 17, clone hRPK.1096_G_20, complete sequence.//9.7e-17:180:78//AC005410
R-OVARC1001044
R-OVARC1001051//H.sapiens mRNA for homologue to yeast ribosomal protein L41.//3.7e-15:124:88//Z12962
R-OVARC1001055//Homo sapiens, clone hRPK.15_A_1, complete sequence.//2.0e-30:292:76//AC006213
R-OVARC1001062//Sequence 65 from patent US 5691147.//2.6e-54:312:92//I76237
R-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.//2.3e-95:463:98//AF082657
R-OVARC1001072//Gallus gallus chicken brain factor-2 (CBF-2) mRNA, complete cds.//0.92:272:59//U47276
R-OVARC1001074//HS_2205_A1_D07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2205 Col=13 Row=G, genomic survey sequence.//1.3e-35:205:94//AQ184530

R-OVARC1001085

R-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone I MAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).//4.5e-95:325:98//AJ005897

R-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds.//1.0e-73:386:95//AF051782

R-OVARC1001117//Homo sapiens chromosome 7 clone UWGC:g3586a160 from 7p14-15, complete sequence.//6.1e-37:314:81//AC005272

R-OVARC1001118//Homo sapiens chromosome 5, P1 clone 1195e2 (LBNL H73), complete sequence.//1.5e-44:390:77//AC005372

R-OVARC1001129//Rickettsia prowazekii strain Madrid E, complete genome; segment 1/4.//0.81:461:57//AJ235270

R-OVARC1001161//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 850H21, WORKING DRAFT SEQUENCE.//4.6e-08:342:64//AL031680

R-OVARC1001162//CIT-HSP-2171J2.TR CIT-HSP Homo sapiens genomic clone 2171J2, genomic survey sequence.//5.9e-48:347:85//B89781

R-OVARC1001167//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUENCE, 15 unordered pieces.//1.3e-28:427:70//AC004963

R-OVARC1001169//RPCI11-36P6.TV RPCI-11 Homo sapiens genomic clone RPCI-11-36P6, genomic survey sequence.//0.56:113:72//AQ045859

R-OVARC1001170//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete sequence.//8.8e-39:301:85//AC002549

R-OVARC1001173//Human clone HS2.30 Alu-Ya5 sequence.//2.4e-35:183:83//U67213

R-OVARC1001180//Homo sapiens 12q24.1 NOVECTOR P443K8 () complete sequence.//9.1e-41:516:72//AC005907

R-OVARC1001188//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//1.2e-14:134:85//AC004796

R-OVARC1001200//ALS-85 kda insulin-like growth factor binding protein-3

complex acid-labile subunit [baboons, liver, mRNA Partial, 1818 nt].//0.

12:345:60//S83462

R-OVARC1001232//Bovine tyrosine hydroxylase mRNA, complete cds.//0.66:25

7:59//M36794

R-OVARC1001240//Homo sapiens chromosome 17, clone hCIT.124_H_2, complete
sequence.//1.4e-41:284:87//AC006071

R-OVARC1001243//HS_2055_B2_C01_MR CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=2055 Col=2 Row=F, genomic survey s
equence.//0.59:83:75//AQ243142

R-OVARC1001261//Crocodylus porosus mRNA for transthyretin.//0.93:121:66/
/AJ223148

R-OVARC1001268

R-OVARC1001270//Plasmodium falciparum MAL3P6, complete sequence.//0.0031
:295:62//Z98551

R-OVARC1001271//Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), c
omplete sequence.//1.6e-107:544:97//AC004494

R-OVARC1001282//Homo sapiens Xp22-39-47 PAC RPC11-199J3 (Roswell Park Ca
ncer Institute Human PAC Library) complete sequence.//0.025:402:59//AC00
6062

R-OVARC1001296//Homo sapiens echinoderm microtubule-associated protein h
omolog HuEMAP mRNA, complete cds.//1.1e-05:319:62//U97018

R-OVARC1001306//Sequence 13 from patent US 5624818.//5.4e-85:577:84//I41
142

R-OVARC1001329//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 30G7, WORKING DRAFT SEQUENCE.//4.2e-71:282:88//AL034402

R-OVARC1001330//Homo sapiens PAC clone DJ0697H17 from 7q11.23-q21.1, com
plete sequence.//0.19:256:59//AC004862

R-OVARC1001339//Homo sapiens 12q13 PAC RPC11-316M24 (Roswell Park Cancer
Institute Human PAC library) complete sequence.//2.5e-49:366:83//AC0042

42

R-OVARC1001341//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 695020, WORKING DRAFT SEQUENCE.//4.8e-26:447:69//AL032818

R-OVARC1001342//Homo sapiens chromosome 10 clone CIT987SK-1175G20 map 10 q25.2-10q25.3, complete sequence.//5.5e-86:569:86//AC005874

R-OVARC1001344//Homo sapiens chromosome 5, BAC clone 261j17 (LBNL H190), complete sequence.//2.8e-46:424:78//AC005350

R-OVARC1001357//Sequence 1 from patent US 5597707.//3.0e-42:250:93//I34297

R-OVARC1001360//Homo sapiens chromosome 17, clone hRPK.786_0_4, complete sequence.//0.20:335:60//AC005863

R-OVARC1001369

R-OVARC1001372//S.scrofa DNA for myogenin 3' flanking region (285 bp).//6.9e-29:249:83//X89210

R-OVARC1001376//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//2.1e-50:491:73//AC004491

R-OVARC1001381//Homo sapiens chromosome 17, clone hRPK.156_L_14, complete sequence.//9.3e-20:422:60//AC005821

R-OVARC1001391

R-OVARC1001399

R-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds.//9.9e-110:561:95//AB006651

R-OVARC1001419//CIT-HSP-2362F16.TR CIT-HSP Homo sapiens genomic clone 2362F16, genomic survey sequence.//7.6e-47:242:98//AQ074668

R-OVARC1001425//Homo sapiens PAC clone DJ1108A12 from 14q24.3, complete sequence.//2.3e-20:211:66//AC005157

R-OVARC1001436//Human DNA flanking 3' end of transposon L1.1.//0.18:148:66//M80341

R-OVARC1001442

R-OVARC1001453//Human PAC clone DJ525N14 from Xq23, complete sequence.//
2.3e-19:181:81//AC002086

R-OVARC1001476//CITBI-E1-2517B6.TR CITBI-E1 Homo sapiens genomic clone 2
517B6, genomic survey sequence.//0.24:308:59//AQ278655

R-OVARC1001480//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 753D4, WORKING DRAFT SEQUENCE.//0.99:294:62//AL031676

R-OVARC1001489//E.caballus microsatellite DNA marker (clone ASB32).//0.8
7:81:71//X93546

R-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete
cds.//9.3e-116:585:96//AF016507

R-OVARC1001506//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-13F4 - c
omplete genomic sequence, complete sequence.//2.6e-40:285:86//AC002039

R-OVARC1001525//Homo sapiens clone NH0215P16, WORKING DRAFT SEQUENCE, 3
unordered pieces.//1.0:320:59//AC006036

R-OVARC1001542//Homo sapiens hJTB mRNA, complete cds.//5.0e-110:566:95//
AB016488

R-OVARC1001547

R-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retropseu
dogene.//5.9e-33:216:92//AF031165

R-OVARC1001600//Human Chromosome X, complete sequence.//3.0e-22:157:89//
AC002418

R-OVARC1001610//HS_3070_A2_A06_MR CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3070 Col=12 Row=A, genomic survey
sequence.//0.47:107:66//AQ103523

R-OVARC1001611//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 1185N5, WORKING DRAFT SEQUENCE.//0.17:236:63//AL034423

R-OVARC1001615//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 310013, WORKING DRAFT SEQUENCE.//1.3e-19:248:70//AL031658

R-OVARC1001668//HS_3228_A2_E12_MR CIT Approved Human Genomic Sperm Libra

ry D Homo sapiens genomic clone Plate=3228 Col=24 Row=I, genomic survey
sequence.//4.6e-13:156:76//AQ188379

R-OVARC1001702//CITBI-E1-2501P16.TR.1 CITBI-E1 Homo sapiens genomic clone
2501P16, genomic survey sequence.//1.6e-41:217:99//AQ241965

R-OVARC1001703

R-OVARC1001711//CITBI-E1-2502N10.TF CITBI-E1 Homo sapiens genomic clone
2502N10, genomic survey sequence.//2.0e-14:220:72//AQ266194

R-OVARC1001726//CIT-HSP-232001.TF CIT-HSP Homo sapiens genomic clone 232
001, genomic survey sequence.//0.021:170:62//AQ038145

R-OVARC1001731//Human mRNA for fibroblast tropomyosin TM30 (pl).//2.5e-7
2:422:90//X05276

R-OVARC1001745//Human DNA sequence from clone 796I11 on chromosome 20q12
. Contains ESTs, an STS and GSSs, complete sequence.//7.6e-44:314:84//AL
031257

R-OVARC1001762//S.cerevisiae N-acetyltransferase (AAA1) mRNA, complete c
ds.//1.6e-08:396:60//M23166

R-OVARC1001766//Homo sapiens eukaryotic translation initiation factor ei
F3, p35 subunit mRNA, complete cds.//3.5e-108:567:94//U97670

R-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds.//6
.3e-108:529:97//AB014575

R-OVARC1001768//Caenorhabditis elegans cosmid Y57G11A, complete sequence
.//0.24:205:64//Z99279

R-OVARC1001791//Homo sapiens BAC clone RG118P15 from 8q21, complete sequ
ence.//4.6e-58:558:76//AC005066

R-OVARC1001795

R-OVARC1001802//Human HLA class III region containing cAMP response elem
ent binding protein-related protein (CREB-RP) and tenascin X (tenascin-X
) genes, complete cds, complete sequence.//1.1e-37:346:78//U89337

R-OVARC1001805//Human DNA sequence from clone 511E16 on chromosome 6p24.

3-25.1. Contains the last coding exon of the gene for P18 component of a minoacyl-tRNA synthetase complex, part of an unknown gene downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence.//3.0e-112:581:95//AL023694

R-OVARC1001812//Human DNA sequence from clone 227L5 on chromosome Xp11.2
2-11.3. Contains a Keratin, Type 1 Cytoskeletal 18 (KRT18, CYK18, K18, C K18) pseudogene and an STS, complete sequence.//6.6e-41:345:81//AL031585

R-OVARC1001813//CITBI-E1-2508J18.TR CITBI-E1 Homo sapiens genomic clone 2508J18, genomic survey sequence.//1.6e-72:386:95//AQ263046

R-OVARC1001820//Human PAC clone DJ525N14 from Xq23, complete sequence.//4.8e-41:320:83//AC002086

R-OVARC1001828//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//3.4e-08:527:58//AC004688

R-OVARC1001846//CIT-HSP-2014F15.TR CIT-HSP Homo sapiens genomic clone 20 14F15, genomic survey sequence.//0.0045:165:67//B58905

R-OVARC1001861//M.musculus mRNA for pMEM2 protein.//9.5e-28:405:68//X953 50

R-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence.//5.9e-104:571:91//AF070611

R-OVARC1001879//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//9.1e-20:206:80//AL031864

R-OVARC1001880//RPCI11-42I15.TJ RPCI11 Homo sapiens genomic clone R-42I1 5, genomic survey sequence.//3.9e-50:287:88//AQ052700

R-OVARC1001883//Homo sapiens chromosome 17, clone hCIT.123_J_14, complete sequence.//6.1e-13:457:63//AC003950

R-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homol

og (TID1) mRNA, complete cds.//2.5e-86:346:90//AF061749
R-OVARC1001901//Homo sapiens testis specific methyl-CpG binding protein
MBD2 (MBD2) mRNA, partial cds.//7.2e-89:421:100//AF072246
R-OVARC1001911//Homo sapiens full length insert cDNA clone ZD52F10.//8.2
e-106:510:98//AF086315
R-OVARC1001916
R-OVARC1001928
R-OVARC1001942//S.cerevisiae N-acetyltransferase (AAA1) mRNA, complete c
ds.//0.0013:231:63//M23166
R-OVARC1001943//Human immunodeficiency virus type 1, strain FRMP329, env
elope glycoprotein V3 region (env) gene, partial cds.//0.14:173:64//U588
26
R-OVARC1001949//Human zinc finger protein 20 (ZNF20) pentanucleotide rep
eat polymorphism.//1.3e-09:306:63//M99593
R-OVARC1001950//Homo sapiens chromosome 17, clone hRPK.112_H_10, complet
e sequence.//8.2e-38:385:75//AC005666
R-OVARC1001987
R-OVARC1001989//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS **
* from clone Y57G11, WORKING DRAFT SEQUENCE.//6.3e-08:355:60//Z92841
R-OVARC1002044//Human DNA sequence from clone 681J21 on chromosome 1q23.
2-24.3 Contains CpG island, complete sequence.//5.0e-42:298:86//AL031286
R-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds.//1.
4e-107:542:96//AB007934
R-OVARC1002066//Arabidopsis thaliana chromosome II BAC F14M4 genomic seq
uence, complete sequence.//0.23:210:61//AC004411
R-OVARC1002082//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6
unordered pieces.//5.4e-99:546:92//AC006015
R-OVARC1002107//Human DNA sequence from PAC 417G15 on chromosome Xq25-Xq
26. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), p

pseudogene, ESTs.//4.4e-34:375:74//AL009174
 R-OVARC1002127
 R-OVARC1002138//CIT-HSP-2290018.TF CIT-HSP Homo sapiens genomic clone 22
 90018, genomic survey sequence.//2.4e-07:316:62//AQ003988
 R-OVARC1002143//RPCI11-54M8.TJ RPCI11 Homo sapiens genomic clone R-54M8,
 genomic survey sequence.//2.3e-35:220:90//AQ083241
 R-OVARC1002156
 R-OVARC1002158//CITBI-E1-2514D4.TF CITBI-E1 Homo sapiens genomic clone 2
 514D4, genomic survey sequence.//1.6e-12:140:79//AQ265720
 R-OVARC1002165//CIT-HSP-2307C9.TF CIT-HSP Homo sapiens genomic clone 230
 7C9, genomic survey sequence.//5.0e-59:291:99//AQ020420
 R-OVARC1002182//P. falciparum SD17 gene for knob-associated histidine-ri
 ch protein.//0.74:161:65//Y00060
 R-PLACE1000004//D.discoideum gene for protein kinase.//0.00081:263:59//Z
 37981
 R-PLACE1000005//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 geno
 mic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0082:477:58
 //AC005507
 R-PLACE1000007//Homo sapiens clone 24422 mRNA sequence.//1.2e-14:100:97/
 /AF070557
 R-PLACE1000014//Homo sapiens genomic DNA, chromosome 21q22.2, p1 clone:
 T1212 and T1601, WORKING DRAFT SEQUENCE.//2.8e-44:405:77//D83253
 R-PLACE1000031//Homo sapiens clone UWGC:y23c049 from 6p21, complete sequ
 ence.//1.8e-24:291:73//AC006162
 R-PLACE1000040//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS **
 * from clone Y105C5, WORKING DRAFT SEQUENCE.//0.00039:289:61//Z98855
 R-PLACE1000048//Human BAC clone RG210I04, complete sequence.//4.7e-83:51
 8:89//AC002462
 R-PLACE1000050//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic

sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.98:73:76//AC005505

R-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//5.9e-21:125:98//L22154

R-PLACE1000066

R-PLACE1000078//Homo sapiens chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.2e-87:456:95//AC005848

R-PLACE1000081

R-PLACE1000094//RPCI11-91K6.TV RPCI11 Homo sapiens genomic clone R-91K6, genomic survey sequence.//2.3e-83:409:98//AQ282619

R-PLACE1000133//Homo sapiens chromosome 17, clone hRPK.746_E_8, complete sequence.//1.8e-06:420:57//AC005358

R-PLACE1000142

R-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds.//1.3e-112:594:94//AF058291

R-PLACE1000185

R-PLACE1000213//CIT-HSP-2308A18.TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey sequence.//8.2e-80:410:97//AQ022149

R-PLACE1000214//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-09, complete sequence.//1.6e-05:548:59//AL008989

R-PLACE1000236//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 695020, WORKING DRAFT SEQUENCE.//2.2e-16:118:91//AL032818

R-PLACE1000246//X.laevis mRNA for XLCL2 protein.//6.5e-13:66:95//Z14122

R-PLACE1000292//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 111B22, WORKING DRAFT SEQUENCE.//6.6e-41:322:84//Z98200

R-PLACE1000332//Homo sapiens chromosome 17, clone hCIT.281_F_24, complete sequence.//1.8e-16:598:62//AC004706

R-PLACE1000347//Homo sapiens PAC clone DJ1090P18 from 7q21-q22, complete sequence.//2.3e-11:237:69//AC005326

R-PLACE1000374//Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence.//8.7e-09:492:58//AC005278

R-PLACE1000380//Plasmodium falciparum chromosome 2, section 1 of 73 of the complete sequence.//0.59:354:59//AE001364

R-PLACE1000383//Mus musculus myotubularin related protein 1 (Mtmr1) mRNA, complete cds.//0.55:65:84//AF073997

R-PLACE1000401//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.6e-17:152:83//AC005015

R-PLACE1000406//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence.//0.51:346:58//AB020742

R-PLACE1000420//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 2/15, WORKING DRAFT SEQUENCE.//1.5e-25:243:79//AP000009

R-PLACE1000421//HS_2251_B2_G12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2251 Col=24 Row=N, genomic survey sequence.//1.4e-82:430:95//AQ192807

R-PLACE1000424//Human PAC clone DJ515N1 from 22q11.2-q22, complete sequence.//1.8e-36:483:71//AC002073

R-PLACE1000435//Homo sapiens chromosome 21q22.2 cosmid clone Q71A3, complete sequence.//2.6e-37:371:76//AF015724

R-PLACE1000444//Homo sapiens chromosome 17, clone hRPK.227_G_15, complete sequence.//1.0e-54:429:81//AC005899

R-PLACE1000453//Murine genomic DNA; partially digested Sau3A fragment, cloned into cosmid vector pEMBLcos2, complete sequence.//0.66:103:72//AF059580

R-PLACE1000481//Human DNA sequence from clone 960017 on chromosome Xp11.21-11.22 Contains EST, CA repeat(DXS991), STS, GSS, complete sequence.//0.019:171:66//AL022166

R-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, comp

lete cds.//3.2e-17:221:72//U35245

R-PLACE1000540//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.00045:480:60//AC005308

R-PLACE1000547//Homo sapiens chromosome 19, cosmid F17987, complete sequence.//9.6e-32:231:85//AC004790

R-PLACE1000562//, complete sequence.//1.8e-45:280:92//AC005409

R-PLACE1000564//Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds.//0.0079:180:65//U41302

R-PLACE1000583//Homo sapiens chromosome 17, clone hRPK.799_N_11, complete sequence.//1.5e-37:414:74//AC005323

R-PLACE1000588//Human guanylate binding protein isoform I (GBP-2) mRNA, complete cds.//1.9e-77:542:82//M55542

R-PLACE1000596//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00019:482:59//AC005506

R-PLACE1000599//Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S2A1T, TCRBV6S5A1N1, TCRBV30S1P, TCRBV31S1, TCRBV13S5, TCRBV6S1A1N1, TCRBV32S1P, TCRBV5S5P, TCRBV1S1A1N1, TCRBV12S2A1T, TCRBV21S1, TCRBV8S4P, TCRBV12S3, TCRBV21S3A2N2T, TCRBV8S5P, TCRBV13S1 genes from bases 1 to 267156 (section 1 of 3).//5.6e-51:369:85//U66059

R-PLACE1000610//HS_3071_A1_C05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=9 Row=E, genomic survey sequence.//0.051:147:65//AQ103341

R-PLACE1000636//HS_3220_B2_E09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220 Col=18 Row=J, genomic survey

sequence.//0.010:253:64//AQ181157

R-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//1.6e-99:506:96//AF102265

R-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin)).//4.5e-101:559:92//AJ005896

R-PLACE1000706//nuclear protein TIF1 [mice, mRNA, 3951 nt].//9.1e-10:331:63//S78219

R-PLACE1000712//Homo sapiens full length insert cDNA clone ZD76G10.//1.0e-69:345:98//AF086408

R-PLACE1000716//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//1.0:174:62//AC002300

R-PLACE1000748//Plasmodium falciparum MAL3P3, complete sequence.//1.0e-06:337:60//Z98547

R-PLACE1000749//cSRL-15g9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-15g9, genomic survey sequence.//8.8e-26:236:80//B02791

R-PLACE1000755//HS_2183_B1_H11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=21 Row=P, genomic survey sequence.//0.47:151:65//AQ064202

R-PLACE1000769//Homo sapiens clone DJ0647J21, WORKING DRAFT SEQUENCE, 10 unordered pieces.//7.0e-38:492:74//AC004847

R-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//2.6e-101:513:96//AB014548

R-PLACE1000786//Human putative outer mitochondrial membrane 34 kDa translocase hTOM34 mRNA, complete cds.//0.078:180:68//U58970

R-PLACE1000793

R-PLACE1000798//Homo sapiens cosmid D66B10, chromosome 21 5' of IFNAR1.//5.1e-26:348:72//AF039904

R-PLACE1000841//Human guanine nucleotide regulatory protein (NET1) mRNA,
complete cds.//1.4e-26:110:95//U02081

R-PLACE1000849//Homo sapiens full length insert cDNA clone ZD55D10.//1.4
e-13:93:96//AF086334

R-PLACE1000856//Anopheles quadrimaculatus NADH dehydrogenase subunits (1
-4, 4L, 5-6); cytochrome oxidase subunits (1-3); adenosine triphosphatas
e subunits (6,8); cytochrome b; transfer RNA; ribosomal RNA (large and s
mall subunits).//2.7e-09:484:59//L04272

R-PLACE1000863

R-PLACE1000909//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic
sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//3.0e-05:274:60//
AC005505

R-PLACE1000931//RPCI11-66P7.TK RPCI11 Homo sapiens genomic clone R-66P7,
genomic survey sequence.//3.4e-73:369:97//AQ237489

R-PLACE1000948//RPCI11-64K15.TK RPCI11 Homo sapiens genomic clone R-64K1
5, genomic survey sequence.//6.6e-06:258:62//AQ239337

R-PLACE1000972//Homo sapiens chromosome 17, clone hRPK.112_J_9, complete
sequence.//8.3e-20:223:76//AC005553

R-PLACE1000977//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic
sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00030:448:59//
AC005506

R-PLACE1000979

R-PLACE1001000//CIT-HSP-2297I8.TF CIT-HSP Homo sapiens genomic clone 229
7I8, genomic survey sequence.//7.0e-07:64:95//AQ004997

R-PLACE1001007//Human endothelial nitric oxide synthase gene, complete c
ds.//0.0078:215:64//D26607

R-PLACE1001010

R-PLACE1001015//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 150C2, WORKING DRAFT SEQUENCE.//1.5e-16:452:63//AL022318

R-PLACE1001024//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 417M14, WORKING DRAFT SEQUENCE.//0.99:186:63//AL024498

R-PLACE1001036//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.5e-15:313:68//AC005377

R-PLACE1001062//Homo sapiens chromosome 17, clone hCIT54K19, complete sequence.//7.3e-16:119:84//AC003664

R-PLACE1001076

R-PLACE1001088//Human DNA sequence from cosmid 203C2, between markers DX S6791 and DXS8038 on chromosome X contains ESTs.//0.97:332:59//Z74696

R-PLACE1001092//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//6.2e-07:302:62//AC005139

R-PLACE1001104//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//0.057:280:60//AE001372

R-PLACE1001118//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6 q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence.//4.9e-06:334:60//Z84480

R-PLACE1001136//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.1e-31:331:75//AC005412

R-PLACE1001168//HS_2036_A1_H04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2036 Col=7 Row=0, genomic survey sequence.//0.40:144:63//AQ230662

R-PLACE1001171

R-PLACE1001185

R-PLACE1001238//Human coxVIb gene, last exon and flanking sequence.//3.4e-36:349:76//X58139

R-PLACE1001241//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-20, complete sequence.//0.11:258:61//AL008972

R-PLACE1001257//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4
, BAC clone B4P3; HTGS phase 1, WORKING DRAFT SEQUENCE, 9 unordered piec
es.//1.9e-46:484:73//AC000016

R-PLACE1001272//Homo sapiens chromosome 21q22.3 PAC 191P10, complete seq
uence.//0.89:119:65//AF045448

R-PLACE1001279//Caenorhabditis elegans cosmid Y39A1C, complete sequence.
//0.99:95:69//AL023839

R-PLACE1001280//CIT-HSP-2328B24.TF CIT-HSP Homo sapiens genomic clone 23
28B24, genomic survey sequence.//5.4e-24:147:76//AQ042129

R-PLACE1001294//M.musculus GEG-154 mRNA.//1.3e-22:472:65//X71642

R-PLACE1001304//Homo sapiens chromosome 19, overlapping cosmids F18547,
F11133, R27945, R28830 and R32804, complete sequence.//2.2e-22:139:77//A
C003682

R-PLACE1001311//Loligo pealei repeat region.//0.84:232:64//Z18286

R-PLACE1001323//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6
q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein
Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSS,
complete sequence.//7.2e-39:308:83//Z84480

R-PLACE1001351//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS **
* from clone Y39B6, WORKING DRAFT SEQUENCE.//0.0018:408:59//Z95399

R-PLACE1001366//Human Na+/phosphate co-transporter gene, exon 1, partial
sequence.//2.2e-46:369:82//D89927

R-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds.//7.1e-8
0:431:93//AF009615

R-PLACE1001383//Homo sapiens clone 24538 mRNA sequence.//3.6e-35:192:97/
/AF055030

R-PLACE1001384//Homo sapiens mRNA for multi PDZ domain protein.//2.6e-86
:456:94//AJ001319

R-PLACE1001387

R-PLACE1001395//Nyctalus leisleri mitochondrial D-loop, partial sequence
./0.054:148:68//U95355

R-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING
DRAFT SEQUENCE, 2 ordered pieces./6.7e-70:352:98//AC005412

R-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence./
/8.0e-44:242:95//AF091087

R-PLACE1001414//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete
sequence./0.12:53:84//AC006241

R-PLACE1001440//Homo sapiens Xq28 genomic DNA in the region of the ALD 1
ocus containing the genes for creatine transporter (SLC6A8), CDM, adreno
leukodystrophy (ALD), Na+-isocitrate dehydrogenase gamma subunit (IDH),
and translocon-associated protein delta (TRAP) genes, complete cds, plex
in related protein (PLEXR) and serine kinase (SK) genes, partial cds, Xq
28lul gene and cytochrome C (CCp) pseudogene./1.0:250:61//U52111

R-PLACE1001456//Borrelia burgdorferi (section 16 of 70) of the complete
genome./0.0077:173:62//AE001130

R-PLACE1001468//HS_3050_A2_D07_MR CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3050 Col=14 Row=G, genomic survey
sequence./0.00023:202:65//AQ133920

R-PLACE1001484//Homo sapiens Xq28 BAC PAC and cosmid clones containing F
MR2 gene exons 1,2, and 3, complete sequence./7.2e-17:180:80//AC002368

R-PLACE1001502//RPCI11-24F2.TP RPCI-11 Homo sapiens genomic clone RPCI-1
1-24F2, genomic survey sequence./0.15:203:66//B84401

R-PLACE1001503//HS_2183_A1_B10_MR CIT Approved Human Genomic Sperm Libra
ry D-Homo sapiens genomic clone Plate=2183 Col=19 Row=C, genomic survey
sequence./1.3e-38:181:82//AQ022613

R-PLACE1001517//Homo sapiens hGAA1 mRNA, complete cds./6.4e-56:339:90//
AB006969

R-PLACE1001534//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c

lone 620E11, WORKING DRAFT SEQUENCE.//8.6e-59:304:97//AL031667
R-PLACE1001545//Homo sapiens chromosome 3, clone hRPK.165_I_16, complete
sequence.//2.6e-18:171:82//AC005669
R-PLACE1001551
R-PLACE1001570//M.capricolum DNA for CONTIG MC188.//0.0043:305:57//Z3313
5
R-PLACE1001602//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of
hepatocellular colorectal and non-small cell lung cancer , segment 3/11.
//2.5e-82:408:98//AB020860
R-PLACE1001603//Homo sapiens KE05 protein mRNA, complete cds.//1.5e-40:2
95:84//AF064605
R-PLACE1001610//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7
unordered pieces.//2.5e-39:307:82//AC005037
R-PLACE1001611//Homo sapiens histone macroH2A1.2 mRNA, complete cds.//4.
9e-41:217:97//AF054174
R-PLACE1001632//Human DNA binding protein (HPF2) mRNA, complete cds.//1.
4e-08:178:65//M27878
R-PLACE1001634//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS **
* from clone H06C16, WORKING DRAFT SEQUENCE.//0.00026:221:62//Z92791
R-PLACE1001640//Homo sapiens chromosome 17, clone hRPK.651_L_9, complete
sequence.//2.6e-83:441:95//AC005971
R-PLACE1001672//H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA2
6H8.//0.91:115:69//Z79253
R-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48
-18) mRNA, complete cds.//1.5e-111:545:97//AF069250
R-PLACE1001692//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 u
nordered pieces.//1.0e-46:478:75//AC005077
R-PLACE1001705//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 250D10, WORKING DRAFT SEQUENCE.//0.79:91:73//Z99716

R-PLACE1001716//Homo sapiens Xp22 PAC RPC11-167A22 (from Roswell Park Cancer Center) complete sequence.//0.96:172:66//AC002349

R-PLACE1001720

R-PLACE1001729//Human interleukin-13 (IL-13) precursor gene, complete cds.//0.79:280:60//U31120

R-PLACE1001739//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.0:109:65//AC005261

R-PLACE1001740//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete sequence.//5.3e-11:249:67//AC006027

R-PLACE1001745

R-PLACE1001746//Homo sapiens chromosome 4 clone B200N5 map 4q25, complete sequence.//6.0e-05:337:61//AC005509

R-PLACE1001748//Homo sapiens metalloprotease 1 (MPI) mRNA, complete cds.//1.3e-91:540:89//AF061243

R-PLACE1001756//Human BAC clone RG302F04 from 7q31, complete sequence.//0.074:344:62//AC002463

R-PLACE1001761

R-PLACE1001771//Homo sapiens full length insert cDNA clone ZD79C11.//4.4e-57:298:96//AF086426

R-PLACE1001781//T.thermophila micronuclear DNA containing to chromosomal breakage sequence Cbs-1, clone Tt819.//4.6e-05:282:61//M15711

R-PLACE1001799//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.015:331:58//AC004710

R-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//4.1e-92:463:95//AF058953

R-PLACE1001821//***ALU WARNING: Human Alu-J subfamily consensus sequence.//3.6e-36:281:82//U14567

R-PLACE1001845//Mus musculus Paneth cell enhanced expression PCEE mRNA,

complete cds.//9.1e-26:313:73//U37351

R-PLACE1001869

R-PLACE1001897//Mus musculus homeobox protein (Dlx5) mRNA, complete cds.
//0.0043:207:64//AF033011

R-PLACE1001912//RPCI11-25F23.TKBR RPCI-11 Homo sapiens genomic clone RPC
I-11-25F23, genomic survey sequence.//6.3e-33:248:67//AQ013567

R-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cd
s.//5.0e-73:363:98//AF070671

R-PLACE1001928//Homo sapiens chromosome 17, clone hRPK.642_C_21, complet
e sequence.//0.98:248:60//AC005245

R-PLACE1001983//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS **
* from clone Y40H7, WORKING DRAFT SEQUENCE.//0.12:157:61//AL021389

R-PLACE1001989//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 968D22, WORKING DRAFT SEQUENCE.//1.4e-44:376:80//AL023755

R-PLACE1002046//CITBI-E1-2520J24.TF CITBI-E1 Homo sapiens genomic clone
2520J24, genomic survey sequence.//4.5e-20:144:89//AQ280117

R-PLACE1002052//Human DNA sequence from cosmid U160A4, between markers D
XS366 and DXS87 on chromosome X contains STS.//0.025:362:57//Z80900

R-PLACE1002066//Leishmania tarentolae maxicircle DNA fragment.//0.0034:1
97:62//X02438

R-PLACE1002072//Homo sapiens chromosome 5, P1 clone 854b11 (LBNL H44), c
omplete sequence.//9.7e-06:414:60//AC004763

R-PLACE1002073

R-PLACE1002090//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4 -
complete genomic sequence, complete sequence.//1.8e-06:278:63//AC002302

R-PLACE1002115//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone Y214H10, WORKING DRAFT SEQUENCE.//6.0e-12:327:64//AL022344

R-PLACE1002119//Mus musculus IER5 (Ier5) mRNA, complete cds.//5.1e-67:44
2:86//AF079527

R-PLACE1002140//Homo sapiens DNA sequence from PAC 454M7 on chromosome X q25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//2.2e-80:403:97//AL022162

R-PLACE1002150//Human DNA sequence from PAC 145B12 on chromosome Xq27-Xq28. Contains EST, CA repeat and STS.//0.043:455:59//AL008706

R-PLACE1002157//Human DNA sequence from Fosmid 65B7 on chromosome 22q11.2-qter. Contains exons 6-12 of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter), complete sequence.//9.8e-58:384:79//Z83849

R-PLACE1002163//Canis familiaris MHC class IIA DLA-DQA (DQA 1 allele) gene, exon 2, partial cds.//0.82:96:70//U44785

R-PLACE1002171//Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence.//0.83:196:65//AC004456

R-PLACE1002205//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLRS1). Contains ESTs, an STS and GSSs, complete sequence.//0.0017:193:61//Z94056

R-PLACE1002213//Homo sapiens chromosome 19, fosmid 37308, complete sequence.//8.0e-42:330:81//AC004152

R-PLACE1002227//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//2.1e-10:126:80//AC003071

R-PLACE1002256//Homo sapiens clone DJ0853H20, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.7e-06:478:57//AC004907

R-PLACE1002259//Human DNA sequence from cosmid U75A4 on chromosome X.//6.5e-81:501:88//Z82255

R-PLACE1002319//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00023:549:58//

AC005505

R-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds.//4.9e-94:501:93//AB018271

R-PLACE1002395//Homo sapiens chromosome 19, cosmid R34382, complete sequence.//1.4e-69:385:93//AC005329

R-PLACE1002399//Human HepG2 3' region cDNA, clone hmd5d06.//2.4e-71:411:92//D16939

R-PLACE1002433//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 173D1, WORKING DRAFT SEQUENCE.//0.85:176:63//AL031984

R-PLACE1002437//Human BAC clone RG114A06 from 7q31, complete sequence.//0.0040:213:63//AC002542

R-PLACE1002438//CITBI-E1-2501M20.TF.1 CITBI-E1 Homo sapiens genomic clone 2501M20, genomic survey sequence.//0.70:247:61//AQ242104

R-PLACE1002450//Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3.//0.00060:471:59//AJ229041

R-PLACE1002465//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//2.5e-10:98:81//AC004854

R-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//1.7e-25:199:71//U69262

R-PLACE1002477//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//1.2e-11:382:63//Z92545

R-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds.//1.1e-53:307:91//AF042273

R-PLACE1002499//Plasmodium falciparum MAL3P6, complete sequence.//0.56:270:60//Z98551

R-PLACE1002500//CIT-HSP-2337C20.TR CIT-HSP Homo sapiens genomic clone 2337C20, genomic survey sequence.//3.2e-42:297:85//AQ037614

R-PLACE1002514//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 212A2, WORKING DRAFT SEQUENCE.//7.8e-16:221:73//Z95114

R-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//1.6e-86:582:85//AB018256

R-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1, complete sequence.//9.0e-91:453:97//AC004774

R-PLACE1002537//Hansenula wingei mitochondrial gene for NADH dehydrogenase subunit 5, complete cds.//0.0042:489:60//D16253

R-PLACE1002571//Apis mellifera ligustica complete mitochondrial genome.//0.034:493:55//L06178

R-PLACE1002578//Homo sapiens chromosome 5, Pac clone 9c13 (LBNL H127), complete sequence.//2.5e-44:292:84//AC006084

R-PLACE1002583//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//3.1e-17:517:61//AF045555

R-PLACE1002591

R-PLACE1002598//Caenorhabditis elegans cosmid Y37D8A, complete sequence.//0.080:308:60//AL032626

R-PLACE1002604//Human cosmid LL12NC01-88A9, ETV6 gene, exons 6, 7 and 8 and partial cds.//0.0013:176:65//U63313

R-PLACE1002625//HS_2233_B2_H04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2233 Col=8 Row=P, genomic survey sequence.//5.2e-13:137:79//AQ146663

R-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//5.8e-46:272:94//AF079765

R-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//1.2e-77:390:97//AF068180

R-PLACE1002714//Mus musculus clone OST2473, genomic survey sequence.//1.3e-35:328:78//AF046656

R-PLACE1002722//Sequence 1 from patent US 5686597.//1.7e-42:276:89//I737

23

R-PLACE1002768//Homo sapiens Xp22 bins 169-171 BAC GSHB-383H3 (Genome Systems Human BAC Library) complete sequence.//0.0098:197:64//AC005185

R-PLACE1002772//Homo sapiens PAC clone DJ0560014 from 7q21.1-q21.2, complete sequence.//6.7e-49:378:82//AC006145

R-PLACE1002782

R-PLACE1002794

R-PLACE1002811//CIT-HSP-2316H11.TF CIT-HSP Homo sapiens genomic clone 2316H11, genomic survey sequence.//6.0e-50:250:100//AQ034981

R-PLACE1002815//Sequence 2 from patent US 5747660.//2.7e-59:312:84//AR005279

R-PLACE1002816//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.3e-59:339:93//AC004466

R-PLACE1002834//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//1.4e-78:413:95//M27877

R-PLACE1002839//Homo sapiens PAC clone DJ0015I23 from 22, complete sequence.//6.5e-25:301:74//AC004819

R-PLACE1002851//CIT-HSP-2317M9.TR CIT-HSP Homo sapiens genomic clone 2317M9, genomic survey sequence.//0.0011:210:61//AQ040519

R-PLACE1002853//Human interleukin 6 (IL6) gene, 3' flank.//5.8e-06:327:61//J03049

R-PLACE1002881

R-PLACE1002908//HS_3064_A1_D04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=7 Row=G, genomic survey sequence.//1.9e-09:156:72//AQ142985

R-PLACE1002941

R-PLACE1002962

R-PLACE1002968//Human DNA sequence from clone 109F14 on chromosome 6p21.

2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF 127 LIKE gene, and the PPARD for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUC1, PPARB). Contains three putative CpG islands, ESTs, STSs, GSSs and a ca repeat polymorphism, complete sequence.//1.9e-32:314:77//AL022721

R-PLACE1002991//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//1.6e-42:343:81//AL023755

R-PLACE1002993//Homo sapiens PAC clone DJ0899E09 from 7q11.23-q21.1, complete sequence.//0.56:88:72//AC004921

R-PLACE1002996//HS_2064_A1_A05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2064 Col=9 Row=A, genomic survey sequence.//4.9e-18:117:95//AQ243211

R-PLACE1003025//Homo sapiens PAC clone DJ0560014 from 7q21.1-q21.2, complete sequence.//0.26:428:58//AC006145

R-PLACE1003027//Homo sapiens chromosome 17, clone hRPK.700_H_6, complete sequence.//1.3e-95:465:98//AC005920

R-PLACE1003044

R-PLACE1003092//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-89, complete sequence.//3.6e-05:358:60//AL010266

R-PLACE1003100//HS_2244_A2_H12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2244 Col=24 Row=0, genomic survey sequence.//2.3e-42:288:86//AQ084224

R-PLACE1003108//Homo sapiens clone DJ0781A18, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00066:233:61//AC004885

R-PLACE1003136//Plasmodium falciparum MAL3P2, complete sequence.//0.019:429:57//AL034558

R-PLACE1003145

R-PLACE1003153//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human B

AC library) complete sequence.//3.2e-05:390:58//AC004616
R-PLACE1003174//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone
: MTE17, complete sequence.//2.4e-06:390:60//AB015479
R-PLACE1003176
R-PLACE1003190//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 u
nordered pieces.//4.0e-78:406:81//AC005095
R-PLACE1003200//Plasmodium falciparum MAL3P6, complete sequence.//0.016:
411:57//Z98551
R-PLACE1003205//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic
sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.00084:288:61//
AC005139
R-PLACE1003238//Homo sapiens full length insert cDNA clone ZD79H11.//7.6
e-114:567:96//AF086432
R-PLACE1003249//Human Chromosome X, complete sequence.//1.3e-45:317:85//
AC002416
R-PLACE1003256//Homo sapiens chromosome 17, clone HCIT421K24, complete s
equence.//1.0e-45:328:85//AC004099
R-PLACE1003258
R-PLACE1003296//Diphtheria sp. 16S ribosomal RNA gene, mitochondrial ge
ne encoding mitochondrial rRNA, partial sequence.//0.050:228:59//U39952
R-PLACE1003302//Figure 2. Nucleotide and translated protein sequences of
HPF1, -2, and -9.//1.7e-91:458:96//M27877
R-PLACE1003334//Homo sapiens DNA sequence from BAC 217C2 on chromosome 2
2q13-q13.33. Contains a gene for the presumptive isolog of Rat RTP60 (nuc
lear pore complex protein Npap60). Contains ESTs, complete sequence.//4.
3e-34:370:71//Z82243
R-PLACE1003342//CIT-HSP-2311D21.TF CIT-HSP Homo sapiens genomic clone 23
11D21, genomic survey sequence.//1.0:159:68//AQ020460
R-PLACE1003343//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic

sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.1e-05:330:61//
AC004153
R-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//3.4e-98:469:98//U92715
R-PLACE1003361
R-PLACE1003366//Homo sapiens CAG repeated sequence.//0.018:319:61//AJ006805
R-PLACE1003369//T18H17-T7 TAMU Arabidopsis thaliana genomic clone T18H17, genomic survey sequence.//0.050:155:63//B20174
R-PLACE1003373//Homo sapiens chromosome 17, clone hRPC.1050_D_4, complete sequence.//1.2e-62:434:83//AC004771
R-PLACE1003375//Dictyostelium discoideum golgesin (gol) gene, complete cds.//0.042:263:57//U89350
R-PLACE1003383//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 10/10.//1.7e-83:429:96//AB020878
R-PLACE1003401//Homo sapiens chromosome 17, clone hRPK.85_B_7, complete sequence.//2.4e-13:175:76//AC005695
R-PLACE1003420//Homo sapiens PAC clone DJ0988G15 from 7q33-q35, complete sequence.//2.1e-05:340:61//AC005587
R-PLACE1003454//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-64, complete sequence.//0.47:411:58//AL009014
R-PLACE1003478//M.capricolum DNA for CONTIG MC175.//0.51:253:59//Z33125
R-PLACE1003493//Homo sapiens chromosome 17, clone hRPK.394_K_10, complete sequence.//4.6e-37:319:81//AC006080
R-PLACE1003516//CIT-HSP-2295M19.TF CIT-HSP Homo sapiens genomic clone 2295M19, genomic survey sequence.//1.0e-40:251:90//AQ007480
R-PLACE1003519//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a.//2.7e-29:163:89//AF064859

R-PLACE1003521//HS_3252_A2_G05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=10 Row=M, genomic survey sequence.//0.00017:274:60//AQ221562

R-PLACE1003528//HS_2041_B1_B07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2041 Col=13 Row=D, genomic survey sequence.//6.6e-40:219:83//AQ230483

R-PLACE1003537//Drosophila melanogaster mitochondrial cytochrome c oxidase subunits, ATPase6, 7 tRNAs (Trp, Cys, Tyr, Leu(UUR), Lys, Asp, Gly) genes, and unidentified reading frames A61, 2 and 3.//8.3e-05:300:61//J01404

R-PLACE1003553//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 97P20, WORKING DRAFT SEQUENCE.//2.7e-87:450:96//AL031297

R-PLACE1003566

R-PLACE1003575//Homo sapiens chromosome 16, cosmid clone 325D7, complete sequence.//4.7e-20:148:78//AC003965

R-PLACE1003583//Human DNA sequence from PAC 388N15 on chromosome Xq21.1.//3.5e-18:287:68//Z99571

R-PLACE1003584

R-PLACE1003592//Homo sapiens cosmid 223D9 from Xq28, complete sequence.//2.5e-10:153:73//AF061032

R-PLACE1003593//Human BAC clone RG030H15 from 7q31, complete sequence.//6.9e-07:240:65//AC002066

R-PLACE1003596//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS ** * from clone Y87G2, WORKING DRAFT SEQUENCE.//0.13:393:60//AL022597

R-PLACE1003602//Homo sapiens mRNA expressed in placenta.//2.4e-95:576:88//D83200

R-PLACE1003605//Homo sapiens BAC clone RG331C24 from 7q21, complete sequence.//2.9e-19:302:71//AC002081

R-PLACE1003611

R-PLACE1003618//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 191E19, WORKING DRAFT SEQUENCE.//8.3e-57:469:80//AL034451

R-PLACE1003625//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.1e-05:339:62//AC004688

R-PLACE1003638//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1104E15, WORKING DRAFT SEQUENCE.//2.5e-38:279:84//AL022312

R-PLACE1003669//HS_3054_A2_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=14 Row=I, genomic survey sequence.//0.014:265:61//AQ132713

R-PLACE1003704//HS_3213_A1_D12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=23 Row=G, genomic survey sequence.//0.80:195:61//AQ176784

R-PLACE1003709//Human BAC clone RG126M09 from 7q21-q22, complete sequence.//0.018:152:61//AC002067

R-PLACE1003711//Human endothelial nitric oxide synthase gene, complete cds.//1.7e-61:366:89//D26607

R-PLACE1003723//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//2.7e-44:505:73//AL022336

R-PLACE1003738//H.sapiens DNA sequence.//0.93:185:60//Z22357

R-PLACE1003760//Human globin gene.//5.9e-97:538:91//M69023

R-PLACE1003762//Homo sapiens chromosome 17, clone HCIT39G8, complete sequence.//4.6e-13:134:79//AC003070

R-PLACE1003768//Homo sapiens chromosome 17, clone hRPK.142_H_19, complete sequence.//5.4e-12:189:71//AC005919

R-PLACE1003771//Homo sapiens BAC clone GS164B05 from 7p21-p22, complete sequence.//1.7e-119:619:95//AC004160

R-PLACE1003783

R-PLACE1003784//Homo sapiens chromosome 19, CIT-HSP-87m17 BAC clone, complete sequence.//5.6e-15:204:74//AC004659

R-PLACE1003795//CIT-HSP-2374C8.TR CIT-HSP Homo sapiens genomic clone 2374C8, genomic survey sequence.//7.0e-37:234:89//AQ114933

R-PLACE1003833//Homo sapiens full length insert cDNA clone ZE15C06.//4.4e-59:313:95//AF086558

R-PLACE1003850

R-PLACE1003858

R-PLACE1003864

R-PLACE1003870//Homo sapiens Chromosome 22q11.2 Cosmid Clone 15a10 In DG CR Region, complete sequence.//8.7e-33:285:81//AC000072

R-PLACE1003885

R-PLACE1003886

R-PLACE1003888//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//0.73:127:65//AC004069

R-PLACE1003900//Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.//1.9e-05:239:59//L78810

R-PLACE1003903//Homo sapiens full length insert cDNA clone ZD78D11.//8.1e-74:369:97//AF086422

R-PLACE1003915//Mus musculus bone morphogenetic protein-6 (BMP-6) gene, exons 6 and 7 and complete cds.//0.56:247:61//U73520

R-PLACE1003923//Caenorhabditis elegans cosmid Y57G11C, complete sequence.//0.67:213:63//Z99281

R-PLACE1003932//Human DNA sequence from cosmid U90B3, on chromosome Xp11, contains ESTs.//8.7e-49:342:85//Z74022

R-PLACE1003936//H.sapiens gene for ventricular myosin light chain 2.//2.6e-09:394:61//Z15030

R-PLACE1003968//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***

from contig 4-62, complete sequence.//1.3e-07:245:65//AL010247

R-PLACE1004104

R-PLACE1004114//Human PAC clone RG212D03, complete sequence.//5.0e-07:336:61//AC002485

R-PLACE1004118//HS_3092_B1_B01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=1 Row=D, genomic survey sequence.//0.80:207:60//AQ128151

R-PLACE1004128//Rattus norvegicus guanine nucleotide binding protein beta 4 subunit mRNA, partial cds.//1.8e-06:193:66//AF022085

R-PLACE1004149//HS_2253_A2_F11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=22 Row=K, genomic survey sequence.//2.4e-59:315:95//AQ129711

R-PLACE1004156//Homo sapiens Xp22 bins 3-5 PAC RPC14-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//8.3e-53:299:76//AC005295

R-PLACE1004161

R-PLACE1004183//Homo sapiens for TOM1-like protein.//1.3e-80:434:93//AJ010071

R-PLACE1004197//RPC111-69N15.TK RPC111 Homo sapiens genomic clone R-69N15, genomic survey sequence.//0.0078:170:65//AQ265515

R-PLACE1004203//Homo sapiens semaphorin L (SEMAL) mRNA, complete cds.//3.4e-105:501:98//AF030698

R-PLACE1004242//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6 q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//6.1e-65:373:86//AL021326

R-PLACE1004256//Homo sapiens BAC clone NH0044G14 from 7q11.23-21.1, complete sequence.//0.011:383:61//AC006031

R-PLACE1004257//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence.//3.4e-09:576:59//AC004470

R-PLACE1004258//HS_3034_A1_B12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3034 Col=23 Row=C, genomic survey sequence.//1.4e-35:359:77//AQ128936

R-PLACE1004270//CITBI-E1-2504K14.TR CITBI-E1 Homo sapiens genomic clone 2504K14, genomic survey sequence.//2.7e-06:150:74//AQ261108

R-PLACE1004274//Homo sapiens BAC clone NH0436H22 from 2, complete sequence.//0.025:116:72//AC005234

R-PLACE1004277//Homo sapiens two pore domain K⁺ channel (TASK-2) mRNA, complete cds.//4.4e-106:581:91//AF084830

R-PLACE1004284//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.59:231:60//AC005308

R-PLACE1004289//Homo sapiens chromosome 17, clone hRPK.700_H_6, complete sequence.//5.8e-31:340:75//AC005920

R-PLACE1004302//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.4e-90:572:86//AC005095

R-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//1.9e-113:590:94//Y11588

R-PLACE1004336//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1013A10, WORKING DRAFT SEQUENCE.//2.3e-65:292:82//AL033383

R-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//2.4e-70:379:93//AF100153

R-PLACE1004376//CIT-HSP-2287M8.TF CIT-HSP Homo sapiens genomic clone 2287M8, genomic survey sequence.//0.47:173:61//AQ000837

R-PLACE1004384//CIT-HSP-2316J11.TF CIT-HSP Homo sapiens genomic clone 2316J11, genomic survey sequence.//0.035:109:69//AQ037817

R-PLACE1004388//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-82, complete sequence.//4.2e-06:381:60//AL010149

R-PLACE1004405//Homo sapiens clone GS512I21, WORKING DRAFT SEQUENCE, 9 u

nordered pieces.//0.20:270:60//AC005027
R-PLACE1004425//Homo sapiens PAC clone DJ0733B09 from 7p14-p13, complete
sequence.//1.3e-96:516:94//AC005532
R-PLACE1004428//Human DNA sequence from clone 888M10 on chromosome 1p36.
11-36.31 Contains part of gene KIAA0453, EST, STS, GSS, complete sequenc
e.//5.8e-10:279:65//AL031296
R-PLACE1004437//Human NAD⁺-specific isocitrate dehydrogenase beta subuni
t precursor, mRNA, nuclear gene encoding mitochondrial protein, complete
cds.//2.9e-88:516:88//U49283
R-PLACE1004451//HS_2258_B2_F01_MR CIT Approved Human Genomic Sperm Libra
ry D.Homo sapiens genomic clone Plate=2258 Col=2 Row=L, genomic survey s
equence.//0.82:172:61//AQ221189
R-PLACE1004460
R-PLACE1004467//Syrian hamster carbamoylphosphate synthetase-aspartate t
ranscarbamylase-dihydroorotase (CAD) gene, exons 1 and 2.//1.2e-24:311:6
2//M31621
R-PLACE1004471//Homo Sapiens Chromosome X clone bWXD75, complete sequenc
e.//2.1e-34:333:70//AC004389
R-PLACE1004473
R-PLACE1004491//Drosophila melanogaster Oregon-R mitochondrial A+T regio
n.//1.0e-08:485:60//U11584
R-PLACE1004506
R-PLACE1004510//Plasmodium falciparum chromosome 2, section 64 of 73 of
the complete sequence.//0.0094:543:56//AE001427
R-PLACE1004516//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, compl
ete sequence.//0.00011:343:59//AC003071
R-PLACE1004518
R-PLACE1004548//Homo sapiens Xp22 BAC GS-551019 (Genome Systems Human BA
C library) and cosmids U199A7 and U209F2 (Lawrence Livermore X chromosom

e cosmid library) containing part of human chloride channel 4 gene, complete sequence.//4.9e-40:245:80//AC003666

R-PLACE1004550

R-PLACE1004564//B.taurus mRNA for cleavage and polyadenylation specificity factor.//2.7e-82:532:86//X75931

R-PLACE1004629//Homo sapiens chromosome 7 clone UWGC:g3586a230 from 7p14-15, complete sequence.//0.015:437:59//AC004800

R-PLACE1004645//CIT-HSP-2370D6.TR CIT-HSP Homo sapiens genomic clone 2370D6, genomic survey sequence.//0.033:76:75//AQ110136

R-PLACE1004646//Homo sapiens cosmid 120C12 from Xq28, complete sequence.//2.0e-23:237:79//AF036876

R-PLACE1004658//Homo sapiens Chromosome 12p13.3 BAC RPCI11-21K20 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//7.1e-09:94:87//AC005343

R-PLACE1004664//RPCI11-79G23.TV RPCI11 Homo sapiens genomic clone R-79G23, genomic survey sequence.//2.2e-81:433:94//AQ283692

R-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//2.7e-24:263:74//U07561

R-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds.//1.1e-89:513:91//AF035606

R-PLACE1004681//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//1.3e-96:498:95//AB020860

R-PLACE1004686

R-PLACE1004691//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 2/11.//2.1e-33:290:80//AB020859

R-PLACE1004693//Caenorhabditis elegans cosmid Y2H9A, complete sequence.//1.0:195:60//AL021448

R-PLACE1004716//CITBI-E1-2519C14.TR CITBI-E1 Homo sapiens genomic clone
2519C14, genomic survey sequence.//5.0e-43:245:93//AQ276965

R-PLACE1004722//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic
sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0022:360:60
//AC005507

R-PLACE1004736

R-PLACE1004740

R-PLACE1004743//Homo sapiens ubiquitin-protein ligase E3-alpha (UBR1) mRNA,
partial cds.//5.4e-105:575:92//AF061556

R-PLACE1004751//Homo sapiens Xq28 BACs 360 F12, GSHB-555C13, complete
sequence.//9.0e-26:317:76//AC002523

R-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds.//8.5e-
88:437:96//AF084367

R-PLACE1004777//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome
region), segment 3/15, WORKING DRAFT SEQUENCE.//0.050:138:65//AP0000
10

R-PLACE1004793//Human endogenous retrovirus HERV-K(HML6) proviral clone
HML6.17 putative polymerase and envelope genes, partial cds, and 3'LTR./
//5.1e-58:313:80//U60269

R-PLACE1004804//Homo sapiens mRNA for KIAA0606 protein, partial cds.//5.
8e-98:580:88//AB011178

R-PLACE1004813//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic
sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//5.3e-09:256:
64//AC005140

R-PLACE1004814//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-
18) mRNA, complete cds.//3.5e-107:358:99//AF069250

R-PLACE1004815//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete
sequence.//3.8e-61:353:89//AC004126

R-PLACE1004824//Homo sapiens chromosome 17, clone hCIT.468_F_23, WORKING

DRAFT SEQUENCE, 3 unordered pieces.//5.7e-42:364:79//AC004666

R-PLACE1004827//Homo sapiens Xp22 BAC GS-594A7 (Genome Systems Human BAC library) contains Bmx gene, complete sequence.//2.7e-14:156:79//AC003669

R-PLACE1004836//HS_2270_A2_H10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=20 Row=0, genomic survey sequence.//8.6e-51:267:96//AQ164110

R-PLACE1004838//CIT-HSP-2343E10.TR CIT-HSP Homo sapiens genomic clone 2343E10, genomic survey sequence.//0.071:168:63//AQ058544

R-PLACE1004840//Sequence 4 from patent US 5728819.//1.6e-26:150:98//I92820

R-PLACE1004868//Human Chromosome X clone bWXd342, complete sequence.//0.57:344:59//AC004072

R-PLACE1004885//HS_3235_B2_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=14 Row=J, genomic survey sequence.//1.1e-38:175:78//AQ210193

R-PLACE1004900//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.0e-44:334:84//AL022577

R-PLACE1004902

R-PLACE1004913//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//7.7e-58:377:87//Z82209

R-PLACE1004918//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//0.00084:373:60//AC004605

R-PLACE1004930//Homo sapiens MDC-3.13 isoform 1 mRNA, complete cds.//2.0e-100:532:93//AF099936

R-PLACE1004934//Homo sapiens clone RG062N11, WORKING DRAFT SEQUENCE, 2 u

nordered pieces.//0.00030:198:66//AC005683
 R-PLACE1004937//Caenorhabditis elegans SEL-10 (sel-10) mRNA, complete cds.//1.3e-13:367:61//AF020788
 R-PLACE1004969//Human DNA sequence from clone LUCA7 on chromosome 3, complete sequence.//0.97:116:71//Z84494
 R-PLACE1004972
 R-PLACE1004979//Plasmodium falciparum MAL3P4, complete sequence.//0.74:304:60//AL008970
 R-PLACE1004982//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7e-05:495:57//AC005308
 R-PLACE1004985//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 451B21, WORKING DRAFT SEQUENCE.//2.5e-10:410:60//AL033522
 R-PLACE1005026//Homo sapiens PAC clone DJ0907C10 from 7q31-3q32, complete sequence.//2.7e-56:158:99//AC004925
 R-PLACE1005027
 R-PLACE1005046//Homo sapiens chromosome 19, cosmid F20237, complete sequence.//3.1e-63:438:86//AC005775
 R-PLACE1005052//Homo sapiens chromosome Xp22-135-136 clone GSHB-567I1, WORKING DRAFT SEQUENCE, 35 unordered pieces.//6.1e-87:301:98//AC005867
 R-PLACE1005066//Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVP2 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSs and GSSs and an AAAT repeat polymorphism, complete sequence.//1.1e-09:453:61//AL023584
 R-PLACE1005077//H.sapiens genes for semenogelin I and semenogelin II.//2.6e-05:199:66//Z47556
 R-PLACE1005085//Homo sapiens chromosome 17, clone hRPK.293_K_20, complete sequence.//2.1e-42:384:69//AC005495

R-PLACE1005086//RPCI11-30H10.TV RPCI-11 Homo sapiens genomic clone RPCI-11-30H10, genomic survey sequence.//0.13:112:67//B87788

R-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds.//2.5e-97:531:92//L40401

R-PLACE1005102//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//1.3e-91:504:92//AC004476

R-PLACE1005108//Homo sapiens BAC129, complete sequence.//4.0e-28:232:84//U85195

R-PLACE1005111//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 566H6, WORKING DRAFT SEQUENCE.//3.0e-18:174:74//AL031845

R-PLACE1005128

R-PLACE1005146

R-PLACE1005162//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//2.4e-07:273:61//AC005140

R-PLACE1005176//Rat alternatively spliced mRNA.//8.1e-20:185:82//M93018

R-PLACE1005181//HS_2182_B2_B05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=10 Row=D, genomic survey sequence.//4.9e-05:193:65//AQ030787

R-PLACE1005187//Arabidopsis thaliana chromosome II BAC T14A4 genomic sequence, complete sequence.//0.00073:264:60//AC006161

R-PLACE1005206//Homo sapiens full length insert cDNA YN66A06.//6.3e-64:343:93//AF075043

R-PLACE1005232//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 25J6, WORKING DRAFT SEQUENCE.//1.3e-34:286:81//Z84476

R-PLACE1005243

R-PLACE1005261//Caenorhabditis elegans cosmid ZK666, complete sequence.//0.66:180:60//Z49132

R-PLACE1005266//Homo sapiens clone RG122E10, complete sequence.//1.3e-15

:166:78//AC005067

R-PLACE1005277//CITBI-E1-2514D4.TF CITBI-E1 Homo sapiens genomic clone 2
514D4, genomic survey sequence.//2.5e-34:358:74//AQ265720

R-PLACE1005287//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***
from MALIP1, WORKING DRAFT SEQUENCE.//4.1e-07:495:60//AL031744

R-PLACE1005305//HS_3180_B2_D02_MR CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3180 Col=4 Row=H, genomic survey s
equence.//1.1e-42:308:85//AQ169443

R-PLACE1005308

R-PLACE1005313//Human Chromosome 11 pac pDJ227b23, WORKING DRAFT SEQUENC
E, 19 unordered pieces.//0.00048:320:60//AC000383

R-PLACE1005327//chromosome 1 specific transcript KIAA0491.//5.4e-103:537
:94//AB007960

R-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569, complete sequ
ence.//2.2e-94:536:91//AC004794

R-PLACE1005335//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE,
2 unordered pieces.//5.3e-32:313:79//AC000380

R-PLACE1005373//Homo sapiens BAC129, complete sequence.//8.8e-10:229:68/
/U85195

R-PLACE1005374//Homo sapiens chromosome 17, clone hRPK.401_0_9, complete
sequence.//3.0e-44:434:77//AC005291

R-PLACE1005409//Human BAC clone RG167B05 from 7q21, complete sequence.//
8.8e-105:529:96//AC003991

R-PLACE1005453//Human PAC clone DJ327A19 from Xq25-q26, complete sequenc
e.//4.7e-39:302:82//AC002477

R-PLACE1005467//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 167P19, WORKING DRAFT SEQUENCE.//1.1e-40:328:81//Z93014

R-PLACE1005471//Human DNA sequence from clone 395P12 on chromosome 1q24-
25. Contains the TXGP1 gene for tax-transcriptionally activated glycopro

tein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Aminotransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//6.4e-68:409:90//AL022310

R-PLACE1005477//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 32B1, WORKING DRAFT SEQUENCE.//0.020:216:66//AL023693

R-PLACE1005480//Homo sapiens chromosome 19, CIT-HSP BAC 490g23 (BC338531), complete sequence.//2.8e-44:327:70//AC005392

R-PLACE1005481//Homo sapiens chromosome 17, clone hRPC.1164_0_3, complete sequence.//4.2e-23:284:74//AC004703

R-PLACE1005494//Danio rerio homeobox protein LIM-3 (lim3) gene, exon 4.//0.19:468:60//AF031631

R-PLACE1005502//Homo sapiens formin binding protein 21 mRNA, complete cds.//1.6e-55:277:98//AF071185

R-PLACE1005526//Human mRNA for alpha-1 type II collagen.//0.10:227:63//X16468

R-PLACE1005528//Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SEQUENCE.//2.3e-76:395:96//AP000038

R-PLACE1005530//C.familiaris CA repeat sequence (isolate).//0.023:90:75//X86184

R-PLACE1005550//Fugu rubripes GSS sequence, clone 048A08bH1, genomic survey sequence.//2.0e-09:235:64//AL025928

R-PLACE1005554//Homo sapiens chromosome 17, clone hRPK.215_P_18, complete sequence.//0.069:305:60//AC005969

R-PLACE1005557//Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence.//4.3e-105:587:91//AC004707

R-PLACE1005574//Human BAC 367D17 from chromosome 18, complete sequence.//1.5e-17:274:67//AC003971

R-PLACE1005584//Homo sapiens PAC clone DJ1186C01 from 7q21.2-q31.1, comp

lete sequence.//2.7e-15:191:77//AC004991
R-PLACE1005595//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete sequence.//6.4e-90:453:96//AC004126
R-PLACE1005603//Homo sapiens cosmid clone U169D2 from Xp22.1-22.2, complete sequence.//0.69:322:61//U72788
R-PLACE1005611//Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds.//0.059:473:56//U42599
R-PLACE1005623//Homo sapiens full length insert cDNA clone ZD76B03.//1.6e-113:575:95//AF086405
R-PLACE1005630//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.6e-79:270:94//AC005840
R-PLACE1005639//Human BAC clone RG022J17 from 7q21, complete sequence.//8.2e-56:441:83//AC002382
R-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//3.2e-110:585:93//AF083255
R-PLACE1005656//Homo sapiens chromosome 17, clone hRPK.628_E_12, complete sequence.//8.6e-08:505:58//AC005701
R-PLACE1005666//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and polymorphic CA repeat.//3.2e-27:307:72//Z82203
R-PLACE1005698//344B22.TV CIT978SKA1 Homo sapiens genomic clone A-344B22, genomic survey sequence.//0.030:91:70//B15144
R-PLACE1005727//Human variable number tandem repeat (VNTR) region, allele 17R1 3' to collagen type II (COL2A1) gene.//5.2e-10:587:59//L10171
R-PLACE1005730//Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.//0.0039:239:58//L78810
R-PLACE1005739//Mus musculus IFN-gamma induced (MgII) mRNA, complete cds.//2.2e-21:270:72//U15635
R-PLACE1005755//Caenorhabditis elegans cosmid M03F4.//6.9e-08:219:64//U64601

R-PLACE1005763//Human mRNA for KIAA0118 gene, partial cds.//1.0e-45:268:87//D42087

R-PLACE1005799//Human X chromosome mRNA for CCG1 protein inv. in cell proliferation.//0.030:91:78//X07024

R-PLACE1005802//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//1.4e-69:391:92//AC004827

R-PLACE1005803

R-PLACE1005804//Human BAC clone RG341D10 from 7p15-p21, complete sequence.//1.8e-21:175:75//AC002530

R-PLACE1005828//Homo sapiens chromosome 17, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//2.9e-56:333:91//AC004150

R-PLACE1005834//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P2, WORKING DRAFT SEQUENCE.//0.020:513:55//AL031745

R-PLACE1005845//Rabbit mRNA for protein phosphatase 2A-beta.//1.8e-10:182:69//Y00763

R-PLACE1005850

R-PLACE1005851//Homo sapiens clone DJ0789I05, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.5e-06:318:63//AC004887

R-PLACE1005876//B.taurus mRNA for cleavage and polyadenylation specificity factor.//6.7e-28:366:72//X75931

R-PLACE1005884//Human DNA sequence from cosmid V526F1, between markers DXS366 and DXS87 on chromosome X contains STS.//1.0e-06:306:64//Z70281

R-PLACE1005898//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0094:449:59//AC005139

R-PLACE1005921//CITBI-E1-2509N21.TF CITBI-E1 Homo sapiens genomic clone 2509N21, genomic survey sequence.//4.8e-84:494:89//AQ261347

R-PLACE1005923//RPCI11-65N9.TJ RPCI11 Homo sapiens genomic clone R-65N9, genomic survey sequence.//8.3e-97:520:93//AQ237243

R-PLACE1005925//Human DNA sequence from clone 231L4 on chromosome Xq27.1
-27.3 Contains GSS, STS, complete sequence.//5.2e-67:578:78//AL022719

R-PLACE1005932//Caenorhabditis elegans cosmid Y52B11A, complete sequence
./0.0035:176:62//AL032654

R-PLACE1005934

R-PLACE1005936//Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5
cM, complete sequence.//0.00021:272:62//AF069716

R-PLACE1005951

R-PLACE1005953//Caenorhabditis elegans cosmid F09E5.//1.3e-07:349:60//U3
7429

R-PLACE1005955//Human HepG2 3' region MboI cDNA, clone hmdld01m3.//8.3e-
08:128:70//D17131

R-PLACE1005966//Pontia protodice large subunit ribosomal RNA gene, parti
al sequence; tRNA-Val gene, complete sequence; and small subunit ribosom
al RNA gene, partial sequence, mitochondrial genes for mitochondrial RNA
s.//7.0e-09:549:59//AF044863

R-PLACE1005968//Rattus norvegicus mRNA for p47, complete cds.//1.1e-51:3
94:81//AB002086

R-PLACE1005990//Homo sapiens chromosome 12p13.3 clone RPC111-407G6, WORK
ING DRAFT SEQUENCE, 51 ordered pieces.//4.4e-63:369:91//AC005866

R-PLACE1006002//Human cosmid CRI-JC2015 at D10S289 in 10sp13.//5.9e-27:2
99:74//U15177

R-PLACE1006003//Mus musculus clone OST18050, genomic survey sequence.//3
.5e-07:164:67//AF046375

R-PLACE1006011//Mus musculus poly-(ADPribose)-transferase homolog PARP
mRNA, complete cds.//1.1e-32:266:83//AF072521

R-PLACE1006017//Homo sapiens Chromosome 22q11.2 Cosmid Clone 31e In DGCR
Region, complete sequence.//1.8e-17:164:82//AC000077

R-PLACE1006037//Mus musculus B6D2F1 clone 2C11B mRNA.//2.0e-49:557:72//U

01139

R-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//4.3e-13:128:81
//X99906

R-PLACE1006076//Homo sapiens clone DJ0781A18, WORKING DRAFT SEQUENCE, 3
unordered pieces.//3.3e-18:220:74//AC004885

R-PLACE1006119//Plasmodium berghei (STRAIN ANKA) gamma-GCS gene, complet
e CDS.//0.0050:271:63//AJ005122

R-PLACE1006129//Drosophila melanogaster, chromosome 2R, region 31C1-31D6
, P1 clone DS08879, complete sequence.//0.43:178:65//AC005454

R-PLACE1006139//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, complete
sequence.//7.5e-13:222:68//AC004849

R-PLACE1006143//Plasmodium falciparum MAL3P6, complete sequence.//0.0001
9:455:59//Z98551

R-PLACE1006157//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***
from MAL4P1, WORKING DRAFT SEQUENCE.//0.00018:351:60//AL034557

R-PLACE1006159//Homo sapiens chromosome 10 clone LA10NC01_124_D_3 map 10
q25.1, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.0e-113:586:96//AC006
103

R-PLACE1006164//Human hereditary haemochromatosis region, histone 2A-lik
e protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, an
d sodium phosphate transporter (NPT3) gene, complete cds.//1.0e-28:342:7
5//U91328

R-PLACE1006167//Homo sapiens full length insert cDNA clone ZE14E04.//4.6
e-77:426:93//AF086555

R-PLACE1006170//Mouse mRNA for alpha-adaptin (C).//3.0e-46:188:82//X1497
2

R-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds.//1.6e-116:597
:95//AF091433

R-PLACE1006195//Homo sapiens chromosome 19, fosmid 39554, complete seque

nce.//8.8e-11:148:74//AC004410

R-PLACE1006196

R-PLACE1006205//Genomic sequence from Mouse 11, complete sequence.//8.4e-44:332:85//AC000398

R-PLACE1006223//Human DNA sequence from cosmid U74C11, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//0.041:215:61//Z73362

R-PLACE1006225//Caenorhabditis elegans cosmid Y69H2, complete sequence.//9.7e-13:358:63//Z98877

R-PLACE1006236//Plasmodium falciparum MAL3P4, complete sequence.//0.00019:538:58//AL008970

R-PLACE1006239//Homo sapiens BAC clone RG118D07 from 7q31, complete sequence.//3.1e-96:497:95//AC004142

R-PLACE1006246//Homo sapiens clone NH0144M13, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.029:499:56//AC006034

R-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds.//9.2e-96:499:95//AB014548

R-PLACE1006262//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//0.00043:160:66//AC004087

R-PLACE1006288//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20N2, WORKING DRAFT SEQUENCE.//3.5e-120:611:96//AL031320

R-PLACE1006318

R-PLACE1006325//Plasmodium falciparum MAL3P8, complete sequence.//1.0:426:57//AL034560

R-PLACE1006335//Human DNA sequence from PAC 849L7 on chromosome Xq21.//0.96:173:66//AL008987

R-PLACE1006357//P.falciparum complete gene map of plastid-like DNA (IR-B).//1.9e-07:491:58//X95276

R-PLACE1006360//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//0.25:484:56//AE001398

R-PLACE1006368//Caenorhabditis elegans cosmid Y38H6C, complete sequence.
//1.0:240:59//AL031630

R-PLACE1006371//Homo sapiens chromosome 16, cosmid clone 360H6 (LANL), complete sequence.//3.7e-101:574:91//AC004232

R-PLACE1006382

R-PLACE1006385//Mus musculus intersectin-EH binding protein Ibp2 mRNA, partial cds.//1.4e-50:350:86//AF057286

R-PLACE1006412//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//5.1e-51:339:82//AC004854

R-PLACE1006414//Homo sapiens 12p13.3 PAC RPCI5-927J10 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.6e-38:297:84//AC004804

R-PLACE1006438//Homo sapiens full length insert cDNA YH73H06.//7.6e-73:422:90//AF074985

R-PLACE1006445//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018K9, WORKING DRAFT SEQUENCE.//3.0e-07:376:61//AL031726

R-PLACE1006469

R-PLACE1006470//Mouse B1 repetitive sequence DNA.//1.0:96:66//M24152

R-PLACE1006482//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 447C4, WORKING DRAFT SEQUENCE.//3.0e-101:535:94//AL021977

R-PLACE1006492//Homo sapiens chromosome 17, clone hRPK.180_P_8, complete sequence.//0.78:44:95//AC005972

R-PLACE1006506//R.norvegicus BSP gene.//1.0:206:60//X86100

R-PLACE1006521//RPCI11-13L8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13L8, genomic survey sequence.//9.0e-17:414:61//B75158

R-PLACE1006531//Plasmodium falciparum coronin gene, isolate 3D7.//0.98:186:63//AJ002197

R-PLACE1006534//Anopheles gambiae complete mitochondrial genome.//0.051:412:61//L20934

R-PLACE1006540//Homo sapiens clone UWGC:y55c025 from 6p21, complete sequence.//7.5e-41:470:70//AC004209

R-PLACE1006552//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS **
* from clone Y47D3, WORKING DRAFT SEQUENCE.//0.57:355:57//Z98865

R-PLACE1006598//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.016:291:58//AC004710

R-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//2.9e-116:590:95//U97670

R-PLACE1006617//Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.//2.2e-45:209:88//AC004050

R-PLACE1006626//C. elegans cosmid K12H4.//1.2e-16:344:64//L14331

R-PLACE1006629//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//2.8e-25:343:70//AC006128

R-PLACE1006640//CIT-HSP-2169L1.TF CIT-HSP Homo sapiens genomic clone 2169L1, genomic survey sequence.//0.00020:201:62//B90038

R-PLACE1006673//Homo sapiens clone DJ076B20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.4e-42:309:84//AC004882

R-PLACE1006678//Homo sapiens PAC clone DJ1166G19 from 7p12-p11.2, complete sequence.//6.4e-09:454:59//AC006024

R-PLACE1006704//Human DNA sequence from clone 249C1 on chromosome Xq21.1-22.2 Contains GSS, complete sequence.//0.56:226:63//AL022154

R-PLACE1006731//Homo sapiens clone 23923 mRNA sequence.//6.0e-101:486:98//AF038172

R-PLACE1006754//Homo sapiens chromosome 19, cosmid R29124, complete sequence.//1.4e-68:381:93//AC005626

R-PLACE1006760//Homo sapiens clone 24800 mRNA sequence.//6.2e-72:397:92//AF070622

R-PLACE1006779//Rattus norvegicus intestinal trefoil factor gene, promot

er and partial cds.//1.6e-11:420:61//U20984

R-PLACE1006782//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS **
* from clone Y47D3, WORKING DRAFT SEQUENCE.//0.60:321:58//Z98865

R-PLACE1006792//Homo sapiens chromosome 4 clone C0026P05 map 4P16, complete sequence.//2.9e-40:379:77//AC005599

R-PLACE1006795//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//6.2e-07:291:63//AC005083

R-PLACE1006800//HS_2270_B1_D02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=3 Row=H, genomic survey sequence.//4.1e-76:367:99//AQ085793

R-PLACE1006805//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.00058:354:59//AC005507

R-PLACE1006815//HS_3028_B1_B04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3028 Col=7 Row=D, genomic survey sequence.//1.5e-33:251:77//AQ120174

R-PLACE1006819//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments.//1.4e-76:544:84//Z86062

R-PLACE1006829

R-PLACE1006860

R-PLACE1006867//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 323M4, WORKING DRAFT SEQUENCE.//3.2e-107:549:95//AL033378

R-PLACE1006878//Homo sapiens full length insert cDNA clone ZB55G05.//1.4e-46:241:97//AF086155

R-PLACE1006883//Homo sapiens chromosome 16, cosmid clone 360H6 (LANL), complete sequence.//1.3e-38:283:85//AC004232

R-PLACE1006901

R-PLACE1006904//Human DNA sequence from PAC 360E18 on chromosome X contains

ins EST, CpG island and polymorphic CA repeat.//4.1e-15:477:62//Z82203
R-PLACE1006917//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library) complete sequence.//1.3e-42:305:87//AC005184
R-PLACE1006932
R-PLACE1006935//Human DNA sequence from PAC 117P19 on chromosome X.//0.0014:114:74//Z86061
R-PLACE1006958//Mouse mRNA for germ cell specific protein APG-1, complete cds.//9.5e-85:590:83//D49482
R-PLACE1006961//Homo sapiens chromosome 17, clone hRPK.349_A_8, complete sequence.//6.7e-42:295:86//AC005544
R-PLACE1006962//Homo sapiens Xp22 PAC RPC11-167A22 (from Roswell Park Cancer Center) complete sequence.//1.1e-19:302:71//AC002349
R-PLACE1006966//HS_2219_B2_C02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2219 Col=4 Row=F, genomic survey sequence.//0.019:180:63//AQ145873
R-PLACE1006989
R-PLACE1007014
R-PLACE1007021//Homo sapiens chromosome 12p13.3 clone RPC13-454B23, WORKING DRAFT SEQUENCE, 48 unordered pieces.//1.6e-23:362:70//AC005845
R-PLACE1007045//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 32B1, WORKING DRAFT SEQUENCE.//2.3e-90:584:86//AL023693
R-PLACE1007053//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//2.4e-108:550:96//AC004895
R-PLACE1007097//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//1.8e-103:552:93//AL02

1368

R-PLACE1007105//Mus musculus muskelin mRNA, complete cds.//2.7e-32:379:73//U72194

R-PLACE1007111//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.14:422:57//AC004688

R-PLACE1007112//Cynips cornifex cytb gene.//0.020:427:58//AJ228479

R-PLACE1007132//Homo sapiens full length insert cDNA YH77E09.//5.7e-107:535:96//AF074987

R-PLACE1007140//Homo sapiens clone RG030L05, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.36:408:58//AC005050

R-PLACE1007178//Homo sapiens clone HEA4 Cri-du-chat region mRNA.//0.99:63:73//AF009283

R-PLACE1007226

R-PLACE1007238

R-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//2.0e-91:534:89//D50495

R-PLACE1007242//CITBI-E1-2512M9.TF CITBI-E1 Homo sapiens genomic clone 2 512M9, genomic survey sequence.//1.3e-05:117:76//AQ279454

R-PLACE1007243//Prototheca wickerhamii 263-11 complete mitochondrial DNA.//0.21:284:58//U02970

R-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//6.9e-113:607:93//Y15908

R-PLACE1007274//Homo sapiens chromosome 17, clone hRPK.394_K_10, complete sequence.//4.4e-10:135:74//AC006080

R-PLACE1007276//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence.//1.7e-36:435:72//AF069291

R-PLACE1007282//B.garinii (strain TIs1) p83/100 gene (partial).//0.95:183:60//X81533

R-PLACE1007286//RPCI11-13L8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13L8, genomic survey sequence.//6.1e-55:519:76//B75158

R-PLACE1007301//Human DNA sequence from PAC 106H8 on chromosome 1q24. Contains PHOSPHATIDYLINOSITOL-GLYCAN class C (PIG-C) and DYNAMIN-3 genes. Contains ESTs and STSs and a CpG island.//0.75:180:62//Z97195

R-PLACE1007317//Drosophila dasycnemia 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence.//0.59:236:59//U94253

R-PLACE1007342

R-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//3.7e-65:367:91//AF096870

R-PLACE1007367//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.0e-06:385:62//AC005507

R-PLACE1007375//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.10:309:59//AC004709

R-PLACE1007386//Reclinomonas americana mitochondrial DNA, complete genome.//0.0012:403:58//AF007261

R-PLACE1007402//HS_2055_A2_D03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=6 Row=G, genomic survey sequence.//0.0046:88:79//AQ234824

R-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence.//7.6e-112:590:94//AF093771

R-PLACE1007416//Homo sapiens chromosome 19, cosmid R26894, complete sequence.//0.96:98:70//AC005594

R-PLACE1007450//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54B20, WORKING DRAFT SEQUENCE.//1.7e-39:308:82//Z98304

R-PLACE1007452//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//2.6e-59:389:82//AC004081

R-PLACE1007460

R-PLACE1007478//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence.//7.0e-08:335:60//AC004241

R-PLACE1007484

R-PLACE1007488//Glossina morsitans morsitans 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence.//2.5e-05:421:61//AF072373

R-PLACE1007507//Plasmodium falciparum MAL3P7, complete sequence.//2.3e-09:577:57//AL034559

R-PLACE1007511//Homo sapiens chromosome 17, clone hRPC.1110_E_20, complete sequence.//1.2e-79:387:96//AC004231

R-PLACE1007524//Homo sapiens chromosome 19, overlapping cosmid F18547, F11133, R27945, R28830 and R32804, complete sequence.//3.4e-09:148:73//AC003682

R-PLACE1007525//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//4.7e-38:297:82//AC004381

R-PLACE1007544

R-PLACE1007547//Human laminin alpha 4 chain (LAMA4*-1) mRNA, complete cds.//4.0e-17:108:97//U77706

R-PLACE1007557//Human BAC clone RG343P13 from 7q31, complete sequence.//2.2e-45:390:77//AC002465

R-PLACE1007583//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 545L17, WORKING DRAFT SEQUENCE.//1.0e-56:302:95//AL031665

R-PLACE1007598//Homo sapiens clone 23939 mRNA sequence.//1.5e-102:554:93//AF038179

R-PLACE1007618

R-PLACE1007621//Homo sapiens clone 23859 mRNA sequence.//1.4e-103:537:94//AF038176

R-PLACE1007632//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.3e-76:289:94//AC005840

R-PLACE1007645//Homo sapiens full length insert cDNA clone ZD76G10.//0.0080:96:77//AF086408

R-PLACE1007649//CIT-HSP-2308A18.TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey sequence.//1.1e-82:412:97//AQ022149

R-PLACE1007677//Plasmodium falciparum chromosome 2, section 4 of 73 of the complete sequence.//0.0041:470:57//AE001367

R-PLACE1007688

R-PLACE1007690//Human Chromosome 16 BAC clone CIT987SK-A-418G10, complete sequence.//1.3e-22:162:91//AC002044

R-PLACE1007697

R-PLACE1007705//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460J8, WORKING DRAFT SEQUENCE.//4.4e-121:624:95//AL031662

R-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//1.8e-73:374:96//AF061243

R-PLACE1007725//Caenorhabditis elegans cosmid F38A5.//0.070:186:60//U70854

R-PLACE1007729//Human endogenous retrovirus HERV-K(HML6) proviral clone HML6.17 putative polymerase and envelope genes, partial cds, and 3' LTR.//3.8e-53:415:81//U60269

R-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//2.1e-92:556:89//AB014585

R-PLACE1007737//Homo sapiens clone Sb19.12 Alu-Yb8 sequence.//4.0e-43:302:77//AF015169

R-PLACE1007743//Plasmodium falciparum MAL3P8, complete sequence.//1.0e-06:533:59//AL034560

R-PLACE1007746//T.brucei mitochondrial maxicircle DNA encoding cytochrome c oxidase subunit I (COI), and NADH dehydrogenase subunits 4 and 5, co

mplete cds.//0.28:386:58//M14820

R-PLACE1007791//D.discoideum gene for protein kinase.//0.17:263:60//Z379
81

R-PLACE1007807//Human DNA sequence from clone 87808 on chromosome Xq21.1
-21.33. Contains an EST, STSS, a GSS and genomic marker DXS472, complete
sequence.//1.1e-72:324:88//AL031116

R-PLACE1007810//Homo sapiens chromosome 7 common fragile site, complete
sequence.//2.2e-14:325:67//AF017104

R-PLACE1007829//Human BAC clone GS165I04 from 7q21, complete sequence.//
0.00052:455:61//AC002379

R-PLACE1007843//P.falciparum complete gene map of plastid-like DNA (IR-A
)//0.0050:447:57//X95275

R-PLACE1007846//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndr
ome region), segment 3/15, WORKING DRAFT SEQUENCE.//2.2e-111:570:95//AP0
00010

R-PLACE1007852//HS_3028_B2_F04_MR CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3028 Col=8 Row=L, genomic survey s
equence.//1.3e-12:209:71//AQ131021

R-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//6
.6e-110:574:94//AB018309

R-PLACE1007866//Homo sapiens DNA sequence from PAC 454M7 on chromosome X
q25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome pr
oteins OCRL-1. Contains ESTs, STSS and GSSs, complete sequence.//1.6e-43:
551:70//AL022162

R-PLACE1007877//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169),
complete sequence.//1.6e-22:222:78//AC005754

R-PLACE1007897//HS_3113_B2_E04_T7 CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3113 Col=8 Row=J, genomic survey s
equence.//2.9e-72:381:95//AQ186905

R-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0487.//8.8e-88:460:95//AB007956

R-PLACE1007946//Human chromosome Y cosmid 54E8 genomic sequence, WORKING
DRAFT SEQUENCE.//4.9e-23:172:78//AC003095

R-PLACE1007954//Homo sapiens BAC clone NH0414C23 from Y, complete sequen
ce.//1.7e-27:303:75//AC006157

R-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, com
plete cds.//3.9e-102:513:95//AF084530

R-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B)
mRNA, partial cds.//2.2e-87:465:93//AF079529

R-PLACE1007969//Mus musculus myelin gene expression factor (MEF-2) mRNA,
partial cds.//4.8e-72:556:81//U13262

R-PLACE1007990//E.tenella antigen LPMC61 mRNA, partial cds.//0.043:273:6
3//M30933

R-PLACE1008000//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 668J24, WORKING DRAFT SEQUENCE.//8.8e-10:453:62//AL034346

R-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4
unordered pieces.//9.0e-114:563:96//AC005628

R-PLACE1008044//Rattus norvegicus nuclear pore complex protein NUP107 mR
NA, complete cds.//2.6e-44:509:72//L31840

R-PLACE1008045//Homo sapiens chromosome 5, BAC clone 79a6 (LBNL H172), c
omplete sequence.//0.32:137:66//AC005592

R-PLACE1008080//Arabidopsis thaliana chromosome II BAC F10A12 genomic se
quence, complete sequence.//0.082:292:59//AC006232

R-PLACE1008095//Homo sapiens BAC clone NH0364H22 from 2, complete sequen
ce.//5.4e-27:260:76//AC005036

R-PLACE1008111//Human variable number tandem repeat (VNTR) region, allel
e 12R1 3' to collagen type II (COL2A1) gene.//2.2e-07:444:59//L10157

R-PLACE1008122//Homo sapiens chromosome 17, clone hRPK.142_H_19, complet

e sequence.//1.9e-11:384:63//AC005919

R-PLACE1008129//Homo sapiens clone DJ1087M19, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.0e-10:189:66//AC004955

R-PLACE1008132//Human HepG2 3' region cDNA, clone hmd5d06.//7.4e-47:320:86//D16939

R-PLACE1008177//Mouse mRNA for meiosis-specific nuclear structural protein 1 (MNS1), complete cds.//2.6e-32:410:70//D14849

R-PLACE1008181//Caenorhabditis elegans cosmid C31H2.//0.055:358:60//U41748

R-PLACE1008198

R-PLACE1008201//Homo sapiens mRNA for KIAA0530 protein, partial cds.//4.8e-103:551:93//AB011102

R-PLACE1008209//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1125A11, WORKING DRAFT SEQUENCE.//4.6e-16:250:71//AL034549

R-PLACE1008231//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.13:341:60//AC004688

R-PLACE1008244//P.falciparum P.195 gene.//0.11:212:66//A04562

R-PLACE1008273//Human MEST mRNA, complete cds.//0.00013:52:100//D78611

R-PLACE1008275

R-PLACE1008280//Homo sapiens chromosome 7 clone UWGC:g3586a160 from 7p14-15, complete sequence.//1.5e-05:104:76//AC005272

R-PLACE1008309//Human 'at'-rich region adjacent to alpha satellite DNA.//0.70:138:63//M80308

R-PLACE1008329//Homo sapiens chromosome 10 clone CIT-HSP-1240G16 map 10q25.1, complete sequence.//0.00061:150:68//AC005886

R-PLACE1008330//Homo sapiens chromosome 19, cosmid F21431, complete sequence.//4.8e-74:252:98//AC005176

R-PLACE1008331//Genomic sequence from Human 13, complete sequence.//1.0:

176:65//AC001226

R-PLACE1008356//Homo sapiens meningioma-expressed antigen 5 (MEA5) mRNA,
3' UTR.//2.5e-98:556:90//AF036145

R-PLACE1008368//HS-1039-A1-C10-MF.abi CIT Human Genomic Sperm Library C
Homo sapiens genomic clone Plate=CT 821 Col=19 Row=E, genomic survey seq
uence.//1.2e-05:375:62//B36336

R-PLACE1008369//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndr
ome region), segment 4/15, WORKING DRAFT SEQUENCE.//2.8e-10:466:61//AP00
0011

R-PLACE1008392//Homo sapiens chromosome 17, clone hRPK.471_L_13, complet
e sequence.//1.0e-46:282:82//AC005244

R-PLACE1008398//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 215D11, WORKING DRAFT SEQUENCE.//4.1e-101:529:94//AL034417

R-PLACE1008401//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4
, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered
pieces.//0.18:379:58//AC004604

R-PLACE1008402//Homo sapiens mRNA for p115, complete cds.//1.6e-101:521:
95//D86326

R-PLACE1008405//Human cosmid CRI-JC2015 at D10S289 in 10sp13.//6.8e-22:3
28:71//U15177

R-PLACE1008424

R-PLACE1008426//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of
hepatocellular colorectal and non-small cell lung cancer , segment 7/11.
//7.5e-101:505:96//AB020864

R-PLACE1008429//Human DNA sequence from clone 20J23 on chromosome Xq26.2
-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ra
s-like protein TC25) EST, CA repeat, STS, CpG island, complete sequence.
//1.2e-11:118:78//AL022576

R-PLACE1008437//H.sapiens genomic DNA (PAC 838L14) from chromosome 11, W

ORKING DRAFT SEQUENCE.//2.2e-06:159:69//Y12335
R-PLACE1008455
R-PLACE1008457//Homo sapiens chromosome 17, Neurofibromatosis 1 locus,
complete sequence.//1.2e-109:588:93//AC004526
R-PLACE1008465//CIT978SK-A-28A11.TVE CIT978SK Homo sapiens genomic clone
A-28A11, genomic survey sequence.//1.1e-10:133:77//B78696
R-PLACE1008488
R-PLACE1008524//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 34B21, WORKING DRAFT SEQUENCE.//7.3e-120:612:95//AL031778
R-PLACE1008531//Homo sapiens wbscr1 (WBSCR1) and replication factor C su
bunit 2 (RFC2) genes, complete cds.//8.5e-96:510:93//AF045555
R-PLACE1008532
R-PLACE1008533
R-PLACE1008568//HS_3218_B2_D08_T7 CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3218 Col=16 Row=H, genomic survey
sequence.//0.0042:295:62//AQ214623
R-PLACE1008584//Human PAC clone DJ0596009 from 7p15, complete sequence./
/5.0e-26:254:66//AC003074
R-PLACE1008621//Homo sapiens chromosome 17, clone hRPK.346_K_10, complet
e sequence.//4.0e-78:498:86//AC006120
R-PLACE1008625
R-PLACE1008626//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 97P20, WORKING DRAFT SEQUENCE.//5.5e-06:228:67//AL031297
R-PLACE1008627//Cricetulus griseus mRNA for Zn finger factor.//3.4e-20:3
35:71//Y12836
R-PLACE1008629//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12
unordered pieces.//0.55:326:58//AC004826
R-PLACE1008630//Homo sapiens genomic DNA, 21q region, clone: B175P11X96,
genomic survey sequence.//0.13:440:55//AG011096

R-PLACE1008643//Human BAC clone RG083J23 from 7q31, complete sequence.//
1.3e-58:356:82//AC004001

R-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//2.4e-88:434:97//AF044333

R-PLACE1008693//CIT-HSP-2025M9.TR CIT-HSP Homo sapiens genomic clone 2025M9, genomic survey sequence.//1.2e-41:300:82//B64742

R-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//4.8e-31:320:75//AF038406

R-PLACE1008715//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 799N4, WORKING DRAFT SEQUENCE.//0.074:478:58//AL022147

R-PLACE1008748//CIT-HSP-2170P12.TR CIT-HSP Homo sapiens genomic clone 2170P12, genomic survey sequence.//8.5e-42:160:86//B90841

R-PLACE1008757//Homo sapiens 12q24.2 PAC RPC14-765H13 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.99:211:61//AC005864

R-PLACE1008790//Rattus norvegicus clonel polymeric immunoglobulin receptor mRNA 3' untranslated region, GA rich region, and microsatellites with GGA-triplet and GAA-triplet repeats.//0.052:108:68//U00762

R-PLACE1008798//Homo sapiens full length insert cDNA clone YZ86C05.//7.7e-58:285:100//AF086088

R-PLACE1008807//CIT-HSP-2366014.TR CIT-HSP Homo sapiens genomic clone 2366014, genomic survey sequence.//3.5e-35:223:89//AQ079210

R-PLACE1008808//Homo sapiens exonuclease homolog RAD1 (RAD1) mRNA, complete cds.//2.3e-97:499:95//AF030933

R-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds.//9.7e-45:394:78//AF032668

R-PLACE1008851//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.9e-28:207:87//AC004581

R-PLACE1008854//CIT-HSP-2172B3.TF CIT-HSP Homo sapiens genomic clone 217
2B3, genomic survey sequence.//8.9e-30:166:97//B93289

R-PLACE1008867//Homo sapiens BAC clone RG054D04 from 7q31, complete sequ
ence.//3.5e-76:404:95//AC005058

R-PLACE1008887//Homo sapiens clone DJ0943F02, WORKING DRAFT SEQUENCE, 3
unordered pieces.//7.7e-37:585:67//AC004932

R-PLACE1008902//Homo sapiens chromosome Y, clone hCIT.494_G_17, complete
sequence.//0.0022:409:60//AC005820

R-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds.//8.
2e-55:344:89//AB018308

R-PLACE1008925//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS **
* from clone Y53F4, WORKING DRAFT SEQUENCE.//0.0014:398:58//Z92860

R-PLACE1008934

R-PLACE1008941//Homo sapiens chromosome 17, clone hRPK.293_K_20, complet
e sequence.//9.8e-84:429:92//AC005495

R-PLACE1008947

R-PLACE1009020

R-PLACE1009027//Human DNA sequence from clone 914P14 on chromosome Xq23
Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat,
GSS, complete sequence.//1.3e-82:434:95//AL031117

R-PLACE1009039//Human DNA sequence from clone 276K20 on chromosome 6p22.
1-22.3. Contains STSS, GSSs and a putative CpG island, complete sequence
.//0.00010:297:58//AL031391

R-PLACE1009045//Homo sapiens chromosome 17, clone hRPC.117_B_12, complet
e sequence.//2.9e-06:160:70//AC004707

R-PLACE1009048//Human DNA sequence from clone 511E16 on chromosome 6p24.
3-25.1. Contains the last coding exon of the gene for P18 component of a
minoacyl-tRNA synthetase complex, part of an unknown gene downstream of
a putative CpG island, and an STS with a CA repeat polymorphism, complet

e sequence.//1.3e-16:339:66//AL023694

R-PLACE1009050//Aedes aegypti gene sequence, primary transcript.//0.40:393:59//L17023

R-PLACE1009060//Mus musculus mRNA for Alix-SF (ALG-2-interacting protein X, short form, complete CDS.//0.00075:79:83//AJ005074

R-PLACE1009090//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC262482), complete sequence.//6.7e-13:212:73//AC004783

R-PLACE1009094//Caenorhabditis elegans cosmid C49F8, complete sequence.//0.49:221:61//Z70206

R-PLACE1009099

R-PLACE1009110//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//5.1e-17:301:66//AC004025

R-PLACE1009111//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//1.2e-06:234:61//AC005140

R-PLACE1009130//Plasmodium falciparum MAL3P6, complete sequence.//7.5e-06:426:58//Z98551

R-PLACE1009150//Homo sapiens *** SEQUENCING IN PROGRESS ***, WORKING DRAFT SEQUENCE.//2.3e-118:614:95//AJ011929

R-PLACE1009155//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SEQUENCE.//1.4e-107:584:93//AP000031

R-PLACE1009158//Homo sapiens full length insert cDNA clone YP10D03.//1.9e-105:539:95//AF085876

R-PLACE1009166//Homo sapiens chromosome 17, clone hRPK.180_P_8, complete sequence.//2.8e-44:360:71//AC005972

R-PLACE1009172//Human cosmid QLL2C9 from Xq28.//4.1e-37:401:74//Z47046

R-PLACE1009174//Homo sapiens PAC clone DJ0907C10 from 7q31-3q32, complete sequence.//2.1e-17:140:81//AC004925

R-PLACE1009183//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6

q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8). LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSS, complete sequence.//1.9e-46:572:69//Z84480

R-PLACE1009186//Human Chromosome X, complete sequence.//0.016:322:61//AC004070

R-PLACE1009190//Plasmodium falciparum MAL3P8, complete sequence.//0.050:487:58//AL034560

R-PLACE1009200//H.sapiens mRNA for sortilin.//1.0e-31:195:92//X98248

R-PLACE1009230//Homo sapiens chromosome 19, CIT-HSP BAC 490g23 (BC338531), complete sequence.//1.8e-75:364:85//AC005392

R-PLACE1009246//Cricetulus griseus SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2) mRNA, complete cds.//6.6e-44:525:71//U22818

R-PLACE1009308

R-PLACE1009319//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.00010:132:75//AC004801

R-PLACE1009328//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//3.3e-87:576:85//AC006120

R-PLACE1009335//Borrelia burgdorferi (section 62 of 70) of the complete genome.//0.32:315:60//AE001176

R-PLACE1009338//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//6.8e-05:411:59//AC005140

R-PLACE1009368//Homo sapiens PAC clone DJ1179J19 from 7q11.23-q21, complete sequence.//0.00040:280:61//AC004989

R-PLACE1009375//D. yakuba mitochondrial DNA for origin of replication, small ribosomal RNA, transfer RNAs tRNA-fMet, tRNA-Gln, tRNA-Ile and tRNA-A-Val.//1.1e-08:444:60//X05915

R-PLACE1009388

R-PLACE1009398//Homo sapiens BAC clone GS011E15 from 5q31, complete sequence.//0.065:279:61//AC002427

R-PLACE1009404//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.0e-06:253:64//AC005038

R-PLACE1009410//Homo sapiens chromosome 17, clone hRPK.142_H_19, complete sequence.//9.8e-112:561:96//AC005919

R-PLACE1009434//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence.//2.2e-21:126:79//AL031120

R-PLACE1009443//Homo sapiens nucleolar protein Nop30 and cytoplasmic protein Myp (NOP) gene, alternatively spliced products, complete cds.//4.5e-14:117:91//AF064598

R-PLACE1009444//Homo sapiens phosphatidylinositol 4-kinase mRNA, complete cds.//9.6e-85:479:90//L36151

R-PLACE1009459

R-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence.//5.6e-101:540:94//AC004531

R-PLACE1009477//Homo sapiens, clone hRPK.15_A_1, complete sequence.//3.4e-46:284:91//AC006213

R-PLACE1009493//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//5.5e-107:581:92//U91321

R-PLACE1009524//Homo sapiens DNA sequence from PAC 63G5 on chromosome 22 q12.3-13.1. Contains part of a gene for a human SEC7 homolog B2-1 (cytohesin-2, Arno, ARF exchange factor) LIKE protein, an unknown gene and a gene coding for a Leucine rich protein. Contains ESTs, STSs and GSSs, complete sequence.//0.74:301:61//Z94160

R-PLACE1009539//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167A19, WORKING DRAFT SEQUENCE.//5.7e-29:357:74//AL031427

R-PLACE1009542//CIT-HSP-2166P10.TRB CIT-HSP Homo sapiens genomic clone 2166P10, genomic survey sequence.//2.6e-10:145:75//B89614

R-PLACE1009571//RPCI11-61J16.TK RPCI11 Homo sapiens genomic clone R-61J16, genomic survey sequence.//0.016:68:80//AQ202146

R-PLACE1009581

R-PLACE1009595//Homo sapiens clone DJ56J10, complete sequence.//1.8e-38:365:79//AC005006

R-PLACE1009596//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 501A4, WORKING DRAFT SEQUENCE.//1.2e-29:314:76//Z98051

R-PLACE1009607//cSRL-77g9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-77g9, genomic survey sequence.//2.1e-05:142:69//B06230

R-PLACE1009613//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-89, complete sequence.//3.6e-08:434:59//AL010266

R-PLACE1009621//Sequence 50 from patent US 5691147.//1.5e-20:235:73//I76222

R-PLACE1009622//CIT-HSP-2023D13.TFB CIT-HSP Homo sapiens genomic clone 2023D13, genomic survey sequence.//0.72:176:62//B81271

R-PLACE1009637//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.0068:396:59//X95276

R-PLACE1009639//Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project).//0.013:521:58//AL021811

R-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds.//1.0e-107:589:92//AB011159

R-PLACE1009665//Human PAC clone DJ0658N05 from 7p21, complete sequence.//8.4e-72:487:85//AC003075

R-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//2.0e-61:310:97//AF062534

R-PLACE1009708//Homo sapiens clone DJ0935K16, complete sequence.//2.8e-1

03:542:94//AC006011

R-PLACE1009721//Human Cosmid g0771a222 from 7q31.3, complete sequence.//
4.6e-85:518:88//AC000109

R-PLACE1009731//Homo sapiens DNA sequence from PAC 434014 on chromosome
1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehyd
rogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF
6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains
ESTs and GSSs, complete sequence.//0.0033:215:65//AL022398

R-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds.//6.2e-116:5
98:95//AF046024

R-PLACE1009794

R-PLACE1009798//Human DNA sequence from clone 1189B24 on chromosome Xq25
-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3,
EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein
Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part o
f a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C
. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.//7
.5e-88:191:96//AL030996

R-PLACE1009845//Homo sapiens DNA sequence from PAC 234H5 on chromosome 6
q21. Contains an unknown gene, ESTs and STSs, complete sequence.//8.7e-1
9:226:69//Z98172

R-PLACE1009879//Homo sapiens genomic DNA, 21q region, clone: 149C3A68, g
enomic survey sequence.//2.1e-29:230:76//AG002672

R-PLACE1009886//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, com
plete sequence.//0.99:203:61//AC004945

R-PLACE1009888//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323),
complete sequence.//5.3e-91:577:88//AC006116

R-PLACE1009908

R-PLACE1009921//Homo sapiens cosmid clone HDAB (1S149) insert DNA, compl

ete cosmid.//4.7e-81:385:84//M63005

R-PLACE1009924//HS_3151_B1_B10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3151 Col=19 Row=D, genomic survey sequence.//5.5e-47:240:99//AQ167412

R-PLACE1009925//CIT978SK-A-931F6.TV CIT978SK Homo sapiens genomic clone A-931F6, genomic survey sequence.//0.00010:159:68//B51673

R-PLACE1009935//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.081:238:65//AC005308

R-PLACE1009947//Homo sapiens PAC clone 248015 from 13q12-q13, complete sequence.//1.0:353:58//AC002483

R-PLACE1009971//Homo sapiens full length insert cDNA clone ZD38E12.//3.7e-11:152:75//AF086247

R-PLACE1009992

R-PLACE1009995//Plasmodium falciparum chromosome 2, section 4 of 73 of the complete sequence.//0.0019:305:61//AE001367

R-PLACE1009997//Homo sapiens chromosome 10 clone CIT987SK-1175G20 map 10q25.2-10q25.3, complete sequence.//1.8e-43:462:76//AC005874

R-PLACE1010023//HS_3018_B1_H10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=19 Row=P, genomic survey sequence.//0.00013:198:63//AQ093513

R-PLACE1010031//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence.//7.4e-115:581:96//AL031775

R-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein.//1.9e-05:136:74//X84692

R-PLACE1010069//CIT-HSP-2328B12.TF CIT-HSP Homo sapiens genomic clone 23

28B12, genomic survey sequence.//2.6e-60:324:94//AQ042094
R-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds./
/4.6e-87:543:88//AF065482
R-PLACE1010076//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4
, BAC clone C0473M13; HTGS phase 1, WORKING DRAFT SEQUENCE, 4 unordered
pieces.//6.3e-08:489:58//AC005699
R-PLACE1010083
R-PLACE1010089//F19F22-Sp6 IGF Arabidopsis thaliana genomic clone F19F22
, genomic survey sequence.//0.14:400:59//B10583
R-PLACE1010096//R.norvegicus mRNA for 100 kDa protein.//4.3e-91:562:87//
X64411
R-PLACE1010102//Apis mellifera tRNA-Leu cytochrome oxidase II intergenic
spacer region, mitochondrial sequence.//1.5e-08:357:60//AF039556
R-PLACE1010105//Plasmodium falciparum chromosome 2, section 11 of 73 of
the complete sequence.//4.0e-09:510:59//AE001374
R-PLACE1010106//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 54B20, WORKING DRAFT SEQUENCE.//1.4e-12:194:73//Z98304
R-PLACE1010134
R-PLACE1010148//HS_3128_A1_D09_MR CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3128 Col=17 Row=G, genomic survey
sequence.//0.17:281:61//AQ140790
R-PLACE1010152//Mouse mRNA for arylhydrocarbon receptor, complete cds.//
3.1e-45:351:81//D38417
R-PLACE1010181//Homo sapiens clone DJ0914M06, WORKING DRAFT SEQUENCE, 1
unordered pieces.//3.6e-06:207:66//AC004928
R-PLACE1010194//HS_2232_B1_H10_MR CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=2232 Col=19 Row=P, genomic survey
sequence.//2.4e-08:134:74//AQ185425
R-PLACE1010202//Human DNA sequence from clone 227L5 on chromosome Xp11.2

2-11.3. Contains a Keratin, Type 1 Cytoskeletal 18 (KRT18, CYK18, K18, C K18) pseudogene and an STS, complete sequence.//0.00035:383:61//AL031585
R-PLACE1010231//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 287G14, WORKING DRAFT SEQUENCE.//1.2e-95:519:94//AL033377
R-PLACE1010261
R-PLACE1010270//H.sapiens CpG island DNA genomic MseI fragment, clone 85.
a6, reverse read cpg85a6.rtl1a.//0.068:171:63//Z63482
R-PLACE1010274//S.douglasii gene for cytochrome b.//4.5e-07:276:63//X592
80
R-PLACE1010293//Homo sapiens chromosome 2 PAC RPCI3-417E16 (Roswell Park
Cancer Institute Human PAC library) complete sequence.//4.7e-91:522:90/
/AC004464
R-PLACE1010321
R-PLACE1010324//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS **
* from clone Y38E10, WORKING DRAFT SEQUENCE.//5.7e-08:484:57//AL021149
R-PLACE1010329//Homo sapiens Chromosome 22q11.2 Cosmid Clone 50d10 In IG
LC Region, complete sequence.//7.9e-35:328:79//AC000024
R-PLACE1010341//Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21
unordered pieces.//1.3e-31:418:66//AC004971
R-PLACE1010362
R-PLACE1010364//Mus cookii mitochondrion DNA fragment.//0.23:162:64//M77
098
R-PLACE1010383//Homo sapiens chromosome 17, clone hCIT.186_H_2, complete
sequence.//1.4e-105:543:95//AC004675
R-PLACE1010401//Human Chromosome 15q11-q13 PAC clone pDJ223c9 from the P
rader-Willi/Angelman Syndrome region, complete sequence.//0.00017:268:62
//AC004137
R-PLACE1010481//Bos taurus C5-glucuronyl epimerase mRNA, partial cds.//8
.6e-79:556:83//AF003927

R-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds.//7.3e-88:438:96//AF039081

R-PLACE1010492//HS_3169_B2_B04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3169 Col=8 Row=D, genomic survey sequence.//0.98:171:63//AQ169892

R-PLACE1010522//WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.34:407:62//AC006082

R-PLACE1010547

R-PLACE1010562//CITBI-E1-2503B16.TF CITBI-E1 Homo sapiens genomic clone 2503B16, genomic survey sequence.//6.4e-17:152:84//AQ265929

R-PLACE1010579//Torulopsis glabrata mitochondrial gene for ribosomal protein var1.//1.7e-05:271:65//X02893

R-PLACE1010580

R-PLACE1010599

R-PLACE1010616//Human BAC clone RG343P13 from 7q31, complete sequence.//3.0e-13:151:75//AC002465

R-PLACE1010622//Arabidopsis thaliana BAC F1104.//0.00031:366:60//AF096370

R-PLACE1010624//Homo sapiens chromosome 7q22 sequence, complete sequence.//8.2e-34:322:79//AF053356

R-PLACE1010628//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//2.3e-97:515:94//AC004846

R-PLACE1010629//HS_3003_A2_C08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=16 Row=E, genomic survey sequence.//5.6e-60:321:95//AQ130493

R-PLACE1010630//Plasmodium falciparum chromosome 2, section 19 of 73 of the complete sequence.//0.051:372:59//AE001382

R-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds.//2.6e-92:497:93//AB011102

R-PLACE1010661//CIT-HSP-2008K15.TR CIT-HSP Homo sapiens genomic clone 20
08K15, genomic survey sequence.//5.7e-27:160:95//B57089

R-PLACE1010662//Caenorhabditis elegans cosmid C12C8, complete sequence./
/9.4e-09:151:73//Z81467

R-PLACE1010702//CIT-HSP-2314C3.TR CIT-HSP Homo sapiens genomic clone 231
4C3, genomic survey sequence.//1.3e-90:459:96//AQ028536

R-PLACE1010714//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-
Phe genes, partial sequence, and Varlp (var1) gene, mitochondrial gene e
ncoding mitochondrial protein, complete cds.//5.3e-08:478:58//U49822

R-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mR
NA, partial cds.//3.8e-55:300:95//AF092564

R-PLACE1010739//Human DNA sequence from clone 393P23 on chromosome Xq21.
1-21.33. Contains GSSs, complete sequence.//3.4e-89:507:90//Z95400

R-PLACE1010743

R-PLACE1010761//Homo sapiens chromosome 17, clone hRPK.294_J_22, complet
e sequence.//3.0e-103:511:97//AC005921

R-PLACE1010771

R-PLACE1010786

R-PLACE1010800//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE, 30
unordered pieces.//1.8e-43:545:71//AC005682

R-PLACE1010802//Phoebeis agarithe large subunit ribosomal RNA gene, parti
al sequence; tRNA-Val gene, complete sequence; and small subunit ribosom
al RNA gene, partial sequence, mitochondrial genes for mitochondrial RNA
s.//1.9e-09:492:59//AF044862

R-PLACE1010811//Homo sapiens Xp22 BAC GSHB-257G1 (Genome Systems BAC Lib
rary) complete sequence.//0.041:415:59//AC002524

R-PLACE1010833

R-PLACE1010856//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic
sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0022:512:55//A

C004153

R-PLACE1010857//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 11/11 .//4.9e-85:507:90//AB020868

R-PLACE1010870//RPCI11-59K21.TK RPCI11 Homo sapiens genomic clone R-59K2 1, genomic survey sequence.//8.2e-85:422:97//AQ195697

R-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//7.0e-100:501:96//AB011182

R-PLACE1010891//Homo sapiens chromosome X, clone 592, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.10:162:61//AC002489

R-PLACE1010896//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00032:409:59//AC005505

R-PLACE1010900//Homo sapiens DNA, trinucleotide repeats region.//3.2e-07 :180:71//AB018488

R-PLACE1010916//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//0.041:205:60//AL034557

R-PLACE1010917

R-PLACE1010925//HS_2027_B2_B09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=18 Row=D, genomic survey sequence.//1.6e-46:404:77//AQ247031

R-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds.//4.2e-65:402:89//AB011126

R-PLACE1010942//Homo sapiens intersectin short form mRNA, complete cds./ /1.9e-80:441:93//AF064243

R-PLACE1010944

R-PLACE1010947//D.discoideum rasG gene.//0.00044:181:65//Z11533

R-PLACE1010954//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//3.0e-51:518:74//AC005077

R-PLACE1010960//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 451B21, WORKING DRAFT SEQUENCE.//0.022:292:63//AL033522

R-PLACE1010965//Human mariner1 transposase gene, complete consensus sequence.//1.0e-64:444:84//U52077

R-PLACE1011026//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//0.59:345:61//AJ235272

R-PLACE1011032//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//0.62:82:75//Z93242

R-PLACE1011041//H.sapiens DNA sequence.//0.051:162:66//Z22248

R-PLACE1011046//Homo sapiens mRNA for KIAA0581 protein, partial cds.//2.9e-100:563:91//AB011153

R-PLACE1011054//Human DNA sequence from PAC 46H23, BRCA2 gene region chromosome 13q12-13 contains Klotho, ESTs.//4.7e-29:280:73//Z84483

R-PLACE1011056//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 341D10, WORKING DRAFT SEQUENCE.//1.7e-39:288:84//Z97985

R-PLACE1011057//CIT-HSP-2014F10.TF CIT-HSP Homo sapiens genomic clone 2014F10, genomic survey sequence.//2.4e-60:370:90//B58896

R-PLACE1011090//Homo sapiens chromosome 4 clone B200N5 map 4q25, complete sequence.//0.12:489:59//AC005509

R-PLACE1011109//Homo sapiens chromosome Y, clone 486, 0, 2, complete sequence.//8.4e-43:427:76//AC002531

R-PLACE1011114//Homo sapiens mRNA from HIV associated non-Hodgkin's lymphoma (clone hl1-14).//1.7e-29:179:94//Y16709

R-PLACE1011133//HS-1058-B1-H02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 780 Col=3 Row=P, genomic survey sequence.//1.0:133:63//B44006

R-PLACE1011143//H.sapiens CpG island DNA genomic MseI fragment, clone 127a4, forward read cpgl27a4.ft1a.//1.0:127:67//Z56550

R-PLACE1011160//Homo sapiens HRIHFB2038 mRNA, partial cds.//2.4e-95:534:

91//AB015333

R-PLACE1011165//Human Cosmid g5129s232 from 7q31.3, complete sequence.//
0.47:355:58//AC003968

R-PLACE1011185//Homo sapiens clone DJ0038I10, WORKING DRAFT SEQUENCE, 5
unordered pieces.//1.3e-26:403:70//AC004820

R-PLACE1011203//paramecium species 4.51er mt dna dimer: replication init.
. region, clone 1.//1.0e-10:379:60//K00908

R-PLACE1011219//HS_3036_B1_F08_MR CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3036 Col=15 Row=L, genomic survey
sequence.//2.6e-39:253:88//AQ104587

R-PLACE1011221//Homo sapiens T-cell receptor alpha delta locus from base
s 250472 to 501670 (section 2 of 5) of the Complete Nucleotide Sequence.
//0.32:279:60//AE000659

R-PLACE1011229//HS_3002_B1_E10_MR CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3002 Col=19 Row=J, genomic survey
sequence.//9.3e-31:317:74//AQ303626

R-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21, complete sequ
ence.//1.2e-109:571:94//AC005014

R-PLACE1011273//Saccharomyces douglasii mitochondrial cytochrome c oxida
se subunit I (COX1) gene, complete cds.//0.00027:337:61//M97514

R-PLACE1011291

R-PLACE1011296//H.sapiens steroid reductase pseudogene.//4.2e-37:326:80/
/M68887

R-PLACE1011310//H.sapiens 5' flanking sequence of gene for corticotropin
.//0.0017:416:60//X67661

R-PLACE1011325//Plasmodium falciparum chromosome 2, section 35 of 73 of
the complete sequence.//3.0e-10:511:59//AE001398

R-PLACE1011332//Homo sapiens chromosome 17, clone HCIT3L16, WORKING DRAF
T SEQUENCE, 7 unordered pieces.//8.3e-06:250:64//AC002344

R-PLACE1011340//Human BAC clone RG341D10 from 7p15-p21, complete sequence.//0.67:290:58//AC002530

R-PLACE1011375//Mus musculus Kv3.4 gene, exon 4.//6.8e-23:190:86//AJ010310

R-PLACE1011399//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.22:359:60//AC005140

R-PLACE1011419//Human DNA sequence from cosmid U90B3, on chromosome Xp11, contains ESTs.//5.1e-32:282:81//Z74022

R-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds.//1.5e-112:600:94//AB011102

R-PLACE1011452//Homo sapiens clone DJ0945F02, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.9e-77:303:85//AC006013

R-PLACE1011465

R-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds.//7.9e-103:515:96//AB018255

R-PLACE1011492//A-837A4.TP CIT978SK Homo sapiens genomic clone A-837A4, genomic survey sequence.//6.5e-37:234:82//B14085

R-PLACE1011503//Homo sapiens chromosome 17, clone hRPC.1171_I_10, complete sequence.//0.99:267:60//AC004687

R-PLACE1011520//Homo sapiens clone DJ1119N05, complete sequence.//2.0e-116:591:96//AC004968

R-PLACE1011563//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.2e-13:566:59//AC004688

R-PLACE1011567//Plasmodium falciparum MAL3P6, complete sequence.//0.62:358:61//Z98551

R-PLACE1011576//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//8.7e-45:400:78//AC003973

R-PLACE1011586//Homo sapiens chromosome 17, clone HRPC890E16, complete sequence.//2.2e-59:338:93//AC004477

R-PLACE1011635//C.pasteurianum pfl gene and act gene.//0.71:288:60//X93463

R-PLACE1011641//Mycoplasma genitalium random genomic clone sg11, partial cds.//0.023:232:60//U02205

R-PLACE1011643//Homo sapiens chromosome 19, cosmid R33590, complete sequence.//1.4e-21:432:67//AC005620

R-PLACE1011649//Homo sapiens clone 24432 mRNA sequence.//7.8e-72:414:91//AF070535

R-PLACE1011650//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//5.1e-27:174:79//AC002477

R-PLACE1011664//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460D19, WORKING DRAFT SEQUENCE.//7.4e-05:238:65//AL031905

R-PLACE1011675//CIT-HSP-2370M16.TR CIT-HSP Homo sapiens genomic clone 2370M16, genomic survey sequence.//1.3e-27:233:81//AQ108283

R-PLACE1011682//H.sapiens HLA-DMB gene.//2.3e-22:390:67//X76776

R-PLACE1011719//Homo sapiens 12q24.2 BAC RPCI11-360E11 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//3.1e-24:409:66//AC004806

R-PLACE1011725//Homo sapiens unknown mRNA downregulated by induced differentiation with 13-cis retinoic acid.//0.13:143:65//AF026526

R-PLACE1011729//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE.//1.1e-15:157:82//AL022345

R-PLACE1011749//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.5e-38:314:81//AC005089

R-PLACE1011762//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//1.9e-35:538:68//AC002383

R-PLACE1011778//CIT-HSP-2326C17.TV CIT-HSP Homo sapiens genomic clone 23

26C17, genomic survey sequence.//2.8e-58:346:91//AQ028782

R-PLACE1011783//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 229A8, WORKING DRAFT SEQUENCE.//4.6e-38:288:84//Z86090

R-PLACE1011858//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//4.1e-104:524:97//AL031321

R-PLACE1011874//Homo Sapiens Chromosome X clone bWDX312, complete sequence.//2.1e-100:511:95//AC004478

R-PLACE1011875

R-PLACE1011891//Human lens membrane protein (mp19) gene, exon 11.//0.0011:195:64//L04193

R-PLACE1011896//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//0.010:110:74//AL022398

R-PLACE1011922//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence.//3.5e-10:152:74//AF042090

R-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds.//7.0e-98:546:92//AF059617

R-PLACE1011962//CIT-HSP-2294L24.TF CIT-HSP Homo sapiens genomic clone 2294L24, genomic survey sequence.//0.31:131:63//AQ006352

R-PLACE1011964//Homo sapiens chromosome 17, clone HRPC987K16, complete sequence.//2.5e-08:393:63//AC002994

R-PLACE1011982//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone : MDJ14, complete sequence.//9.6e-09:463:62//AB016889

R-PLACE1011995//Human Down Syndrome region of chromosome 21, clone A12H1-2H4.//2.7e-39:294:82//U44738

R-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds.//2.5e-104:540:95//AB018256

R-PLACE2000003//Human PAC clone DJ404F18 from Xq23, complete sequence.//
4.9e-10:439:63//AC004000

R-PLACE2000007//Human fibroblast growth factor receptor 3 (FGFR3) gene,
intron 3.//1.0:151:66//L78722

R-PLACE2000011//Homo sapiens clone 614 unknown mRNA, complete sequence./
/1.5e-103:524:95//AF091080

R-PLACE2000015//Homo sapiens PAC clone DJ269005 from Xq23, complete sequ
ence.//0.94:372:57//AC005191

R-PLACE2000017//Homo sapiens chromosome 17, clone hCIT.162_E_12, complet
e sequence.//3.0e-55:299:86//AC006236

R-PLACE2000021//CIT-HSP-2343C18.TR CIT-HSP Homo sapiens genomic clone 23
43C18, genomic survey sequence.//4.5e-54:295:94//AQ058140

R-PLACE2000033//H.sapiens gene for mitochondrial ATP synthase c subunit
(P1 form).//6.5e-38:298:82//X69907

R-PLACE2000034//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4
unordered pieces.//5.3e-34:200:79//AC005628

R-PLACE2000039//Homo sapiens BAC clone RG060N22 from 7q21, complete sequ
ence.//1.8e-49:274:89//AC003083

R-PLACE2000047//CIT-HSP-2373C2.TR CIT-HSP Homo sapiens genomic clone 237
3C2, genomic survey sequence.//1.8e-48:389:79//AQ112243

R-PLACE2000050//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 1177I5, WORKING DRAFT SEQUENCE.//0.0027:95:76//AL022315

R-PLACE2000061//Homo sapiens mRNA for KIAA0575 protein, complete cds.//2
.9e-39:429:72//AB011147

R-PLACE2000062//Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10
unordered pieces.//5.9e-40:310:84//AC004832

R-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//1
.9e-109:550:95//AF027219

R-PLACE2000097//Homo sapiens chromosome 12p13.3 clone RPC111-189M20, WOR

KING DRAFT SEQUENCE, 39 unordered pieces.//1.6e-106:553:95//AC005910
R-PLACE2000100//Human DNA sequence from clone 301K23 on chromosome 1p35.
1-36.21. Contains the 5' part of a novel gene similar to predicted yeast
and worm genes. Contains ESTs and GSSs, complete sequence.//1.8e-38:285
:84//AL031730
R-PLACE2000103//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 20208, WORKING DRAFT SEQUENCE.//4.3e-113:559:97//AL031848
R-PLACE2000111//Rat MLC1V gene encoding alkali myosin ventricel light ch
ain, exon 1.//0.00041:347:61//X16325
R-PLACE2000115//Cervus elaphus MHC class II DRB pseudogene, intron 2 mic
rosatellite.//0.50:165:63//U63067
R-PLACE2000132
R-PLACE2000136//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS.***
from contig 3-30, complete sequence.//0.0032:310:61//AL008974
R-PLACE2000140//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 11703, WORKING DRAFT SEQUENCE.//1.1e-111:566:96//AL020995
R-PLACE2000164
R-PLACE2000170//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4
, BAC clone C0024K08; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered
pieces.//3.9e-40:390:76//AC005598
R-PLACE2000172
R-PLACE2000176
R-PLACE2000187//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 268H5, WORKING DRAFT SEQUENCE.//8.7e-45:298:87//AL008718
R-PLACE2000216//Dog nonerythroid beta-spectrin mRNA, 3' end.//5.6e-88:49
5:92//L02897
R-PLACE2000223
R-PLACE2000235//HS_3159_B1_B06_T7 CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3159 Col=11 Row=D, genomic survey

sequence.//1.8e-88:454:96//AQ179271

R-PLACE2000246//Homo sapiens chromosome 3p clone RPC14-544D10, WORKING DRAFT SEQUENCE, 58 unordered pieces.//9.1e-41:282:86//AC005902

R-PLACE2000264//Homo sapiens DNA sequence from PAC 95C20 on chromosome X p11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//8.3e-35:305:80//Z97181

R-PLACE2000274//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence.//3.5e-18:325:67//AC002394

R-PLACE2000302//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//1.5e-39:287:85//AC003043

R-PLACE2000305//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 169I5, WORKING DRAFT SEQUENCE.//1.2e-43:295:85//Z93015

R-PLACE2000317//Human DNA sequence from clone 245G19 on chromosome Xp22.11-22.2 Contains serine-threonine kinase (Tsp3) gene, a pseudogene similar to ALPHA-1 PROTEIN ((CONNEXIN 43, CX43, GAP JUNCTION 43 KD HEART PROTEIN)), and the 3' end of the RS1 (X-linked juvenile retinoschisis precursor protein) gene. Contains ESTs, STSs and GSSs, complete sequence.//4.0e-05:284:65//Z92542

R-PLACE2000335//Homo sapiens clone DJ0755D09, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.5e-26:334:70//AC006147

R-PLACE2000342//Fugu rubripes cosmid 258N02 containing IGFII, TH, NAP2 genes.//4.0e-05:254:64//AL021880

R-PLACE2000347//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 799N4, WORKING DRAFT SEQUENCE.//1.6e-82:504:88//AL022147

R-PLACE2000359//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 40E16, WORKING DRAFT SEQUENCE.//2.0e-36:314:80//AL031963

R-PLACE2000366//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 796F18, WORKING DRAFT SEQUENCE.//2.0e-48:389:80//AL031291

R-PLACE2000371

R-PLACE2000373//Human DNA, sequence *** SEQUENCING IN PROGRESS *** from clone 324M8, WORKING DRAFT SEQUENCE.//0.61:231:61//AL008734

R-PLACE2000379//Homo sapiens clone DJ0892G19, complete sequence.//3.5e-11:287:67//AC004917

R-PLACE2000394//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete sequence.//6.8e-108:553:96//AL031432

R-PLACE2000398//Homo sapiens clone RG074A24, WORKING DRAFT SEQUENCE, 25 unordered pieces.//2.9e-26:326:73//AC005059

R-PLACE2000399

R-PLACE2000404//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//6.5e-84:434:96//AC005216

R-PLACE2000411//P.clarkii mRNA; repeat region (ID 2R).//0.47:104:70//Z54273

R-PLACE2000419

R-PLACE2000425//Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions.//1.9e-40:447:74//AF003528

R-PLACE2000427

R-PLACE2000433//Human Chromosome 15 pac pDJ24m8, complete sequence.//3.5e-40:286:85//AC000379

R-PLACE2000435

R-PLACE2000438//Homo sapiens full length insert cDNA clone ZE04D01.//2.2e-107:523:98//AF086521

R-PLACE2000450

4.1e-42:328:79//AG006257

R-PLACE2000455

R-PLACE2000458//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//5.1e-116:570:97//AC005740

R-PLACE2000465//Human BAC clone RG191D16, complete sequence.//6.3e-37:40
8:75//AC002460

R-PLACE2000477//M.musculus tex264 mRNA (3' region).//7.5e-06:117:76//X804
27

R-PLACE3000004

R-PLACE3000029//Human DNA sequence from PAC 506G2 contains STSs and a Cp
G island.//5.8e-34:308:78//Z82976

R-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//1.1
e-36:273:87//Y17267

R-PLACE3000070//Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148),
complete sequence.//2.3e-10:181:71//AC004648

R-PLACE3000103//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 30A23, WORKING DRAFT SEQUENCE.//1.2e-48:495:74//AL022156

R-PLACE3000119//Homo sapiens Chromosome 22q12 BAC Clone 58b8 In Meningio
ma Deletion Region, complete sequence.//3.4e-39:283:85//AC000026

R-PLACE3000124//Homo sapiens chromosome 5, P1 clone 793c5 (LBNL H57), co
mplete sequence.//9.2e-23:171:76//AC005200

R-PLACE3000136//U.arctos microsatellite DNA, clone UarMU23.//0.00052:171
:65//Y09645

R-PLACE3000142//HS_3037_B2_B02_MR CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3037 Col=4 Row=D, genomic survey s
equence.//0.88:121:66//AQ097023

R-PLACE3000147//Mus musculus DNA for ADAMTS-1, complete cds.//3.3e-23:47
2:66//AB001735

R-PLACE3000148//Human DNA from cosmid L27h9, Huntington's Disease Region
, chromosome 4p16.3 contains CpG island.//3.5e-11:176:73//Z49237

R-PLACE3000155//Homo sapiens chromosome 17, clone hRPK.597_M_12, complet
e sequence.//6.9e-106:549:94//AC005277

R-PLACE3000156//Homo sapiens BAC clone RG067E13 from 7q21, complete sequ

ence.//7.0e-38:545:70//AC002383
R-PLACE3000157
R-PLACE3000158//, complete sequence.//1.4e-33:283:81//AC005500
R-PLACE3000160
R-PLACE3000169//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete se
quence.//5.2e-43:229:85//AC006130
R-PLACE3000194
R-PLACE3000197//Homo sapiens chromosome 17, clone hRPK.401_0_9, complete
sequence.//7.2e-61:394:89//AC005291
R-PLACE3000199//Homo sapiens Xq28 genomic DNA in the region of the L1CAM
locus containing the genes for neural cell adhesion molecule L1 (L1CAM)
, arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyltran
sferase related protein (TE2), renin-binding protein (RbP), host cell fa
ctor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes
, complete cds, and Xq28lu2 gene.//0.23:309:57//U52112
R-PLACE3000207//CIT-HSP-384B14.TR CIT-HSP Homo sapiens genomic clone 384
B14, genomic survey sequence.//1.1e-15:156:81//B54637
R-PLACE3000208//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 591N18, WORKING DRAFT SEQUENCE.//1.3e-16:139:87//AL031594
R-PLACE3000218//HS_3185_B1_B01_T7 CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3185 Col=1 Row=D, genomic survey s
equence.//3.5e-07:120:75//AQ155720
R-PLACE3000220//Homo sapiens chromosome 17, clone HRPC1096F1, complete s
equence.//2.4e-44:363:80//AC004167
R-PLACE3000226//Caenorhabditis elegans cosmid M01G5.//0.88:95:77//AF0787
86
R-PLACE3000230//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and
ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, pa
rtial cds, complete sequence.//5.3e-69:536:81//U95626

R-PLACE3000242//Sequence 1 from patent US 5599918.//3.2e-62:546:78//I354
89

R-PLACE3000244//M.musculus mRNA for 200 kD protein.//1.7e-45:404:75//X80
169

R-PLACE3000254//Human mRNA for KIAA0309 gene, partial cds.//7.5e-28:174:
94//AB002307

R-PLACE3000271//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 423B22, WORKING DRAFT SEQUENCE.//3.9e-54:492:77//AL034379

R-PLACE3000276//Homo sapiens PAC clone DJ0320J15 from Xq23, complete seq
uence.//5.4e-12:176:69//AC004081

R-PLACE3000304//Homo sapiens chromosome 19, cosmid R26660, complete sequ
ence.//5.7e-114:555:97//AC005328

R-PLACE3000310//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 467L1, WORKING DRAFT SEQUENCE.//6.2e-51:314:84//Z98884

R-PLACE3000320//Homo sapiens elastin gene, exons 5-27 and alternatively
spliced products, partial cds.//2.5e-44:289:90//U93037

R-PLACE3000322//Human argininosuccinate lyase (ASL) gene, exon 3.//5.9e-
20:153:88//M21006

R-PLACE3000331//Homo sapiens clone DJ0592G07, WORKING DRAFT SEQUENCE, 3
unordered pieces.//1.1e-43:230:84//AC005480

R-PLACE3000339

R-PLACE3000341//Homo sapiens 3p22 Contig 7 PAC RPC14-672N11 (Roswell Par
k Cancer Institute Human PAC Library) complete sequence.//2.5e-111:550:9
7//AC006055

R-PLACE3000350//Human DNA sequence from clone 243E7 on chromosome 22q12.
1. Contains ESTs, STSs and GSSs, complete sequence.//1.5e-44:314:78//AL0
22323

R-PLACE3000352//HS_3095_B1_E09_MR CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3095 Col=17 Row=J, genomic survey

sequence.//8.5e-73:356:99//AQ123142

R-PLACE3000353//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS **
* from clone Y22F5, WORKING DRAFT SEQUENCE.//0.21:194:63//Z99712

R-PLACE3000362//Plasmodium falciparum coronin gene, isolate 3D7.//0.26:3
60:60//AJ002197

R-PLACE3000363

R-PLACE3000365//Human BAC clone RG343P13 from 7q31, complete sequence.//
4.6e-52:487:76//AC002465

R-PLACE3000373//HS_3202_B1_G05_T7 CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3202 Col=9 Row=N, genomic survey s
equence.//2.4e-75:437:90//AQ252699

R-PLACE3000388//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 732E4, WORKING DRAFT SEQUENCE.//6.4e-61:515:81//AL008722

R-PLACE3000399//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6
unordered pieces.//0.00098:444:60//AC005231

R-PLACE3000400//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic
sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.78:155:66//AC0
05506

R-PLACE3000401//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25
unordered pieces.//8.0e-47:223:81//AC006023

R-PLACE3000402//Homo sapiens chromosome 17, clone 104H12, complete seque
nce.//1.0:179:63//AC000003

R-PLACE3000405//Homo sapiens chromosome 7qtelo BAC F6, complete sequence
.//2.4e-44:466:74//AF104455

R-PLACE3000406//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 268H5, WORKING DRAFT SEQUENCE.//7.7e-49:471:75//AL008718

R-PLACE3000413

R-PLACE3000416//Homo sapiens *** SEQUENCING IN PROGRESS *** from PAC 157
7, WORKING DRAFT SEQUENCE.//5.4e-42:416:77//AJ009612

R-PLACE3000425//Human DNA sequence from PAC 130G2 on chromosome 6p22.2-2
2.3. Contains ribosomal protein L29 pseudogene, ESTs and STSS.//1.1e-41:
366:78//AL008627

R-PLACE3000455//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 469D22, WORKING DRAFT SEQUENCE.//3.8e-98:549:92//AL031284

R-PLACE3000475//Human signal transducing adaptor molecule STAM mRNA, com
plete cds.//1.9e-82:440:92//U43899

R-PLACE3000477

R-PLACE4000009//R.norvegicus mRNA encoding 45kDa protein which binds to
heyman nephritis antigen gp330.//6.6e-17:344:68//Z11995

R-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds.//2.
7e-83:433:95//AB018352

R-PLACE4000034//cSRL-51C5-u cSRL flow sorted Chromosome 11 specific cosm
id Homo sapiens genomic clone cSRL-51C5, genomic survey sequence.//0.54:
116:66//B04984

R-PLACE4000049//Human BAC clone GS165I04 from 7q21, complete sequence.//
0.29:313:59//AC002379

R-PLACE4000052//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***
from MAL4P1, WORKING DRAFT SEQUENCE.//0.0058:466:57//AL034557

R-PLACE4000063//Homo sapiens chromosome 7q22 sequence, complete sequence
.//0.98:246:61//AF053356

R-PLACE4000089//RPCI11-15I1.TVB RPCI-11 Homo sapiens genomic clone RPCI-
11-15I1, genomic survey sequence.//3.2e-07:284:60//B82414

R-PLACE4000093//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic
sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.4e-07:429:60//
AC005506

R-PLACE4000100

R-PLACE4000106//Homo sapiens clone 24561 unknown mRNA, partial cds.//9.3
e-100:419:91//AF055010

R-PLACE4000128//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence.//9.6e-45:284:90//AC003007

R-PLACE4000129//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500.//1.6e-19:118:100//AB007969

R-PLACE4000147//Homo sapiens BAC clone NH0342K06 from 2, complete sequence.//8.9e-17:208:73//AC005034

R-PLACE4000156//Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family protein. Contains ESTs, STSs and GSSs, complete sequence.//3.7e-43:281:90//AL021939

R-PLACE4000192

R-PLACE4000222//Homo sapiens clone DJ1129J21, WORKING DRAFT SEQUENCE, 25 unordered pieces.//5.4e-44:280:82//AC005631

R-PLACE4000233//Homo sapiens full length insert cDNA YH59G06.//1.8e-79:414:97//AF074981

R-PLACE4000247//Homo sapiens chromosome 17, clone hRPK.156_L_14, complete sequence.//5.7e-59:558:76//AC005821

R-PLACE4000250//CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey sequence.//1.7e-44:313:84//AQ037381

R-PLACE4000252//Homo sapiens chromosome 17, clone hRPK.700_H_6, complete sequence.//1.5e-39:311:83//AC005920

R-PLACE4000261//H.sapiens BF1P-glH03np gene for immunoglobulin heavy chain in variable region.//0.33:197:61//Z80410

R-PLACE4000269//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//1.4e-31:327:68//AC005510

R-PLACE4000270//Homo sapiens DNA for amyloid precursor protein, complete cds.//2.3e-32:345:74//D87675

R-PLACE4000300//Sequence 61 from patent US 5744300.//0.0017:51:98//AR003

339

R-PLACE4000320//Human DNA sequence from clone 441J1 on chromosome 6p24 C
ontains STS, GSS, complete sequence.//8.2e-41:295:85//Z99495

R-PLACE4000323//Human chromosome 11 187a8 cosmid, complete sequence.//1.
3e-32:404:75//U73640

R-PLACE4000326

R-PLACE4000344//Homo sapiens PAC clone DJ0988G15 from 7q33-q35, complete
sequence.//0.32:135:68//AC005587

R-PLACE4000367//H.sapiens gene encoding RING finger protein.//0.61:146:6
7//Y07829

R-PLACE4000369//HS_3181_A1_B02_MR CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3181 Col=3 Row=C, genomic survey s
equence.//7.1e-80:424:94//AQ173222

R-PLACE4000379//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 1104E15, WORKING DRAFT SEQUENCE.//1.7e-05:160:65//AL022312

R-PLACE4000387//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6
unordered pieces.//2.4e-47:351:81//AC004913

R-PLACE4000392//Human DNA sequence from clone 751H9 on chromosome 6q13.
Contains part of an unknown gene, ESTs, STSs and GSSs, complete sequence
.//8.5e-88:541:88//AL034377

R-PLACE4000401//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ23
9b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//2.7e-17:143:83//AC00
0406

R-PLACE4000411

R-PLACE4000445//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4
unordered pieces.//0.028:91:78//AC005628

R-PLACE4000465//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 30A23, WORKING DRAFT SEQUENCE.//1.6e-43:532:71//AL022156

R-PLACE4000489//Plasmodium falciparum chromosome 2, section 64 of 73 of

the complete sequence.//4.1e-06:357:61//AE001427

R-PLACE4000494//Homo sapiens 12p13.3 PAC RPCI5-1063M23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.7e-37:416:74//AC005865

R-PLACE4000522

R-PLACE4000548//Homo sapiens 12p13.3 PAC RPCI5-1096D14 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.0020:383:60//AC005342

R-PLACE4000558//Homo sapiens 12q24 BAC RPCI11-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//2.9e-44:465:75//AC002996

R-THYRO1000026//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 37E16, WORKING DRAFT SEQUENCE.//2.2e-43:354:82//Z83844

R-THYRO1000034//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence.//0.022:327:60//AE001422

R-THYRO1000035//HS_3018_B2_F10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=20 Row=L, genomic survey sequence.//2.3e-36:228:91//AQ092318

R-THYRO1000040//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.0:367:56//AC004157

R-THYRO1000070//***ALU WARNING: Human Alu-Sq subfamily consensus sequence.//1.1e-44:284:89//U14573

R-THYRO1000072//***ALU WARNING: Human Alu-J subfamily consensus sequence.//6.6e-33:150:83//U14567

R-THYRO1000085

R-THYRO1000092//Homo sapiens chromosome 7qtelo BAC F6, complete sequence.//3.3e-36:301:78//AF104455

R-THYRO1000107//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c

lone 125I3, WORKING DRAFT SEQUENCE.//1.4e-35:282:82//AL033528
R-THYR01000111//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10,
complete sequence.//4.0e-32:351:65//AC002300
R-THYR01000121//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete
sequence.//6.6e-77:507:85//U91318
R-THYR01000124//High throughput sequencing of human chromosome 12, WORKI
NG DRAFT SEQUENCE, 1 ordered pieces.//0.66:334:59//AC005840
R-THYR01000129//Homo sapiens TED protein (TED) mRNA, complete cds.//2.3e
-88:449:96//AF087142
R-THYR01000132//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 212A2, WORKING DRAFT SEQUENCE.//1.1e-40:298:84//Z95114
R-THYR01000156//Homo sapiens chromosome 17, clone hRPK.849_N_15, complet
e sequence.//3.4e-37:425:73//AC005703
R-THYR01000163//RPCI11-1B20.TVB RPCI-11 Homo sapiens genomic clone RPCI-
11-1B20, genomic survey sequence.//8.4e-38:276:84//B63536
R-THYR01000173//Human DNA sequence from PAC 323B6 on chromosome X contai
ns ESTs CpG island.//1.1e-70:553:81//Z83841
R-THYR01000186//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 410I8, WORKING DRAFT SEQUENCE.//6.7e-41:345:81//AL031732
R-THYR01000187//Human thymopoietin (TMPO) gene, partial exon 6, complete
exon 7, partial exon 8, and partial cds for thymopoietin beta.//1.3e-43
:356:80//U18271
R-THYR01000190//Homo sapiens chromosome 17, clone HRPC843B9, complete se
quence.//2.6e-40:386:77//AC004139
R-THYR01000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//1.
1e-108:535:97//AJ005698
R-THYR01000199//Homo sapiens mRNA for KIAA0652 protein; complete cds.//1
.4e-113:559:97//AB014552
R-THYR01000206//Rat PMSG-induced ovarian mRNA, 3' sequence, N4.//4.0e-43:

318:86//D84482

R-THYRO1000221//Human DNA from overlapping chromosome 19 cosmids R31396, F25451, and R31076 containing COX6B and UPKA, genomic sequence, complete sequence.//2.7e-44:452:76//AC002115

R-THYRO1000241//Homo sapiens Cosmid Clone p129d11 unknown chromosomal location, complete sequence.//4.8e-58:447:81//AC000039

R-THYRO1000242

R-THYRO1000253//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//3.4e-56:300:84//Z95152

R-THYRO1000270

R-THYRO1000279//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 531H16, WORKING DRAFT SEQUENCE.//4.8e-113:584:96//AL031664

R-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//1.1e-98:566:91//AB016068

R-THYRO1000320//HS_2033_B1_A07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=13 Row=B, genomic survey sequence.//0.97:211:63//AQ233366

R-THYRO1000327//Sequence 1 from patent US 5541298.//2.8e-52:289:93//I24058

R-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//1.1e-111:559:96//AB018333

R-THYRO1000358//Human selenium-binding protein (hsBP) mRNA, complete cds.//4.6e-47:317:87//U29091

R-THYRO1000368//HS_3049_A1_E12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3049 Col=23 Row=I, genomic survey sequence.//7.0e-11:111:83//AQ126777

R-THYRO1000381

R-THYRO1000387//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//2.4e-101:545:93//AC006019

R-THYRO1000394//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.6e-46:233:88//AC006078

R-THYRO1000395//Mouse MIPP mRNA for a placenta-expressed gene.//2.3e-57:395:85//X58523

R-THYRO1000401

3.3e-111:546:97//AF051907

R-THYRO1000438//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.7e-44:289:89//AC005231

R-THYRO1000452//Homo sapiens chromosome 17, clone hRPK.243_K_12, complete sequence.//6.7e-27:222:82//AC005668

R-THYRO1000471//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 102D24, WORKING DRAFT SEQUENCE.//2.4e-36:369:76//AL021391

R-THYRO1000484//Homo sapiens clone DJ1099N07, complete sequence.//1.6e-43:288:81//AC004962

R-THYRO1000488//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//1.6e-95:512:94//AC005740

R-THYRO1000501//HS_2208_A1_G11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=21 Row=M, genomic survey sequence.//0.0063:189:63//AQ091586

R-THYRO1000502//Homo sapiens eIF-1A, Y isoform (EIF1AY) mRNA, complete cds.//0.19:468:60//AF000987

R-THYRO1000505//Homo sapiens chromosome 19, cosmid R31546, complete sequence.//0.20:214:58//AC004798

R-THYRO1000558

R-THYRO1000569

R-THYRO1000570//Homo sapiens full length insert cDNA clone ZD76G10.//4.3
e-41:209:100//AF086408

R-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete
cds.//8.2e-107:533:97//AF075587

R-THYRO1000596//Mus musculus mitochondrial DNA polymerase accessory subu
nit (MtPolB) mRNA, nuclear gene encoding mitochondrial protein, partial
cds.//0.36:170:67//AF006072

R-THYRO1000602//Homo sapiens DNA for amyloid precursor protein, complete
cds.//2.2e-53:289:92//D87675

R-THYRO1000605

R-THYRO1000625//Homo sapiens chromosome 19, cosmid R29425, complete sequ
ence.//1.3e-31:261:82//AC005546

R-THYRO1000637//Human DNA sequence from clone 243E7 on chromosome 22q12.
1. Contains ESTs, STSs and GSSs, complete sequence.//4.0e-06:249:63//AL0
22323

R-THYRO1000641//P.falciparum glutamic acid-rich protein gnen, complete c
ds.//3.1e-08:244:68//J03998

R-THYRO1000658//***ALU WARNING: Human Alu-Sp subfamily consensus sequenc
e.//3.9e-49:282:93//U14572

R-THYRO1000662

R-THYRO1000666//Homo sapiens DNA sequence from PAC 329E20 on chromosome
1p34.4-36.13. Contains endothelin-converting-enzyme 1 (ECE-1), EST, STS,
CA repeat, complete sequence.//1.9e-20:215:77//AL031005

R-THYRO1000676//Homo sapiens chromosome 4 clone B71M12 map 4q25, complet
e sequence.//1.2e-06:227:64//AC004069

R-THYRO1000684

R-THYRO1000699

R-THYRO1000712

R-THYRO1000734//Human BAC clone RG191D16, complete sequence.//3.7e-14:46

8:64//AC002460
R-THYRO1000748//Homo sapiens cosmid 123E15, complete sequence.//2.6e-11:
182:73//AF024533
R-THYRO1000756//Sequence 21 from patent US 5552281.//1.4e-15:106:98//I25
660
R-THYRO1000777//Plasmodium falciparum MAL3P2, complete sequence.//1.0:17
5:66//AL034558
R-THYRO1000783//CIT-HSP-2335P6.TF CIT-HSP Homo sapiens genomic clone 233
5P6, genomic survey sequence.//1.2e-81:391:99//AQ038226
R-THYRO1000787//Homo sapiens chromosome Y, clone 264,M,20, complete sequ
ence.//9.4e-07:494:58//AC004617
R-THYRO1000793
R-THYRO1000796//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 167P19, WORKING DRAFT SEQUENCE.//1.7e-42:379:79//Z93014
R-THYRO1000805//Human Chromosome 11 pac pDJ610i20, WORKING DRAFT SEQUENC
E, 18 unordered pieces.//4.7e-40:362:76//AC002555
R-THYRO1000815//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 316D5, WORKING DRAFT SEQUENCE.//4.0e-58:295:92//Z82199
R-THYRO1000829//Sequence 7 from patent US 5716622.//0.97:362:61//I87788
R-THYRO1000843//Homo sapiens Chromosome 15q11-q13 PAC clone pDJ351h23 fr
om the Prader-Willi/Angelman Syndrome region, complete sequence.//3.3e-5
7:522:76//AC004738
R-THYRO1000852//Homo sapiens chromosome 11 clone CIT-HSP-1337H24, WORKIN
G DRAFT SEQUENCE, 9 unordered pieces.//4.2e-17:291:69//AC005849
R-THYRO1000855//Human DNA sequence from clone 366B10 on chromosome 22q12
.2-12.3. Contains GSSs, complete sequence.//1.1e-41:419:75//AL031592
R-THYRO1000865//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 1125A11, WORKING DRAFT SEQUENCE.//9.0e-47:294:84//AL034549
R-THYRO1000895//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c

lone 380F5, WORKING DRAFT SEQUENCE.//3.7e-111:569:96//AL031719

R-THYRO1000916//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.0e-97:554:92//AC006015

R-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//9.6e-109:566:94//AF079529

R-THYRO1000934//Homo sapiens full length insert cDNA clone ZD69A10.//1.6e-104:539:95//AF086378

R-THYRO1000951//Homo sapiens Chromosome 11q12 pac pDJ57114, WORKING DRAFT SEQUENCE, 29 unordered pieces.//8.9e-61:479:81//AC004229

R-THYRO1000952//Human autoimmune thyroid disease-related antigen mRNA.//5.3e-16:116:93//M28639

R-THYRO1000974//Homo sapiens ribosomal protein L33-like protein mRNA, complete cds.//3.2e-59:321:95//AF047440

R-THYRO1000975//Homo sapiens chromosome 19, cosmid F18718, complete sequence.//1.9e-44:396:79//AC006126

R-THYRO1000983//Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence.//0.99:71:78//AC005562

R-THYRO1000984//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//6.7e-42:320:84//AC006078

R-THYRO1000988//Homo sapiens DNA sequence from PAC 230G1 on chromosome X p11.3. Contains EST, STS and GSS, complete sequence.//6.7e-39:292:78//Z84466

R-THYRO1001003//HS_3051_B1_H01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=P, genomic survey sequence.//2.5e-39:310:83//AQ253727

R-THYRO1001031//Homo sapiens DNA sequence from PAC 230G1 on chromosome X p11.3. Contains EST, STS and GSS, complete sequence.//2.5e-50:300:88//Z84466

R-THYRO1001033//CIT-HSP-2007J14.TF CIT-HSP Homo sapiens genomic clone 20
07J14, genomic survey sequence.//5.1e-26:143:100//B56677

R-THYRO1001062//CIT-HSP-2386P3.TF.1 CIT-HSP Homo sapiens genomic clone 2
386P3, genomic survey sequence.//1.4e-48:316:87//AQ239882

R-THYRO1001093

R-THYRO1001100//Homo sapiens BAC clone RG152G17 from 7q22-q31.1, complet
e sequence.//0.47:102:73//AC005070

R-THYRO1001120

R-THYRO1001121//Homo sapiens mRNA for beta-tubulin folding cofactor D.//
8.9e-81:429:94//AJ006417

R-THYRO1001133//CIT-HSP-2381I10.TR CIT-HSP Homo sapiens genomic clone 23
81I10, genomic survey sequence.//4.7e-12:237:67//AQ111077

R-THYRO1001134

R-THYRO1001142//H.sapiens CpG island DNA genomic MseI fragment, clone 81
d1, reverse read cpg81d1.rt1a.//0.95:214:60//Z56037

R-THYRO1001173//cSRL-27c11-u cSRL flow sorted Chromosome 11 specific cos
mid Homo sapiens genomic clone cSRL-27c11, genomic survey sequence.//4.6
e-26:262:77//B04145

R-THYRO1001177

R-THYRO1001189//Homo sapiens DNA from chromosome 19, BAC 33152, complete
sequence.//1.0e-41:281:87//AC003973

R-THYRO1001204

R-THYRO1001213//Human Alu repeat sequence A6.//3.8e-38:236:88//U12581

R-THYRO1001262//Homo sapiens, clone hRPK.16_A_1, complete sequence.//8.7
e-53:442:79//AC006227

R-THYRO1001271//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4
, BAC clone C0224P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 13 unordered
pieces.//0.53:330:61//AC004630

R-THYRO1001290

R-THYRO1001313//H.sapiens CpG island DNA genomic MseI fragment, clone 195h3, forward read cpg195h3.ft1b.//0.046:126:66//Z57783

R-THYRO1001320//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING DRAFT SEQUENCE.//3.0e-58:476:80//Z82207

R-THYRO1001321//Plasmodium falciparum MAL3P2, complete sequence.//1.0e-08:408:62//AL034558

R-THYRO1001322

R-THYRO1001347//Homo sapiens mRNA for KIAA0745 protein, partial cds.//3.2e-08:266:64//AB018288

R-THYRO1001363//cSRL-72f5-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-72f5, genomic survey sequence.//1.7e-85:471:92//B05884

R-THYRO1001365//Homo sapiens chromosome 10 clone CIT987SK-1163G10 map 10q25, complete sequence.//1.8e-109:584:94//AC005660

R-THYRO1001374

R-THYRO1001401//Human pigment epithelium-derived factor gene, complete cds.//4.2e-51:333:88//U29953

R-THYRO1001403//Human PAC clone DJ222H05 from Xq25-q26, complete sequence.//8.7e-38:307:82//AC002377

R-THYRO1001405

R-THYRO1001406//RPCI11-69F22.TK RPCI11 Homo sapiens genomic clone R-69F22, genomic survey sequence.//1.9e-67:400:90//AQ238297

R-THYRO1001411//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 80N2, WORKING DRAFT SEQUENCE.//2.2e-06:349:63//AL031123

R-THYRO1001426//*** SEQUENCING IN PROGRESS *** Homo sapiens genomic DNA (PAC 1118i22) from chromosome 11; HTGS phase 1, WORKING DRAFT SEQUENCE.//2.2e-89:506:86//AJ002553

R-THYRO1001434//Microcentus caryae 12S mitochondrial ribosomal RNA, small subunit, mitochondrial gene, partial sequence.//1.0:176:61//U77877

R-THYRO1001458//Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GS S, CpG island, complete sequence.//3.3e-07:196:67//AL021578

R-THYRO1001480//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.2e-99:517:95//AC006001

R-THYRO1001487//Homo sapiens, WORKING DRAFT SEQUENCE, 97 unordered pieces.//8.5e-14:221:70//AC004085

R-THYRO1001534//HS_2242_B2_H04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=8 Row=P, genomic survey sequence.//0.00012:141:68//AQ182326

R-THYRO1001537//Human DNA sequence from clone 111F4 on chromosome Xq23 C contains GSSs, complete sequence.//0.42:323:60//AL023876

R-THYRO1001541//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.7e-42:370:78//AC005077

R-THYRO1001559//Homo sapiens 12q24.2 PAC RPCI5-944M2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0:144:67//AC005868

R-THYRO1001570//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.43:268:61//AC005308

R-THYRO1001573//M.avium rpsL gene.//0.98:131:66//X80120

R-THYRO1001584//A.longa plastid genes for ribosomal proteins and tRNAs.//0.29:502:58//X75653

R-THYRO1001595//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//1.5e-33:319:78//AL023808

R-THYRO1001602//Homo sapiens chromosome 17, clone hRPK.142_H_19, complete sequence.//4.4e-13:320:67//AC005919

R-THYRO1001605//Human DNA sequence from PAC 358H7 on chromosome X.//1.9e-32:391:76//Z77249

R-THYRO1001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT).//1.9e-81:448:92//AJ002190

R-THYRO1001637//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 688G8, WORKING DRAFT SEQUENCE.//5.4e-41:381:78//AL031671

R-THYRO1001656//HS_2201_B2_A08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2201 Col=16 Row=B, genomic survey sequence.//0.096:162:63//AQ293168

R-THYRO1001661//Human immunoglobulin-associated (B29) gene, promoter and exon 1, partial cds.//1.0:229:62//U22954

R-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//4.8e-110:562:95//AJ225089

R-THYRO1001673//CIT-HSP-2327D12.TR CIT-HSP Homo sapiens genomic clone 2327D12, genomic survey sequence.//1.5e-17:224:68//AQ042426

R-THYRO1001703//Homo sapiens clone 198 unknown mRNA, partial sequence.//1.6e-44:251:93//AF091072

R-THYRO1001706//Homo sapiens clone DJ0935K16, complete sequence.//1.8e-26:378:68//AC006011

R-THYRO1001721//, complete sequence.//1.3e-101:571:92//AC005500

R-THYRO1001738

R-THYRO1001745//Homo sapiens chromosome 5, PAC clone 247f3 (LBNL H85), complete sequence.//1.1e-15:193:70//AC004777

R-THYRO1001746//Human inter-alpha-trypsin inhibitor light chain (ITI) gene, exon 3.//0.54:260:61//M88244

R-THYRO1001772//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30A23, WORKING DRAFT SEQUENCE.//1.6e-12:285:64//AL022156

R-THYRO1001793

R-THYRO1001809//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1071N3, WORKING DRAFT SEQUENCE.//2.5e-43:486:74//AL031728

R-THYRO1001854//Homo sapiens chromosome 17, clone hRPK.74_E_22, complet

e sequence.//5.0e-41:245:87//AC005696

R-THYR01001895//Human Chromosome 11p14.3 PAC clone 6-106f23, complete sequence.//4.4e-12:419:61//AC005137

R-THYR01001907//Homo sapiens Chromosome 22q11.2 Cosmid Clone 24b In DGCR Region, complete sequence.//8.1e-35:340:78//AC000075

R-VESEN1000122//Homo sapiens Luman mRNA, complete cds.//1.3e-23:138:98//AF009368

R-Y79AA1000013

R-Y79AA1000033//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete sequence.//9.9e-112:551:97//AC006027

R-Y79AA1000037//CIT-HSP-2334F3.TR CIT-HSP Homo sapiens genomic clone 233 4F3, genomic survey sequence.//0.16:308:60//AQ036673

R-Y79AA1000059//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//6.1e-56:314:88//AC002300

R-Y79AA1000065//Human carboxylesterase gene, exon 5.//0.64:203:63//D21079

R-Y79AA1000131//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4 , BAC clone C0548N01: HTGS phase 1, WORKING DRAFT SEQUENCE, 31 unordered pieces.//7.0e-18:169:79//AC004795

R-Y79AA1000181//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//1.1e-106:474:98//AL031864

R-Y79AA1000202//CIT978SK-A-518G2.TP CIT978SK Homo sapiens genomic clone A-518G2, genomic survey sequence.//1.0e-10:78:97//B68074

R-Y79AA1000214//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//6.5e-59:386:90//AC004854

R-Y79AA1000230//Cytauxzoon felis 18S ribosomal RNA.//1.0:167:62//L19080

R-Y79AA1000231//HS_3009_A1_H03_T7 CIT Approved Human Genomic Sperm Libra

ry D Homo sapiens genomic clone Plate=3009 Col=5 Row=0, genomic survey s
equence.//6.4e-52:348:88//AQ090225

R-Y79AA1000258//Hepatitis C virus HCV-B9 gene for NS5, partial cds.//0.6
5:127:65//D10558

R-Y79AA1000268//Human DNA sequence from PAC 162H14 on chromosome 22. Con
tains 3' part of a FIBULIN 1 like gene and ESTs, complete sequence.//4.7
e-40:300:84//Z98047

R-Y79AA1000313//Human DNA sequence from PAC 179I15, BRCA2 gene region ch
romosome 13q12-q13 contains Klotho ESTs and CpG island.//5.0e-14:136:83/
/Z92540

R-Y79AA1000328

R-Y79AA1000342//S.clavuligerus linear plasmid pSCL (complete sequence)./
/0.55:189:65//X54107

R-Y79AA1000346//Human MEST mRNA, complete cds.//0.00013:52:100//D78611

R-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//8.8e-36:3
00:81//X84692

R-Y79AA1000355//Human DNA sequence from clone 551E13 on chromosome Xp11.
2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protei
n pseudogene, EST, GSS, complete sequence.//5.7e-45:403:80//AL022163

R-Y79AA1000368

R-Y79AA1000405//RPCI11-16B12.TPB RPCI-11 Homo sapiens genomic clone RPCI
-11-16B12; genomic survey sequence.//0.10:171:65//B88000

R-Y79AA1000410//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 92N15, WORKING DRAFT SEQUENCE.//4.1e-50:361:83//Z93097

R-Y79AA1000420//Plasmodium falciparum merozoite surface protein 4, merozo
ite surface protein 5, merozoite surface protein 2, and adenylosuccinat
e lyase genes, complete cds.//0.071:474:57//AF033037

R-Y79AA1000469//Homo sapiens clone NH0140K04, complete sequence.//1.8e-8
6:221:90//AC005033

R-Y79AA1000480//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//2.1e-14:179:72//AC004057

R-Y79AA1000538//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.//4.5e-43:321:83//AC005282

R-Y79AA1000539//Homo sapiens PAC clone DJ0074M20 from X, complete sequence.//0.0012:275:59//AC006143

R-Y79AA1000540//Z.diploperennis repetitive DNA (clone ZEAR 260).//0.0017:258:62//X53609

R-Y79AA1000560//Mouse mRNA for alpha-adaptin (C).//6.1e-32:390:70//X14972

R-Y79AA1000574//Homo sapiens chromosome 9q34, clone 23B4, complete sequence.//0.96:224:61//AC002325

R-Y79AA1000627//Homo sapiens full length insert cDNA ZA77G02.//6.3e-100:533:94//AF075117

R-Y79AA1000705//RPCI11-76G7.TV RPCI11 Homo sapiens genomic clone R-76G7, genomic survey sequence.//4.6e-88:429:98//AQ268433

R-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds.//2.7e-112:586:95//AF093670

R-Y79AA1000748

R-Y79AA1000752

R-Y79AA1000774//CIT-HSP-2288K24.TF CIT-HSP Homo sapiens genomic clone 2288K24, genomic survey sequence.//5.3e-45:316:86//AQ005014

R-Y79AA1000782//Human mRNA for KIAA0246 gene, partial cds.//5.0e-17:107:100//D87433

R-Y79AA1000784//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00034:520:55//AC005505

R-Y79AA1000794//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 989H11, WORKING DRAFT SEQUENCE.//0.015:322:60//Z83851

R-Y79AA1000800//M.musculus tex264 mRNA (3' region).//1.1e-06:104:78//X804
27

R-Y79AA1000802//CIT-HSP-2295G6.TF CIT-HSP Homo sapiens genomic clone 229
5G6, genomic survey sequence.//0.67:152:62//AQ007605

R-Y79AA1000805//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.
//3.1e-26:423:68//U73642

R-Y79AA1000824//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 329A5, WORKING DRAFT SEQUENCE.//1.1e-08:449:61//Z97832

R-Y79AA1000827//Triticum aestivum heat shock protein 101 kDa (HSP101) mR
NA, complete cds.//1.0:101:69//AF083344

R-Y79AA1000850//Homo sapiens small optic lobes homolog (SOLH) mRNA, comp
lete cds.//0.40:386:59//U85647

R-Y79AA1000962//CIT-HSP-2298N11.TR CIT-HSP Homo sapiens genomic clone 22
98N11, genomic survey sequence.//0.00019:253:65//AQ013111

R-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit
(eIF-2B gamma) mRNA, complete cds.//1.7e-58:446:80//U38253

R-Y79AA1000969

R-Y79AA1000976//CIT-HSP-2350C4.TF CIT-HSP Homo sapiens genomic clone 235
0C4, genomic survey sequence.//3.3e-60:295:100//AQ061422

R-Y79AA1000985//Mus musculus pericentrin mRNA, complete cds.//5.9e-38:34
8:76//U05823

R-Y79AA1001023

R-Y79AA1001041

R-Y79AA1001048

R-Y79AA1001061//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-427H10,
complete sequence.//1.2e-60:537:78//AC004626

R-Y79AA1001068//Homo sapiens P1 clone GSP13996 from 5q12, complete seque
nce.//2.3e-41:405:77//AC005031

R-Y79AA1001077

R-Y79AA1001078//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.0e-09:534:59//AC004801

R-Y79AA1001105//Staphylococcus epidermidis trimethoprim resistance plasmid pSK639.//0.0072:309:63//U40259

R-Y79AA1001145//RPCI11-59N12.TK RPCI11 Homo sapiens genomic clone R-59N12, genomic survey sequence.//3.7e-07:256:64//AQ200068

R-Y79AA1001167//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 5/15, WORKING DRAFT SEQUENCE.//0.55:223:61//AP000012

R-Y79AA1001177//Human gene for Gi3 alpha protein, intron 7 through exon 9, variant U6 gene, and snRNP E protein pseudogene LH87.//7.0e-09:203:69//X54048

R-Y79AA1001185

R-Y79AA1001211//Homo sapiens 12p13.3 BAC RPCI11-543P15 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//2.1e-32:277:81//AC005912

R-Y79AA1001216//Human chromosome 12p13 sequence, complete sequence.//0.98:325:59//U47924

R-Y79AA1001228//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone : MAB16, complete sequence.//0.0034:378:59//AB018112

R-Y79AA1001233//Homo sapiens clone DJ1178G13, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.19:106:72//AC004988

R-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc1101133Q7 (RZPD Berlin)).//3.4e-109:549:95//AJ005892

R-Y79AA1001281

R-Y79AA1001299//Homo sapiens SNF5/INI1 gene, exon 9.//6.3e-24:133:100//Y17126

R-Y79AA1001312//Human immunodeficiency virus type 1 variant 43 polymerase pseudogene, partial cds.//0.0070:284:58//U45372

R-Y79AA1001323//Fugu rubripes GSS sequence, clone 027L23aG3, genomic survey sequence.//0.11:125:70//AL025355

R-Y79AA1001384//W.makrii mitochondrial CYTB and tRNA genes.//0.070:209:65//X66594

R-Y79AA1001391//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P2, WORKING DRAFT SEQUENCE.//0.80:163:62//AL031745

R-Y79AA1001394//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//0.99:241:63//AC004221

R-Y79AA1001402//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.25:81:80//AC005924

R-Y79AA1001493

R-Y79AA1001511//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence.//1.3e-35:207:95//AL034430

R-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//2.7e-44:285:81//D14336

R-Y79AA1001541//Human DNA sequence from clone 113J7 on chromosome Xp11.2-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.//0.70:365:60//AL023574

R-Y79AA1001548//Homo sapiens phosphatidylinositol 4-kinase mRNA, complete cds.//5.9e-95:517:91//L36151

R-Y79AA1001555

R-Y79AA1001585

R-Y79AA1001594//Human DNA sequence from PAC 60G11 on chromosome X; contains STS.//6.6e-19:241:76//Z94722

R-Y79AA1001603//H.sapiens CpG island DNA genomic MseI fragment, clone 72 f8, forward read cpg72f8.ft1a.//3.3e-21:131:96//Z62766

R-Y79AA1001613

R-Y79AA1001647//Human DNA sequence from PAC 36J3, between markers DXS119 2 and DXS102 on chromosome X.//6.3e-08:338:63//Z82975

R-Y79AA1001665//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 1/15, WORKING DRAFT SEQUENCE.//3.2e-11:114:84//AP000008

R-Y79AA1001679//O.cuniculus lambda-crystallin mRNA, complete cds.//3.9e-15:270:68//M22743

R-Y79AA1001692//RPCI11-42M5.TJ RPCI11 Homo sapiens genomic clone R-42M5, genomic survey sequence.//0.013:64:89//AQ052792

R-Y79AA1001696//Apis mellifera ligustica complete mitochondrial genome.//9.3e-09:428:58//L06178

R-Y79AA1001705

R-Y79AA1001711//Mus musculus 60 kDa ribonucleoprotein Ro gene, partial cds.//2.2e-45:554:75//AF042139

R-Y79AA1001781//Plasmodium falciparum chromosome 2, section 39 of 73 of the complete sequence.//1.0:414:57//AE001402

R-Y79AA1001805//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 510D11, WORKING DRAFT SEQUENCE.//2.8e-05:329:61//Z98044

R-Y79AA1001827//Oryctolagus cuniculus PiUS mRNA, complete cds.//2.3e-90:557:89//U74297

R-Y79AA1001846//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//2.1e-34:306:78//Z95152

R-Y79AA1001848//Sequence 11 from patent US 5449616.//1.0:221:59//I14369

R-Y79AA1001866//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence.//0.0089:527:58//AB016874

R-Y79AA1001874

R-Y79AA1001875//M.musculus mRNA for Rab7 protein.//5.8e-45:170:92//X8965
0

R-Y79AA1001923//Human DNA sequence from clone 353H6 on chromosome Xq25-2
6.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related
, matrix associated, actin dependent regulator of chromatin, subfamily a
, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains
ESTs, STSs and GSSs, complete sequence.//1.0:138:68//AL022577

R-Y79AA1002027//Liverwort Marchantia polymorpha chloroplast genome DNA./
/0.71:153:67//X04465

R-Y79AA1002083//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 172B20, WORKING DRAFT SEQUENCE.//1.0:178:64//AL022319

R-Y79AA1002089//Homo sapiens clone GS111G14, WORKING DRAFT SEQUENCE, 5 u
nordered pieces.//6.3e-49:377:81//AC005011

R-Y79AA1002093//Homo sapiens (clone SEL366) 17q YAC (368C7) RNA.//4.0e-3
2:174:99//L77612

R-Y79AA1002103//CIT-HSP-2328I21.TR CIT-HSP Homo sapiens genomic clone 23
28I21, genomic survey sequence.//1.9e-44:245:96//AQ044502

R-Y79AA1002115//CITBI-E1-2514F10.TF CITBI-E1 Homo sapiens genomic clone
2514F10, genomic survey sequence.//1.8e-24:249:78//AQ265752

R-Y79AA1002125//RPCI11-15J6.TV RPCI-11 Homo sapiens genomic clone RPCI-1
1-15J6, genomic survey sequence.//8.5e-21:147:91//B75354

R-Y79AA1002139

R-Y79AA1002204

R-Y79AA1002208//Human ankyrin.G (ANK-3) mRNA, complete cds.//0.040:319:5
9//U13616

R-Y79AA1002209//Psilotum nudum RT gene for reverse transcriptase (PT4)./
/0.99:106:65//X65415

R-Y79AA1002210

R-Y79AA1002211//H.sapiens NGAL gene.//1.0:311:59//X99133

R-Y79AA1002220//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***
 from MAL4P1, WORKING DRAFT SEQUENCE.//5.9e-07:535:57//AL034557

R-Y79AA1002229

R-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//6.
 1e-117:564:98//AB014592

R-Y79AA1002246

R-Y79AA1002258//Homo sapiens mRNA for HIP3, complete cds.//1.3e-92:453:9
 7//AB013384

R-Y79AA1002298//HS_3071_B2_E08_MR CIT Approved Human Genomic Sperm Libra
 ry D Homo sapiens genomic clone Plate=3071 Col=16 Row=J, genomic survey
 sequence.//1.9e-56:384:87//AQ171331

R-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds.//2.
 5e-108:403:99//AB014534

R-Y79AA1002311//Homo sapiens chromosome 10 clone CIT987SK-1173I12 map 10
 q25, complete sequence.//1.1e-07:368:61//AC005887

R-Y79AA1002351

R-Y79AA1002361//H.sapiens CpG island DNA genomic MseI fragment, clone 65
 b9, reverse read cpg65b9.rtl.a.//0.57:59:79//Z62206

R-Y79AA1002399//Homo sapiens chromosome 17, clone hRPK.700_H_6, complete
 sequence.//2.0e-98:385:99//AC005920

R-Y79AA1002407//Homo sapiens chromosome 17, clone hRPC.842_A_23, complet
 e sequence.//5.4e-59:490:76//AC004662

R-Y79AA1002416//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC l
 ibrary) complete sequence.//6.3e-08:103:80//AC004087

R-Y79AA1002431

R-Y79AA1002433//Mouse transcriptional control element.//0.064:84:71//M17
 284

R-Y79AA1002472//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323),
 complete sequence.//1.6e-103:525:96//AC006116

R-Y79AA1002482//Homo sapiens chromosome 18, clone hRPK.474_N_24, complete sequence.//9.7e-38:302:83//AC006238

R-Y79AA1002487//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.23:266:61//X95276

【 0 2 9 4 】

5' 末端クローン配列に対するHuman Unigene相同性検索結果データ

各データは、

クローン配列名、

トップヒットデータのTitle、

P値:比較配列の長さ (base):相同性(%)、

トップヒットデータのAccession No.の順に//で区切って記載した。

なお、相同性のスコアのP値が1より大であった場合はデータは示さない。

F-HEMBA1000005//EST//4.3e-87:422:97//Hs.147830:AI222069

F-HEMBA1000012//Human endosome-associated protein (EEA1) mRNA, complete cds//0.82:170:64//Hs.2864:L40157

F-HEMBA1000020//Homo sapiens beta 2 gene//4.0e-74:529:83//Hs.150244:U83668

F-HEMBA1000030//ESTs//1.1e-91:494:93//Hs.7958:W22078

F-HEMBA1000042//ESTs//3.5e-22:228:77//Hs.145406:AI253247

F-HEMBA1000046//ESTs, Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 [Saccharomyces cerevisiae]//0.00019:192:65//Hs.7900:W22411

F-HEMBA1000050//EST//0.81:74:72//Hs.156298:AI336759

F-HEMBA1000076//ESTs//0.11:252:62//Hs.131939:AI417910

F-HEMBA1000111//ESTs//8.5e-89:449:96//Hs.41105:N66734

F-HEMBA1000129//Human phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds//0.27:342:61//Hs.14207:U86453

F-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds//6.8e-169:791:98//Hs.27197:AB018340

F-HEMBA1000150//Homo sapiens mRNA for KIAA0788 protein, partial cds//1.4

e-37:243:88//Hs.2397:Z70200

F-HEMBA1000156//ESTs, Weakly similar to The KIAA0138 gene product is novel. [H.sapiens]//5.3e-80:383:98//Hs.135552:AI215187

F-HEMBA1000158//Homo sapiens OPA-containing protein mRNA, complete cds//2.1e-07:265:63//Hs.85313:AF071309

F-HEMBA1000168//ESTs//6.1e-35:257:85//Hs.13533:H23079

F-HEMBA1000180//ESTs, Moderately similar to RETROVIRUS-RELATED POLYPROTEIN [H.sapiens]//1.3e-18:111:96//Hs.163863:W28729

F-HEMBA1000185//H.sapiens ERF-2 mRNA//1.0:125:68//Hs.78909:U07802

F-HEMBA1000193//EST//1.5e-48:266:95//Hs.160642:AI240133

F-HEMBA1000201//Human In11 mRNA, complete cds//6.5e-75:440:92//Hs.155626:U04847

F-HEMBA1000213//ESTs//0.21:239:62//Hs.26838:AA527529

F-HEMBA1000216//Homo sapiens clone 23698 mRNA sequence//1.1e-57:529:68//Hs.8136:U81984

F-HEMBA1000227//Human RNA-binding protein CUG-BP/hNab50 (NAB50) mRNA, complete cds//1.3e-05:311:64//Hs.81248:U63289

F-HEMBA1000231

F-HEMBA1000243//EST//5.9e-52:359:85//Hs.141433:N23377

F-HEMBA1000244//H.sapiens mRNA for cytokine inducible nuclear protein//0.0022:350:60//Hs.74019:X83703

F-HEMBA1000251//ESTs//3.2e-84:443:95//Hs.21068:N47460

F-HEMBA1000264//ESTs//0.76:227:61//Hs.5159:AA588562

F-HEMBA1000280//EST//1.7e-12:149:75//Hs.103418:AA035568

F-HEMBA1000282//ESTs//1.7e-16:164:79//Hs.123111:AA813186

F-HEMBA1000288//ESTs//5.4e-06:154:68//Hs.54174:N64406

F-HEMBA1000290//Human novel homeobox mRNA for a DNA binding protein//3.8e-07:412:61//Hs.37035:U07664

F-HEMBA1000302//EST//1.2e-41:238:94//Hs.147245:AI206095

F-HEMBA1000303

F-HEMBA1000304//ESTs//3.5e-11:96:87//Hs.163057:AA728946

F-HEMBA1000307//EST//7.7e-05:280:62//Hs.146462:AI124898

F-HEMBA1000327//ESTs//5.3e-92:435:99//Hs.100605:AA305965

F-HEMBA1000333//Human mRNA for KIAA0206 gene, partial cds//0.84:395:56//
Hs.79299:D86961

F-HEMBA1000338//ESTs, Moderately similar to novel stromal cell protein [M.musculus]//2.4e-38:317:80//Hs.99189:X84712

F-HEMBA1000351//Human Line-1 repeat mRNA with 2 open reading frames//0.0
20:334:59//Hs.23094:M19503

F-HEMBA1000355//Myosin, heavy polypeptide 11, smooth muscle//0.11:336:61
//Hs.78344:AF001548

F-HEMBA1000356//H.sapiens ERF-2 mRNA//0.031:317:59//Hs.78909:U07802

F-HEMBA1000357//Human mRNA for KIAA0118 gene, partial cds//1.2e-50:441:7
8//Hs.154326:D42087

F-HEMBA1000366//ESTs//0.025:56:87//Hs.141629:H74010

F-HEMBA1000369//Homo sapiens PAC clone DJ0669B10 from 7q33-q35//0.99:433
:58//Hs.159899:AC004853

F-HEMBA1000376//Oxytocin receptor//3.4e-43:569:70//Hs.2820:X64878

F-HEMBA1000387//ESTs//8.2e-104:535:94//Hs.78110:AA741320

F-HEMBA1000390//Homo sapiens BAC clone RG119C02 from 7p15//2.3e-141:712:
95//Hs.22900:AC004520

F-HEMBA1000392//Homo sapiens clone 24619 mRNA sequence//1.7e-47:461:74//
Hs.139088:AF070533

F-HEMBA1000396//ESTs, Weakly similar to hypothetical protein [H.sapiens]
//1.2e-26:351:70//Hs.138992:C14008

F-HEMBA1000411//EST//2.8e-27:401:71//Hs.138719:N52915

F-HEMBA1000418//ESTs//0.0094:375:61//Hs.40140:AI079253

F-HEMBA1000422//EST//6.2e-23:225:78//Hs.132635:AI032875

F-HEMBA1000428//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0501//7.6e-31:616:66//Hs.159897:AB007970

F-HEMBA1000434//EST//0.0031:157:64//Hs.162328:AA559034

F-HEMBA1000442//EST//1.0:201:61//Hs.162434:AA577398

F-HEMBA1000456//Fanconi anemia complementation group C//0.58:362:59//Hs.
37953:X66893

F-HEMBA1000459//EST//9.2e-21:157:86//Hs.132635:AI032875

F-HEMBA1000460//ESTs//2.9e-77:409:95//Hs.27135:W49590

F-HEMBA1000464//ESTs//6.6e-17:365:65//Hs.150675:AA127853

F-HEMBA1000469

F-HEMBA1000488//Homo sapiens HIV-1 inducer of short transcripts binding
protein (FBI1) mRNA, complete cds//0.15:253:58//Hs.104640:AF000561

F-HEMBA1000490//Homo sapiens kinectin mRNA, complete cds//0.71:539:56//H
s.82709:Z22551

F-HEMBA1000491//ESTs//2.0e-21:361:65//Hs.152453:AA864970

F-HEMBA1000501//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.5e-3
9:312:77//Hs.5247:AF029750

F-HEMBA1000504//Homo sapiens mRNA for osteoblast specific factor 2 (OSF-
2os)//1.3e-08:57:100//Hs.155095:D13666

F-HEMBA1000505//Homo sapiens KE04p mRNA, complete cds//1.0:197:62//Hs.13
1962:AF064093

F-HEMBA1000508//EST//0.67:156:60//Hs.162898:AA659646

F-HEMBA1000518

F-HEMBA1000519//EST//6.8e-52:300:91//Hs.149580:AI281881

F-HEMBA1000520//ESTs, Weakly similar to coded for by C. elegans cDNA CEE
SB82F [C.elegans]//2.9e-16:132:84//Hs.155871:AA533783

F-HEMBA1000523//ESTs, Highly similar to TESTIS-SPECIFIC PROTEIN PBS13 [
Mus musculus]//2.1e-25:192:87//Hs.22383:R51067

F-HEMBA1000531//ESTs, Weakly similar to heat shock protein [H.sapiens]//

2.4e-57:288:97//Hs.116022:AA455706
 F-HEMBA1000534//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.8e-47:15
 3:88//Hs.113283:AF018080
 F-HEMBA1000540//ESTs//8.6e-07:60:100//Hs.109755:AA180809
 F-HEMBA1000542//Human lysyl oxidase-like protein mRNA, complete cds//0.0
 88:581:57//Hs.65436:U24389
 F-HEMBA1000545//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//
 7.8e-106:731:83//Hs.139107:K00629
 F-HEMBA1000555//Human mRNA for KIAA0242 gene, partial cds//0.75:283:58//
 Hs.77495:D87684
 F-HEMBA1000557//ESTs//3.9e-27:389:71//Hs.125087:AA495729
 F-HEMBA1000561//Homo sapiens mRNA for KIAA0760 protein, partial cds//3.8
 e-64:665:72//Hs.137168:AB018303
 F-HEMBA1000563//ESTs//3.8e-51:257:98//Hs.47122:AI338977
 F-HEMBA1000568//EST//0.12:270:61//Hs.134833:AI091046
 F-HEMBA1000569//H.sapiens mRNA encoding GPI-anchored protein p137//3.8e-
 19:409:62//Hs.119283:Z48042
 F-HEMBA1000575//EST//0.060:156:64//Hs.126277:AA826681
 F-HEMBA1000588//ESTs, Weakly similar to weakly similar to myosin heavy c
 hain [C.elegans]//7.7e-41:217:96//Hs.55084:AA479162
 F-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein//2.3e
 -44:228:97//Hs.155218:AJ007509
 F-HEMBA1000592//ESTs, Weakly similar to sorting nexin 1 [H.sapiens]//1.7
 e-27:463:65//Hs.13794:AA203241
 F-HEMBA1000594//Human clone 230971 defective mariner transposon Hsmar2 m
 RNA sequence//4.0e-68:574:79//Hs.159176:U92019
 F-HEMBA1000604//ESTs//3.3e-21:158:74//Hs.142924:AI092535
 F-HEMBA1000608//Homo sapiens mRNA for KIAA0456 protein, partial cds//3.7
 e-120:561:99//Hs.5003:AB007925

F-HEMBA1000622//Homo sapiens DEC-205 mRNA, complete cds//5.2e-34:592:68/
/Hs.153563:AF011333

F-HEMBA1000636//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.col
i]//7.4e-22:166:84//Hs.26252:AA643235

F-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds//2.1
e-138:639:99//Hs.60103:AB014590

F-HEMBA1000655//ESTs//1.2e-54:503:77//Hs.140864:AA176174

F-HEMBA1000657//Mucin 1, transmembrane//0.99:219:61//Hs.89603:J05582

F-HEMBA1000662//ESTs//2.2e-52:257:99//Hs.63243:AI123912

F-HEMBA1000673//H.sapiens mRNA for translin associated protein X//1.7e-4
7:366:79//Hs.96247:X95073

F-HEMBA1000682//Oxytocin receptor//4.7e-59:673:72//Hs.2820:X64878

F-HEMBA1000686

F-HEMBA1000702

F-HEMBA1000705//EST//0.047:363:60//Hs.136379:AA521309

F-HEMBA1000719//ESTs//2.7e-68:333:98//Hs.146195:AI039850

F-HEMBA1000722//ESTs//0.49:283:60//Hs.21108:N92630

F-HEMBA1000726//EST//1.1e-45:183:87//Hs.149580:AI281881

F-HEMBA1000727//ESTs//4.8e-95:442:100//Hs.22119:AA885491

F-HEMBA1000747

F-HEMBA1000749//ESTs//8.0e-14:108:77//Hs.154892:AI091568

F-HEMBA1000752//EST//1.3e-25:344:69//Hs.160992:H52716

F-HEMBA1000769//ESTs//0.0018:206:63//Hs.153268:AA887239

F-HEMBA1000773//ESTs//0.56:336:58//Hs.105964:N35803

F-HEMBA1000774//EST//4.0e-38:312:79//Hs.162197:AA535216

F-HEMBA1000791//ESTs//2.8e-87:413:99//Hs.112050:AA431300

F-HEMBA1000817//ESTs//5.6e-124:617:96//Hs.101366:AA167536

F-HEMBA1000822//ESTs//0.94:347:58//Hs.23905:AA928542

F-HEMBA1000827//EST//0.064:133:60//Hs.138738:N58367

F-HEMBA1000843

F-HEMBA1000851//Fragile X mental retardation 1//0.014:219:62//Hs.89764:X
69962

F-HEMBA1000852//Arylsulfatase D//6.7e-38:244:75//Hs.43887:X83572

F-HEMBA1000867

F-HEMBA1000869//ESTs//5.1e-33:166:77//Hs.141186:R99609

F-HEMBA1000870//EST//0.032:130:66//Hs.157351:AI367237

F-HEMBA1000872//ESTs//2.4e-20:134:92//Hs.155982:AA406047

F-HEMBA1000876//EST//5.3e-20:233:72//Hs.124339:AA829660

F-HEMBA1000908//ESTs//5.4e-28:219:84//Hs.12247:AI203154

F-HEMBA1000910//Human DNA sequence from clone 1409 on chromosome Xp11.1-
11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a
alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6
-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. C
ontains ESTs, STSs and genomic marker DXS8032//2.8e-11:309:65//Hs.4943:Z
98046

F-HEMBA1000918//ESTs//0.11:234:59//Hs.96499:AA252537

F-HEMBA1000919//Human mRNA for histone H1x, complete cds//0.18:221:64//H
s.109804:D64142

F-HEMBA1000934//Homo sapiens mRNA for KIAA0547 protein, complete cds//3.
8e-09:360:62//Hs.36850:AB011119

F-HEMBA1000942//ESTs, Highly similar to PMS4 homolog mismatch repair pro
tein [H.sapiens]//9.4e-10:77:93//Hs.111445:H00596

F-HEMBA1000943//ESTs, Highly similar to ZINC FINGER PROTEIN 10 [Homo sa
piens]//0.0039:54:92//Hs.58338:AA609476

F-HEMBA1000946//Phosphoribosylglycinamide formyltransferase, phosphoribo
sylglycinamide synthetase, phosphoribosylaminoimidazole synthetase//0.93
:132:66//Hs.82285:X54199

F-HEMBA1000960//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNIN

G ENTRY !!!! [H.sapiens]//0.080:128:71//Hs.118972:AA761369
 F-HEMBA1000968//Human transposon-like element mRNA//2.8e-95:352:87//Hs.8
 4775:M23161
 F-HEMBA1000971//ESTs//8.4e-88:417:98//Hs.128631:AI127903
 F-HEMBA1000972//EST//0.75:134:64//Hs.117228:AA682775
 F-HEMBA1000974//ESTs//1.3e-103:497:98//Hs.126786:U74314
 F-HEMBA1000975//Homo sapiens diacylglycerol kinase iota (DGKi) mRNA, com
 plete cds//1.3e-05:424:59//Hs.159564:AF061936
 F-HEMBA1000985//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
 0492//0.0036:389:60//Hs.127338:AB007961
 F-HEMBA1000986//ESTs//0.00025:272:64//Hs.12364:H09132
 F-HEMBA1000991//Homo sapiens mRNA for Hrs, complete cds//3.9e-24:193:84/
 /Hs.24756:U43895
 F-HEMBA1001007//EST//0.96:70:71//Hs.163258:AA828835
 F-HEMBA1001008//Human G protein-coupled receptor (STRL22) mRNA, complete
 cds//4.9e-43:472:74//Hs.46468:U45984
 F-HEMBA1001009//Immunoglobulin mu//0.18:367:59//Hs.75758:X58529
 F-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds//1.
 4e-140:661:98//Hs.158287:AB007937
 F-HEMBA1001019//EST//4.1e-14:251:68//Hs.148769:AI239572
 F-HEMBA1001020//Von Hippel-Lindau syndrome//2.2e-28:253:69//Hs.78160:AF0
 10238
 F-HEMBA1001022
 F-HEMBA1001024//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
 0501//6.8e-28:376:72//Hs.159897:AB007970
 F-HEMBA1001026//Homo sapiens klotho mRNA, complete cds//1.3e-05:745:57//
 Hs.94592:AB005142
 F-HEMBA1001043//ESTs//2.1e-28:448:67//Hs.112469:AA598515
 F-HEMBA1001051//EST//3.1e-48:310:87//Hs.149580:AI281881

F-HEMBA1001052//EST//0.94:149:67//Hs.131216:AI017971
 F-HEMBA1001059//N-ACETYL GALACTOSAMINE-6-SULFATASE PRECURSOR//4.6e-165:77
 7:98//Hs.159479:U06088
 F-HEMBA1001060//ESTs//6.8e-14:150:78//Hs.24821:AA044813
 F-HEMBA1001071//Alpha-1 type 3 collagen//3.5e-32:181:96//Hs.119571:X1442
 0
 F-HEMBA1001077//ESTs, Moderately similar to transcription intermediary f
 actor 1 [H.sapiens]//1.1e-98:487:97//Hs.147802:R71297
 F-HEMBA1001080//Human N-type calcium channel alpha-1 subunit mRNA, compl
 ete cds//0.013:385:58//Hs.69949:M94172
 F-HEMBA1001085//Human hSIAH2 mRNA, complete cds//0.55:338:59//Hs.20191:U
 76248
 F-HEMBA1001088//Human PINCH protein mRNA, complete cds//7.3e-73:303:78//
 Hs.83987:U09284
 F-HEMBA1001094//Interleukin 8//0.092:530:58//Hs.624:M17017
 F-HEMBA1001099
 F-HEMBA1001109//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.4e-6
 1:341:85//Hs.5247:AF029750
 F-HEMBA1001121//EST//7.3e-13:265:64//Hs.142423:AA412497
 F-HEMBA1001122//Homo sapiens mRNA for KIAA0471 protein, complete cds//0.
 066:649:56//Hs.5347:AB007940
 F-HEMBA1001123//Homo sapiens mRNA for KIAA0448 protein, complete cds//1.
 5e-10:231:68//Hs.27349:AB007917
 F-HEMBA1001133//EST//0.50:222:63//Hs.131018:AI015747
 F-HEMBA1001137//Homo sapiens mRNA for KIAA0798 protein, complete cds//2.
 2e-73:527:77//Hs.159277:AB018341
 F-HEMBA1001140//Homo sapiens mRNA for KIAA0682 protein, complete cds//0.
 020:141:65//Hs.7482:AB014582
 F-HEMBA1001172//EST//0.77:158:60//Hs.158894:AI378457

F-HEMBA1001174//ESTs//1.4e-63:363:92//Hs.132798:AA922226
 F-HEMBA1001197//ESTs, Weakly similar to Rap2 interacting protein 8 [M.mu
 sculus]//5.0e-54:555:71//Hs.55165:AA573499
 F-HEMBA1001208//EST//6.2e-26:213:77//Hs.146964:AI183463
 F-HEMBA1001213//Human mRNA for KIAA0013 gene, complete cds//0.026:569:57
 //Hs.48824:D87717
 F-HEMBA1001226//ESTs//1.9e-11:407:65//Hs.157977:AI369694
 F-HEMBA1001235//ESTs//0.0042:161:63//Hs.155170:AA167748
 F-HEMBA1001247//ESTs//1.2e-91:429:99//Hs.143304:AI084058
 F-HEMBA1001257//Human zinc finger protein (MAZ) mRNA//0.017:330:62//Hs.7
 647:M94046
 F-HEMBA1001265
 F-HEMBA1001281
 F-HEMBA1001286//Natriuretic peptide precursor B//0.76:163:63//Hs.937:AL0
 21155
 F-HEMBA1001289//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//5
 .1e-30:530:64//Hs.154050:AC004131
 F-HEMBA1001294//Homo sapiens mRNA for matrilin-3//0.00023:657:56//Hs.119
 534:AJ224741
 F-HEMBA1001299//Small inducible cytokine A5 (RANTES)//2.2e-27:271:77//Hs
 .155464:AF088219
 F-HEMBA1001302//ESTs, Moderately similar to Cab45a [M.musculus]//3.3e-53
 :272:97//Hs.154563:AI129590
 F-HEMBA1001303//ESTs, Weakly similar to RNA splicing-related protein [R.
 norvegicus]//2.6e-66:241:99//Hs.120847:AA731201
 F-HEMBA1001310//ESTs//2.0e-21:133:93//Hs.159116:W55873
 F-HEMBA1001319//Homo sapiens mRNA for KIAA0758 protein, partial cds//0.2
 3:562:58//Hs.22039:AB018301
 F-HEMBA1001323//Wingless-type MMTV integration site 5A, human homolog//2

.5e-31:165:99//Hs.152213:L20861

F-HEMBA1001326//ESTs, Highly similar to HYPOTHETICAL 55.1 KD PROTEIN IN
FAB1-PES4 INTERGENIC REGION [*Saccharomyces cerevisiae*]//8.9e-08:185:68/
/Hs.108734:AI073427

F-HEMBA1001327//ESTs//0.085:337:60//Hs.114157:AA703013

F-HEMBA1001330//EST//0.0018:225:63//Hs.127987:AA970569

F-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33)
mRNA, complete cds//3.6e-105:516:97//Hs.9006:AF057358

F-HEMBA1001361//ESTs//1.2e-62:317:97//Hs.6639:R39794

F-HEMBA1001375//ESTs//0.93:180:60//Hs.148425:AI198074

F-HEMBA1001377//ESTs//9.2e-87:414:99//Hs.48469:N62156

F-HEMBA1001383//ESTs//0.0023:336:60//Hs.140622:AA844353

F-HEMBA1001387//ESTs, Highly similar to RAS-LIKE PROTEIN TC10 [*Homo sapiens*]
//1.0e-132:643:97//Hs.124217:AA020848

F-HEMBA1001388

F-HEMBA1001391//ESTs//5.6e-32:191:93//Hs.71628:N41660

F-HEMBA1001398

F-HEMBA1001405//EST//1.0:135:63//Hs.146833:AI151117

F-HEMBA1001407//ESTs//0.53:390:57//Hs.150447:AI017798

F-HEMBA1001411//EST//8.8e-06:270:62//Hs.145386:AI253108

F-HEMBA1001413

F-HEMBA1001415//EST//1.3e-12:176:75//Hs.133172:AI051605

F-HEMBA1001432//RING3 PROTEIN//0.57:345:59//Hs.75243:D42040

F-HEMBA1001433//ESTs//1.3e-21:333:69//Hs.131648:AI025726

F-HEMBA1001435//Cytochrome P450, subfamily I (aromatic compound-inducible),
polypeptide 2//1.2e-74:469:80//Hs.1361:M55053

F-HEMBA1001442//EST//0.29:181:64//Hs.116883:AA663031

F-HEMBA1001446//ESTs, Weakly similar to Rap2 interacting protein 8 [*M. musculus*]
//6.8e-47:550:71//Hs.55165:AA573499

F-HEMBA1001450//Homo sapiens GTPase-activating protein (SIP1) mRNA, complete cds//0.82:312:58//Hs.7019:AB005666

F-HEMBA1001454//ESTs//1.2e-46:297:80//Hs.152395:AA533107

F-HEMBA1001455//ESTs//7.3e-103:502:97//Hs.112860:AA442412

F-HEMBA1001463//Human mRNA for KIAA0392 gene, partial cds//8.7e-51:323:88//Hs.40100:AB002390

F-HEMBA1001476//Homo sapiens mRNA for KIAA0572 protein, partial cds//6.2e-104:489:99//Hs.14409:AB011144

F-HEMBA1001478//EST//0.013:205:61//Hs.157309:AI365451

F-HEMBA1001497//Small inducible cytokine A5 (RANTES)//5.9e-45:307:84//Hs.155464:AF088219

F-HEMBA1001510//H.sapiens mRNA for G13 protein//2.1e-71:405:92//Hs.42853:X98054

F-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frames//4.5e-105:773:82//Hs.23094:M19503

F-HEMBA1001517//EST//3.6e-09:271:65//Hs.162347:AA564902

F-HEMBA1001522//ESTs//4.3e-13:85:95//Hs.126707:AI376869

F-HEMBA1001526

F-HEMBA1001533//EST//1.0:75:73//Hs.145360:AI252476

F-HEMBA1001557//EST//3.5e-13:261:64//Hs.161496:N66580

F-HEMBA1001566//EST//3.7e-07:354:64//Hs.43830:N26652

F-HEMBA1001569//Homo sapiens mRNA for vesicle associated membrane protein 2 (VAMP2)//8.0e-68:338:97//Hs.91589:M36205

F-HEMBA1001570//ESTs//1.5e-47:369:82//Hs.107657:AA126814

F-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//7.0e-175:678:99//Hs.159597:AJ012449

F-HEMBA1001581//ESTs//4.4e-07:237:67//Hs.152304:AA605184

F-HEMBA1001585//ESTs//1.1e-11:81:100//Hs.16364:AI357228

F-HEMBA1001589//Human mRNA for KIAA0166 gene, complete cds//0.82:210:64/

/Hs.115778:D79988
 F-HEMBA1001595//Human mRNA for KIAA0128 gene, partial cds//2.6e-110:855:
 78//Hs.90998:D50918
 F-HEMBA1001608//EST//1.0:201:60//Hs.136747:AA749210
 F-HEMBA1001620//ESTs//1.5e-39:211:98//Hs.131063:AI016400
 F-HEMBA1001635//ESTs//4.0e-33:168:100//Hs.122655:AI361870
 F-HEMBA1001636//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNIN
 G ENTRY !!!! [H.sapiens]//0.038:198:64//Hs.34579:AI338536
 F-HEMBA1001640//ESTs//1.1e-24:315:71//Hs.34114:AA776899
 F-HEMBA1001647//Human plectin (PLEC1) mRNA, complete cds//0.00049:629:61
 //Hs.79706:U53204
 F-HEMBA1001651//EST//3.6e-07:285:63//Hs.132558:AA948560
 F-HEMBA1001655//ESTs//1.4e-95:497:96//Hs.59563:AA203283
 F-HEMBA1001658//EST//0.18:251:59//Hs.117724:H47121
 F-HEMBA1001661
 F-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA
 , complete cds//7.9e-146:669:99//Hs.107254:AC005943
 F-HEMBA1001675//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
 0484//2.0e-57:447:79//Hs.158095:AB007953
 F-HEMBA1001678//ESTs//4.0e-50:360:83//Hs.146811:AA410788
 F-HEMBA1001681//EST//1.0:165:58//Hs.136790:AA776060
 F-HEMBA1001702//EST//0.015:312:61//Hs.162839:AA648760
 F-HEMBA1001709//EST//0.85:131:65//Hs.131451:AI023995
 F-HEMBA1001711//ESTs//0.084:425:56//Hs.125346:AI302836
 F-HEMBA1001712//EST//0.26:214:59//Hs.159088:AI383114
 F-HEMBA1001714//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL
 PRECURSOR [Rattus norvegicus]//3.0e-30:195:92//Hs.132948:AA194452
 F-HEMBA1001718//EST//0.0044:275:60//Hs.125969:AA889554
 F-HEMBA1001723//INTERLEUKIN ENHANCER-BINDING FACTOR//0.24:501:57//Hs.101

524:U58197

F-HEMBA1001731//EST//1.2e-06:261:63//Hs.132331:AI028363

F-HEMBA1001734//ESTs//0.018:177:63//Hs.129631:AI000415

F-HEMBA1001744//EST//8.7e-77:420:92//Hs.133226:AI052250

F-HEMBA1001745//Homo sapiens mRNA for TSC403 protein, complete cds//0.37
:300:62//Hs.10887:AB013924

F-HEMBA1001746//ESTs//0.31:168:66//Hs.27237:N68328

F-HEMBA1001761//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapien
s] //0.76:218:60//Hs.135553:N41598

F-HEMBA1001781//Homo sapiens chromosome 19, cosmid R30953//0.98:219:60//
Hs.98776:AC005622

F-HEMBA1001784//Homo sapiens mRNA for KIAA0474 protein, complete cds//6.
4e-09:265:67//Hs.158232:AB007943

F-HEMBA1001791

F-HEMBA1001800//EST//3.1e-41:331:81//Hs.127142:AA937570

F-HEMBA1001803//EST//0.0062:269:59//Hs.49075:N64817

F-HEMBA1001804//Human POU domain protein (Brn-3b) mRNA, complete cds//1.
8e-07:439:59//Hs.266:U06233

F-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0500//2.5e-175:809:98//Hs.118164:AB007969

F-HEMBA1001809//ESTs//6.0e-101:497:97//Hs.155127:AA625305

F-HEMBA1001815

F-HEMBA1001819//Human kruppel-related zinc finger protein (ZNF184) mRNA,
partial cds//4.9e-80:842:70//Hs.158174:U66561

F-HEMBA1001820//EST//0.057:214:62//Hs.148715:AI223845

F-HEMBA1001822//Homo sapiens intersectin short form mRNA, complete cds//
6.7e-42:510:65//Hs.66392:AF064244

F-HEMBA1001824//Homo sapiens OPA-containing protein mRNA, complete cds//
5.2e-13:253:68//Hs.85313:AF071309

F-HEMBA1001835//Human mRNA for KIAA0235 gene, partial cds//0.96:288:60//
Hs.6151:D87078

F-HEMBA1001844//ESTs//1.1e-29:197:80//Hs.155243:N70293

F-HEMBA1001847//Human mRNA for KIAA0326 gene, partial cds//2.0e-23:379:6
8//Hs.6833:AB002324

F-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds//2.
8e-185:865:98//Hs.78946:AB014517

F-HEMBA1001864//EST//0.27:145:63//Hs.162585:AA593121

F-HEMBA1001866//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSY
LTRANSFERASE PRECURSOR [D.melanogaster]//3.2e-39:293:84//Hs.152332:AI141
922

F-HEMBA1001869//ESTs, Weakly similar to ASH1 [D.melanogaster]//8.1e-70:3
67:95//Hs.15423:T84036

F-HEMBA1001888//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0484//5.4e-86:835:76//Hs.158095:AB007953

F-HEMBA1001896

F-HEMBA1001910//Human calpain-like protease (htra-3) mRNA, complete cds/
/0.43:114:71//Hs.6133:U94346

F-HEMBA1001912//ESTs//4.1e-79:398:97//Hs.26660:AI312633

F-HEMBA1001913//Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mR
NA, complete cds//0.00031:200:62//Hs.9573:AF027302

F-HEMBA1001915//EST//0.082:128:64//Hs.126542:AA916511

F-HEMBA1001918//Homo sapiens SEC63 (SEC63) mRNA, complete cds//0.46:374:
59//Hs.31575:AF100141

F-HEMBA1001921//Homo sapiens germinal center kinase related protein kina
se mRNA, complete cds//6.7e-186:855:99//Hs.154934:AF000145

F-HEMBA1001939//ESTs//4.9e-34:342:77//Hs.132711:AI377295

F-HEMBA1001940//ESTs//8.6e-15:149:81//Hs.141129:R86221

F-HEMBA1001942//ESTs//0.0014:271:62//Hs.124514:AI219882

F-HEMBA1001945//EST//0.98:142:64//Hs.161540:N85943
 F-HEMBA1001950//ESTs//0.99:188:64//Hs.28639:R78360
 F-HEMBA1001960//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA
 , complete cds//0.30:85:69//Hs.25674:AF072242
 F-HEMBA1001962//ESTs//0.0012:289:59//Hs.125492:AA938930
 F-HEMBA1001964//EST//0.73:153:64//Hs.112161:AA477708
 F-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.
 2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive iso
 log of a Rat gene) and a novel alternatively spliced gene. Contains a pu
 tative CpG island, ESTs and GSSs//4.6e-156:720:99//Hs.11050:AL031178
 F-HEMBA1001979//ESTs//0.86:184:67//Hs.77208:AA044732
 F-HEMBA1001987//ESTs, Moderately similar to hTAFII68 [H.sapiens]//2.8e-2
 9:151:100//Hs.124106:AA948100
 F-HEMBA1001991//Homo sapiens clone 24540 mRNA sequence//0.049:121:70//Hs
 .153529:AF070581
 F-HEMBA1002003//Keratin 10 (epidermolytic hyperkeratosis; keratosis palm
 aris et plantaris)//9.8e-09:294:63//Hs.99936:X14487
 F-HEMBA1002008//ESTs//0.12:299:59//Hs.132803:W63582
 F-HEMBA1002018//PROTEIN-TYROSINE PHOSPHATASE ZETA PRECURSOR//0.98:212:64
 //Hs.78867:M93426
 F-HEMBA1002022//Human p37NB mRNA, complete cds//0.00044:58:96//Hs.155545
 :U32907
 F-HEMBA1002035//EST//6.4e-07:145:68//Hs.135336:AI049827
 F-HEMBA1002039//EST//0.99:79:67//Hs.98451:AA426057
 F-HEMBA1002049//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
 RY !!!! [H.sapiens]//4.5e-26:223:81//Hs.105292:AA504776
 F-HEMBA1002084
 F-HEMBA1002092
 F-HEMBA1002100//Homo sapiens zinc finger homeodomain protein (ATBF1-A) m

RNA, complete cds//5.6e-21:124:96//Hs.101842:L32832
 F-HEMBA1002102//ESTs, Highly similar to ANKYRIN [Mus musculus]//5.9e-09
 :434:62//Hs.135102:AI190276
 F-HEMBA1002113//ESTs//0.049:255:63//Hs.106137:AI129973
 F-HEMBA1002119
 F-HEMBA1002125//H.sapiens ERF-2 mRNA//0.026:341:59//Hs.78909:U07802
 F-HEMBA1002139//ESTs//0.082:309:60//Hs.36383:W52393
 F-HEMBA1002144//Human mRNA for KIAA0227 gene, partial cds//5.6e-06:601:6
 0//Hs.79170:D86980
 F-HEMBA1002150//Homo sapiens mRNA for KIAA0720 protein, partial cds//5.6
 e-06:353:62//Hs.23741:AB018263
 F-HEMBA1002151
 F-HEMBA1002153//EST//0.014:328:60//Hs.149115:AI244695
 F-HEMBA1002160//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
 0507//5.6e-49:303:79//Hs.158241:AB007976
 F-HEMBA1002161//Myosin, heavy polypeptide 7, cardiac muscle, beta//1.2e-
 40:616:67//Hs.929:M57965
 F-HEMBA1002162//Homo sapiens mRNA for XPR2 protein//3.4e-48:749:67//Hs.4
 4766:AJ007590
 F-HEMBA1002166//Small inducible cytokine A5 (RANTES)//2.1e-60:485:79//Hs
 .155464:AF088219
 F-HEMBA1002177//Homo sapiens yotiao mRNA, complete cds//2.4e-19:151:86//
 Hs.114808:AF026245
 F-HEMBA1002185//EST//0.00011:233:65//Hs.125552:AA884141
 F-HEMBA1002189//EST//5.1e-24:193:81//Hs.163161:AA778363
 F-HEMBA1002191//Homo sapiens mRNA for KIAA0689 protein, partial cds//0.2
 7:382:59//Hs.21992:AB014589
 F-HEMBA1002199//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
 0501//1.2e-14:199:72//Hs.159897:AB007970

F-HEMBA1002204//ESTs//0.46:312:59//Hs.61210:AA024696
 F-HEMBA1002212//ESTs//1.0:191:63//Hs.149752:AI285767
 F-HEMBA1002215//ESTs, Highly similar to TESTIN 2 PRECURSOR [Mus musculus] //1.6e-47:251:96//Hs.59906:AA001281
 F-HEMBA1002226//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//2.4e-57:375:71//Hs.67619:AB007957
 F-HEMBA1002229//Homo sapiens KIAA0395 mRNA, partial cds//7.9e-47:377:80//Hs.43681:AL022394
 F-HEMBA1002237//EST//0.044:137:66//Hs.144448:AA812455
 F-HEMBA1002241
 F-HEMBA1002253//EST//2.2e-41:219:96//Hs.137065:AA888887
 F-HEMBA1002257//Homo sapiens diacylglycerol kinase iota (DGKi) mRNA, complete cds//1.1e-152:731:97//Hs.159564:AF061936
 F-HEMBA1002265//ESTs//5.4e-11:337:65//Hs.112639:AI125420
 F-HEMBA1002267//Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA, complete cds//1.0:395:60//Hs.150926:AF017445
 F-HEMBA1002270//ESTs//2.5e-87:504:89//Hs.124440:H95404
 F-HEMBA1002321//Homo sapiens oxidized low-density lipoprotein receptor mRNA, complete cds//0.17:338:60//Hs.77729:AB010710
 F-HEMBA1002328//ESTs//7.9e-103:480:99//Hs.123318:AI201982
 F-HEMBA1002337//Human mRNA for KIAA0118 gene, partial cds//0.93:220:61//Hs.154326:D42087
 F-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds//7.8e-187:872:98//Hs.6162:AB018314
 F-HEMBA1002348//EST//1.0e-19:285:70//Hs.121860:AA776692
 F-HEMBA1002349//EST//0.011:385:59//Hs.148533:AI200996
 F-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//2.4e-189:872:99//Hs.119023:AF092563
 F-HEMBA1002381//EST//7.9e-34:236:77//Hs.162197:AA535216

F-HEMBA1002389//ESTs//4.3e-59:342:92//Hs.133391:AA535144

F-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784//2.2e-159:775:97//Hs.25527:AC005954

F-HEMBA1002419//EST, Moderately similar to ROD CGMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE BETA-SUBUNIT [H.sapiens]//1.0:144:65//Hs.136096:W27141

F-HEMBA1002430//Human clone 23695 mRNA sequence//2.7e-06:563:59//Hs.90798:U79289

F-HEMBA1002439//EST, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMO LOG [H.sapiens]//0.11:111:67//Hs.162154:AA528561

F-HEMBA1002458//ESTs, Weakly similar to hypothetical protein B, 6.8K [H.sapiens]//1.3e-71:346:98//Hs.136121:W26490

F-HEMBA1002460//ESTs//2.1e-94:484:96//Hs.106441:R53160

F-HEMBA1002462//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//0.00024:240:64//Hs.113286:U77783

F-HEMBA1002469//Human mRNA for KIAA0122 gene, partial cds//1.3e-109:603:92//Hs.154583:D50912

F-HEMBA1002475//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.025:261:63//Hs.89631:U48508

F-HEMBA1002477//Homo sapiens mRNA for KIAA0561 protein, partial cds//2.8e-45:331:83//Hs.6189:AB011133

F-HEMBA1002486//EST//0.00039:174:67//Hs.96680:AA303235

F-HEMBA1002495

F-HEMBA1002498//ESTs//1.2e-91:460:97//Hs.118327:W79161

F-HEMBA1002503//H.sapiens mRNA for MACH-alpha-2 protein//4.8e-13:164:74//Hs.19949:X98173

F-HEMBA1002508//Homo sapiens PYRIN (MEFV) mRNA, complete cds//6.1e-79:460:83//Hs.113283:AF018080

F-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (

JM21)//9.0e-159:738:98//Hs.6764:AJ011972
 F-HEMBA1002515//ESTs//3.6e-08:185:69//Hs.118701:AA420795
 F-HEMBA1002538//ESTs//0.97:68:73//Hs.134672:AI087951
 F-HEMBA1002542//Homo sapiens mRNA for chemokine LEC precursor, complete
 cds//6.1e-46:238:87//Hs.10458:AF088219
 F-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds//1.1e-138
 :655:98//Hs.68900:AF016903
 F-HEMBA1002552//Human Hep27 protein mRNA, complete cds//2.8e-08:173:68//
 Hs.102137:U31875
 F-HEMBA1002555//Homo sapiens mRNA for APC 2 protein, complete cds//0.000
 20:603:57//Hs.20912:AB012162
 F-HEMBA1002558//ESTs//6.0e-25:262:77//Hs.136304:AA431205
 F-HEMBA1002561//Human clone 23574 mRNA sequence//4.7e-17:268:72//Hs.7938
 5:U90905
 F-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete
 cds//4.3e-142:457:99//Hs.151411:AF075587
 F-HEMBA1002583//Homo sapiens UKLF mRNA for ubiquitous Kruppel like facto
 r, complete cds//2.8e-30:156:100//Hs.32170:AB015132
 F-HEMBA1002590//ESTs//1.0e-30:277:77//Hs.139158:AA226159
 F-HEMBA1002592//ESTs//2.4e-20:233:75//Hs.159329:AI378363
 F-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds//1.4
 e-176:820:99//Hs.20141:AB011169
 F-HEMBA1002621//EST//0.99:208:60//Hs.159127:AI384013
 F-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds//9.
 2e-189:632:97//Hs.91338:AB018351
 F-HEMBA1002628//Human mRNA for KIAA0336 gene, complete cds//0.079:231:65
 //Hs.125129:AB002334
 F-HEMBA1002629//Human density enhanced phosphatase-1 mRNA, complete cds/
 /1.3e-07:473:61//Hs.1177:U10886

F-HEMBA1002645//ESTs//2.6e-32:209:88//Hs.141323:N80390
F-HEMBA1002651
F-HEMBA1002659//Human vascular endothelial growth factor related protein
VRP mRNA, complete cds//0.74:223:60//Hs.79141:U43142
F-HEMBA1002661//Human Line-1 repeat mRNA with 2 open reading frames//1.4
e-122:781:85//Hs.23094:M19503
F-HEMBA1002666//ESTs//0.39:117:65//Hs.3794:T08497
F-HEMBA1002678//EST//0.0081:148:64//Hs.156768:A1351368
F-HEMBA1002679//Cyclic nucleotide gated channel (photoreceptor), cGMP ga
ted 1 (alpha)//0.00096:418:61//Hs.1323:S42457
F-HEMBA1002688//Homo sapiens hyperpolarization-activated channel 1 (IH1)
mRNA, partial cds//1.8e-11:541:60//Hs.124161:AF065164
F-HEMBA1002696//Homo sapiens DNA from chromosome 19, cosmid R29144//1.9e
-06:345:61//Hs.155647:AC004221
F-HEMBA1002703//Homo sapiens mRNA for KIAA0455 protein, complete cds//6.
0e-12:327:62//Hs.13245:AB007924
F-HEMBA1002712
F-HEMBA1002716//EST//1.2e-56:284:97//Hs.131329:AA922800
F-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds//3.7
e-127:614:97//Hs.132942:AB014521
F-HEMBA1002730//Homo sapiens microsomal glutathione S-transferase 3 (MGS
T3) mRNA, complete cds//0.21:157:66//Hs.111811:AB007867
F-HEMBA1002742//EST//0.97:138:60//Hs.160545:A1271596
F-HEMBA1002746//Human HOX4C mRNA for a homeobox protein//0.72:347:58//Hs
.74061:X59372
F-HEMBA1002748//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.24:83:74/
/Hs.40806:AA018786
F-HEMBA1002750//ESTs//5.8e-37:185:76//Hs.140577:AA827817
F-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//2.9

e-178:834:98//Hs.74750:AB011126
 F-HEMBA1002770//ESTs, Highly similar to TIP120 [R.norvegicus]//8.0e-98:4
 92:96//Hs.11833:AI299947
 F-HEMBA1002777//Homo sapiens prostate apoptosis response protein par-4 m
 RNA, complete cds//3.9e-05:528:59//Hs.128208:U63809
 F-HEMBA1002779//ESTs//8.1e-134:662:96//Hs.107295:W80392
 F-HEMBA1002780//ESTs//3.8e-41:421:74//Hs.141576:N90326
 F-HEMBA1002794//Protein kinase C, mu//4.8e-06:244:67//Hs.2891:X75756
 F-HEMBA1002801//ESTs//2.1e-24:182:87//Hs.124633:AA856938
 F-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cd
 s//3.4e-169:820:97//Hs.28307:AF071185
 F-HEMBA1002816//ESTs//2.5e-91:387:94//Hs.8008:R52744
 F-HEMBA1002818//Homo sapiens UPH1 (UPH1) mRNA, complete cds//7.0e-122:73
 3:89//Hs.6059:AF093119
 F-HEMBA1002826//ESTs//0.00015:235:62//Hs.119383:AI279904
 F-HEMBA1002833
 F-HEMBA1002850//EST//0.0014:201:65//Hs.156235:AA770550
 F-HEMBA1002863//ESTs//1.2e-50:295:91//Hs.57980:W68823
 F-HEMBA1002876//ESTs, Weakly similar to HYPOTHETICAL 26.4 KD PROTEIN EEE
 D8.8 IN CHROMOSOME II [C.elegans]//4.9e-18:110:94//Hs.13322:AA151730
 F-HEMBA1002886//EST//0.99:184:65//Hs.160684:AI279429
 F-HEMBA1002896//ESTs//2.1e-11:72:100//Hs.149215:AI051679
 F-HEMBA1002921
 F-HEMBA1002924//EST//3.7e-05:291:64//Hs.134677:AI088001
 F-HEMBA1002934//ESTs//2.3e-42:324:80//Hs.141658:N77915
 F-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds//1.6
 e-174:803:99//Hs.14687:AB011148
 F-HEMBA1002937//ESTs, Weakly similar to homologous to mouse gene PC326:G
 enBank Accession Number M95564 [H.sapiens]//8.1e-36:256:85//Hs.36899:AA1

30053

F-HEMBA1002939//H.sapiens mRNA for cytokine inducible nuclear protein//1
.1e-05:479:59//Hs.74019:X83703

F-HEMBA1002944//Human putative endothelin receptor type B-like protein m
RNA, complete cds//0.83:326:58//Hs.27747:U87460

F-HEMBA1002951//ESTs//6.1e-08:137:70//Hs.126762:AA913925

F-HEMBA1002954//ESTs//9.3e-39:249:89//Hs.146185:R19099

F-HEMBA1002968//ESTs//0.73:142:64//Hs.136371:AA506092

F-HEMBA1002970//EST//2.9e-10:103:82//Hs.162580:AA593828

F-HEMBA1002971//ESTs//3.5e-21:190:81//Hs.61170:AA454219

F-HEMBA1002973//Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-
homolog phosphodiesterase E4)//1.5e-37:247:89//Hs.188:L20971

F-HEMBA1002997//Homo sapiens chromosome-associated protein-C (hCAP-C) mR
NA, partial cds//1.7e-05:797:58//Hs.50758:AF092564

F-HEMBA1002999//EST//9.9e-38:453:70//Hs.161635:W22525

F-HEMBA1003021//Small inducible cytokine A5 (RANTES)//4.6e-49:373:81//Hs
.155464:AF088219

F-HEMBA1003033//ESTs//5.0e-64:340:95//Hs.154270:N26486

F-HEMBA1003034//Homo sapiens PYRIN (MEFV) mRNA, complete cds//7.4e-70:33
0:78//Hs.113283:AF018080

F-HEMBA1003035//Homo sapiens mRNA for testican-3//0.041:623:57//Hs.15942
5:AJ001454

F-HEMBA1003037//EST//0.53:59:74//Hs.148011:AI268003

F-HEMBA1003041//ESTs, Weakly similar to F58G11.6 [C.elegans]//1.7e-64:33
7:95//Hs.105907:AA186514

F-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-sub
unit mRNA, complete cds//3.2e-166:777:98//Hs.44097:AF054182

F-HEMBA1003064//ESTs//3.2e-07:320:65//Hs.23466:AI223438

F-HEMBA1003067

F-HEMBA1003071//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.5e-15:611:59//Hs.124161:AF065164

F-HEMBA1003077//Homo sapiens KIAA0405 mRNA, complete cds//2.2e-29:542:62//Hs.48998:AB007865

F-HEMBA1003078//CYTOCHROME P450 IVF3//2.0e-29:452:67//Hs.106242:AB002454

F-HEMBA1003079//EST//2.0e-20:273:73//Hs.138001:AI034461

F-HEMBA1003083//EST//2.0e-48:314:86//Hs.149580:AI281881

F-HEMBA1003086//ESTs//2.6e-20:237:73//Hs.129331:AI090721

F-HEMBA1003096//ESTs, Weakly similar to HMG-box transcription factor [M. musculus]//0.98:216:61//Hs.97865:AA405872

F-HEMBA1003098//EST//2.9e-19:239:73//Hs.152366:AA486721

F-HEMBA1003117//H.sapiens ERF-2 mRNA//0.0048:447:59//Hs.78909:U07802

F-HEMBA1003129//Homo sapiens clone 24407 mRNA sequence//1.9e-06:507:58//Hs.12432:AF070575

F-HEMBA1003133//Homo sapiens mRNA for KIAA0771 protein, partial cds//0.038:288:63//Hs.6162:AB018314

F-HEMBA1003136

F-HEMBA1003142//ESTs//3.6e-112:526:99//Hs.55982:AA284279

F-HEMBA1003148//Homo sapiens mRNA for dachshund protein//2.2e-184:850:99//Hs.63931:AJ005670

F-HEMBA1003166//Homo sapiens mRNA for KIAA0688 protein, complete cds//1.1e-24:171:83//Hs.141874:AB014588

F-HEMBA1003175//EST//0.91:168:60//Hs.123335:AA810740

F-HEMBA1003179//EST, Weakly similar to hypothetical protein in purB 5' region [E.coli]//4.7e-20:118:97//Hs.118831:AA211895

F-HEMBA1003197//ESTs//0.049:265:58//Hs.153718:AI215523

F-HEMBA1003199//SOX-3 PROTEIN//0.00034:383:60//Hs.157429:X71135

F-HEMBA1003202//ESTs//7.1e-84:408:98//Hs.130134:AA905412

F-HEMBA1003204//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.6e-33:15

4:85//Hs.113283:AF018080
 F-HEMBA1003212//ESTs//1.0e-31:159:84//Hs.134067:AI076765
 F-HEMBA1003220//EST//8.6e-29:317:73//Hs.150552:AI053784
 F-HEMBA1003222//ESTs//0.77:208:62//Hs.85451:AA181310
 F-HEMBA1003229//EST//0.084:233:60//Hs.98176:AA417012
 F-HEMBA1003235//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.0005
 4:432:58//Hs.132206:AF039694
 F-HEMBA1003250
 F-HEMBA1003257//Homo sapiens fibroblast growth factor 18 (FGF18) mRNA, complete cds//4.3e-08:426:64//Hs.49585:AF075292
 F-HEMBA1003273//EST//0.00078:195:65//Hs.158019:AA867991
 F-HEMBA1003276//EST//6.6e-09:159:74//Hs.162664:AA605020
 F-HEMBA1003278//ESTs//0.89:257:63//Hs.23207:R42864
 F-HEMBA1003281//ESTs//2.6e-33:175:98//Hs.122278:AA781867
 F-HEMBA1003286//Homo sapiens chromosome 3q13 beta-1,4-galactosyltransferase mRNA, complete cds//2.9e-146:539:97//Hs.13225:AF038662
 F-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds//1.6e-167:799:98//Hs.12836:AB011109
 F-HEMBA1003296//EST//0.0013:49:97//Hs.137157:R44912
 F-HEMBA1003304//ESTs//0.047:164:64//Hs.94448:AA770160
 F-HEMBA1003309//ESTs//7.8e-123:589:98//Hs.105486:AA521012
 F-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds//1.5e-189:865:99//Hs.124224:AB001872
 F-HEMBA1003322//H.sapiens mRNA for sigma 3B protein//4.5e-49:399:80//Hs.154782:X99459
 F-HEMBA1003327//EST//7.7e-10:165:72//Hs.114826:AA056254
 F-HEMBA1003328//EST//0.00023:128:67//Hs.126467:AA913328
 F-HEMBA1003330
 F-HEMBA1003348//Human mRNA for KIAA0331 gene, complete cds//4.8e-26:256:

78//Hs.146395:AB002329

F-HEMBA1003369//Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLF, GCDH, CRTC, and RAD23A genes, genomic sequence//0.37:187:65//Hs.80265:AD000092

F-HEMBA1003370//ESTs//8.2e-36:196:79//Hs.139158:AA226159

F-HEMBA1003373//ESTs//1.0:195:61//Hs.127307:AI263819

F-HEMBA1003376//Clathrin, light polypeptide (Lcb)//2.3e-29:606:64//Hs.73919:X81637

F-HEMBA1003380//ESTs//2.5e-21:303:70//Hs.37528:H58017

F-HEMBA1003384//ESTs//0.14:281:61//Hs.159650:N95552

F-HEMBA1003395//ESTs//0.53:121:70//Hs.144873:AI202488

F-HEMBA1003402//EST//0.029:148:66//Hs.116798:AA633813

F-HEMBA1003403//Adducin 2 (beta) {alternative products} //5.0e-05:445:61//Hs.90951:U43959

F-HEMBA1003408//ESTs//9.0e-12:87:98//Hs.70266:Z78309

F-HEMBA1003417//Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD)//9.5e-05:541:58//Hs.89709:L35546

F-HEMBA1003418//ESTs//3.5e-85:399:100//Hs.154489:AA564962

F-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//2.0e-149:686:99//Hs.25812:AF058696

F-HEMBA1003447//Human mRNA for KIAA0380 gene, complete cds//0.43:271:60//Hs.47822:AB002378

F-HEMBA1003461//Glycoprotein Ib (platelet), beta polypeptide//4.8e-08:775:58//Hs.3847:U59632

F-HEMBA1003463//ESTs//3.3e-22:121:99//Hs.130847:AA058578

F-HEMBA1003480//Homo sapiens mRNA for KIAA0700 protein, partial cds//0.16:321:60//Hs.13999:AB014600

F-HEMBA1003528//ESTs//3.8e-53:315:91//Hs.129688:AA057443

F-HEMBA1003531//Human mRNA for KIAA0033 gene, partial cds//4.9e-51:451:7

8//Hs.22271:D26067
 F-HEMBA1003538//ESTs//1.2e-82:415:96//Hs.162075:AI392811
 F-HEMBA1003545//ISL1 transcription factor, LIM/homeodomain, (islet-1)//5
 .0e-75:736:73//Hs.505:U07559
 F-HEMBA1003548//ESTs//8.7e-77:411:95//Hs.163443:R23311
 F-HEMBA1003555//Human nucleotide-binding protein mRNA, complete cds//3.6
 e-33:562:64//Hs.81469:U01833
 F-HEMBA1003556
 F-HEMBA1003560//EST//3.7e-29:202:86//Hs.136858:AA767122
 F-HEMBA1003568//ESTs//2.4e-06:214:65//Hs.143371:AI342327
 F-HEMBA1003569//Human metastasis-associated mtal mRNA, complete cds//2.0
 e-58:455:66//Hs.101448:U35113
 F-HEMBA1003571//ESTs//0.0025:198:63//Hs.116448:AA648972
 F-HEMBA1003579//ESTs//6.0e-110:513:99//Hs.97372:AA398546
 F-HEMBA1003581//ESTs, Highly similar to TALIN [Mus musculus]//3.6e-19:1
 08:99//Hs.18420:AA599232
 F-HEMBA1003591//ESTs, Weakly similar to R74.5 [C.elegans]//5.2e-85:487:9
 2//Hs.57937:W68285
 F-HEMBA1003595//Membrane cofactor protein (CD46, trophoblast-lymphocyte
 cross-reactive antigen)//2.8e-06:439:62//Hs.83532:X59405
 F-HEMBA1003597//ESTs//0.0025:200:64//Hs.8473:T40827
 F-HEMBA1003598//ESTs//0.18:187:63//Hs.98641:AA429916
 F-HEMBA1003615//ESTs, Highly similar to phosphorylation regulatory prote
 in HP-10 [H.sapiens]//2.4e-133:644:97//Hs.3566:AA314782
 F-HEMBA1003617//Homa sapiens mRNA for HRIHFB2157, partial cds//7.9e-171:
 501:97//Hs.124956:AB015344
 F-HEMBA1003621//Homo sapiens protein inhibitor of activated STAT protein
 PIASx-alpha mRNA, complete cds//4.4e-16:161:78//Hs.111323:AF077954
 F-HEMBA1003622//EST//0.0085:251:62//Hs.97343:AA401750

F-HEMBA1003630//ESTs//7.5e-05:304:61//Hs.87131:AA233159
 F-HEMBA1003637//Homo sapiens homolog of the Aspergillus nidulans sudd gene product mRNA, complete cds//7.9e-26:546:63//Hs.109901:AF013591
 F-HEMBA1003640//ESTs//1.1e-11:267:66//Hs.34359:AI122791
 F-HEMBA1003645
 F-HEMBA1003646
 F-HEMBA1003656
 F-HEMBA1003662
 F-HEMBA1003667//ESTs//1.5e-27:235:81//Hs.55855:AA621381
 F-HEMBA1003679//ESTs//4.3e-49:251:97//Hs.152811:AA630906
 F-HEMBA1003680//Human plectin (PLEC1) mRNA, complete cds//3.4e-06:464:61//Hs.79706:U53204
 F-HEMBA1003684//ESTs, Weakly similar to zinc finger protein C2H2-171 [H. sapiens]//1.6e-100:478:98//Hs.118866:AI017072
 F-HEMBA1003690//Homo sapiens mRNA for KIAA0600 protein, partial cds//9.5e-74:606:77//Hs.9028:AF039691
 F-HEMBA1003692//ESTs//4.2e-43:252:92//Hs.39748:AA487187
 F-HEMBA1003711//Homo sapiens mRNA for KIAA0544 protein, partial cds//0.81:254:62//Hs.32316:AB011116
 F-HEMBA1003714//ESTs//6.4e-98:495:95//Hs.43846:N49995
 F-HEMBA1003715//ESTs//1.3e-11:228:69//Hs.101237:AA708760
 F-HEMBA1003720//Homo sapiens clone 23892 mRNA sequence//5.5e-45:692:68//Hs.91916:AF035317
 F-HEMBA1003725//EST//2.5e-46:228:100//Hs.160069:AA926921
 F-HEMBA1003729//ESTs//4.1e-48:253:96//Hs.26270:AA258839
 F-HEMBA1003733//Human Line-1 repeat mRNA with 2 open reading frames//8.6e-102:753:81//Hs.23094:M19503
 F-HEMBA1003742//Homo sapiens chromosome 19, cosmid R31180//0.16:242:62//Hs.153325:AC005390

F-HEMBA1003758//ESTs//9.3e-12:408:61//Hs.148459:AI198946
 F-HEMBA1003760//Homo sapiens clone 23698 mRNA sequence//9.7e-35:430:69//
 Hs.8136:U81984
 F-HEMBA1003773//EST//0.76:191:61//Hs.127020:AA934920
 F-HEMBA1003783//ESTs, Weakly similar to C01H6.7 [C.elegans]//1.7e-24:224
 :81//Hs.18171:AA524327
 F-HEMBA1003784//ESTs//0.13:120:67//Hs.161993:AA503172
 F-HEMBA1003799//Interleukin 9 receptor//2.0e-17:263:70//Hs.1702:L39064
 F-HEMBA1003803//Homo sapiens calcium-activated potassium channel (KCNN3)
 mRNA, complete cds//0.13:222:61//Hs.89230:AF031815
 F-HEMBA1003804//ESTs//1.4e-112:275:98//Hs.72132:AF039239
 F-HEMBA1003805//Human p62 mRNA, complete cds//1.1e-11:523:60//Hs.119537:
 M88108
 F-HEMBA1003807//ESTs//4.1e-08:279:68//Hs.115679:AI379721
 F-HEMBA1003827//Homo sapiens mRNA for KIAA0616 protein, partial cds//3.3
 e-85:586:87//Hs.6051:AB014516
 F-HEMBA1003836//EST//6.8e-06:98:74//Hs.145447:AI204220
 F-HEMBA1003838//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNIN
 G ENTRY !!!! [H.sapiens]//3.8e-40:151:88//Hs.139007:H74314
 F-HEMBA1003856//ESTs//8.6e-53:286:95//Hs.116645:AI005167
 F-HEMBA1003864//Human mRNA for KIAA0369 gene, complete cds//0.11:144:66/
 /Hs.21355:AB002367
 F-HEMBA1003866//Homo sapiens semaphorin F homolog mRNA, complete cds//4.
 3e-30:580:63//Hs.27621:U52840
 F-HEMBA1003879//Nuclear cap binding protein, 80kD//6.7e-10:87:95//Hs.895
 63:D32002
 F-HEMBA1003880
 F-HEMBA1003885//Homo sapiens mRNA for KIAA0752 protein, partial cds//4.2
 e-18:302:67//Hs.23711:AB018295

F-HEMBA1003893//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN
VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]//1.2e-49:295:92//Hs.114673:
W72675

F-HEMBA1003902//ESTs//1.1e-11:165:74//Hs.54632:AA976236

F-HEMBA1003908//Homo sapiens mRNA for KIAA0525 protein, partial cds//0.0
81:345:58//Hs.78494:AB011097

F-HEMBA1003926//EST//2.5e-32:253:83//Hs.132635:AI032875

F-HEMBA1003937//Human mRNA for KIAA0391 gene, complete cds//2.9e-38:313:
69//Hs.154668:AB002389

F-HEMBA1003939//ESTs//3.4e-07:150:71//Hs.148926:R59562

F-HEMBA1003942//EST, Weakly similar to 24 KD PROTEIN [Xenopus laevis]//0
.0029:222:61//Hs.144236:W52380

F-HEMBA1003950//ESTs//0.98:200:62//Hs.163912:W20055

F-HEMBA1003953//Zinc finger protein 7 (KOX 4, clone HF.16)//0.00014:271:
66//Hs.2076:M29580

F-HEMBA1003958//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING
ENTRY !!!! [H.sapiens]//2.1e-44:243:76//Hs.91146:N73230

F-HEMBA1003959//ESTs//0.067:251:59//Hs.39915:H78567

F-HEMBA1003976//EST//6.7e-09:109:81//Hs.154635:AI138965

F-HEMBA1003978

F-HEMBA1003985//EST//0.32:115:69//Hs.102617:N47009

F-HEMBA1003987//ESTs//7.8e-07:60:100//Hs.66058:AA424456

F-HEMBA1003989//Homo sapiens HIV-1 inducer of short transcripts binding
protein (FBI1) mRNA, complete cds//0.022:349:58//Hs.104640:AF000561

F-HEMBA1004000//EST//7.2e-07:200:66//Hs.119082:AA358468

F-HEMBA1004011//EST//0.019:241:62//Hs.116989:AA676493

F-HEMBA1004012//ESTs//3.6e-09:177:68//Hs.106132:AA812573

F-HEMBA1004015//ESTs//3.0e-86:407:99//Hs.115679:AI379721

F-HEMBA1004024//Homo sapiens mRNA for KIAA0772 protein, complete cds//5.

2e-51:359:84//Hs.15519:AB018315
 F-HEMBA1004038//ESTs//1.2e-58:324:94//Hs.61658:AI239930
 F-HEMBA1004042//EST//0.00088:272:61//Hs.155763:AI312281
 F-HEMBA1004045//EST//2.7e-20:408:66//Hs.162529:AA584160
 F-HEMBA1004048//Transforming growth factor beta//0.026:462:57//Hs.6101:M
 60315
 F-HEMBA1004049//ESTs//8.1e-68:430:86//Hs.146307:AA584638
 F-HEMBA1004055//Human chromosome 3p21.1 gene sequence//1.5e-10:457:58//H
 s.82837:L13435
 F-HEMBA1004056//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, comp
 lete cds//1.5e-46:199:80//Hs.46328:D87942
 F-HEMBA1004074//ESTs//3.0e-23:219:74//Hs.70279:AA757426
 F-HEMBA1004086//EST//0.36:189:62//Hs.156218:AA770107
 F-HEMBA1004097//NADH-CYTOCHROME B5 REDUCTASE//1.0:302:57//Hs.75666:M2871
 3
 F-HEMBA1004111//Human G protein-coupled receptor (STRL22) mRNA, complete
 cds//4.3e-39:335:79//Hs.46468:U45984
 F-HEMBA1004131//Human mRNA for KIAA0202 gene, partial cds//1.9e-24:610:6
 1//Hs.80712:D86957
 F-HEMBA1004132//EST//3.5e-06:143:70//Hs.136799:AA780064
 F-HEMBA1004133//ESTs//1.0:157:68//Hs.161226:AI419759
 F-HEMBA1004138//H.sapiens mRNA for RanGTPase activating protein 1//0.000
 55:343:62//Hs.5923:X82260
 F-HEMBA1004143
 F-HEMBA1004146
 F-HEMBA1004150//EST//0.0046:402:57//Hs.147027:AI186056
 F-HEMBA1004164//Homo sapiens mRNA for KIAA0798 protein, complete cds//1.
 8e-15:591:60//Hs.159277:AB018341
 F-HEMBA1004168//Homo sapiens geminin mRNA, complete cds//1.5e-134:649:97

//Hs.59988:AF067855
 F-HEMBA1004199
 F-HEMBA1004200//ESTs//0.0083:150:66//Hs.116424:AI375427
 F-HEMBA1004202//ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea m
 ays] //1.2e-35:205:94//Hs.10092:AI189282
 F-HEMBA1004203//ESTs//3.9e-14:237:70//Hs.118273:AA626040
 F-HEMBA1004207//Leptin receptor//1.1e-167:791:98//Hs.54515:U50748
 F-HEMBA1004225//ESTs//0.00087:231:64//Hs.13109:AA192514
 F-HEMBA1004227//ESTs, Weakly similar to F55A11.4 [C.elegans] //0.012:156:
 67//Hs.163588:AI073878
 F-HEMBA1004238
 F-HEMBA1004241//ESTs//8.7e-05:51:96//Hs.162826:AA679571
 F-HEMBA1004246//EST//1.2e-36:198:96//Hs.121343:AA758522
 F-HEMBA1004248//Homo sapiens insulin induced protein 1 (INSIG1) gene, co
 mplete cds//1.1e-28:295:72//Hs.56205:U96876
 F-HEMBA1004264//Human HCF1 gene related mRNA sequence//3.1e-07:553:60//H
 s.83634:U52112
 F-HEMBA1004267//Homo sapiens mRNA for KIAA0688 protein, complete cds//4.
 9e-73:490:77//Hs.141874:AB014588
 F-HEMBA1004272
 F-HEMBA1004274//EST//0.43:154:61//Hs.125347:AA876444
 F-HEMBA1004275//Human mRNA for KIAA0333 gene, partial cds//0.71:118:65//
 Hs.155313:AB002331
 F-HEMBA1004276//Homo sapiens mRNA for KIAA0800 protein, complete cds//1.
 0:364:56//Hs.118738:AB018343
 F-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA
 , complete cds//6.9e-187:868:99//Hs.101766:AF022795
 F-HEMBA1004289
 F-HEMBA1004295//EST//0.20:149:62//Hs.162415:AA573484

F-HEMBA1004306//ESTs//0.041:177:64//Hs.158234:AI270047
 F-HEMBA1004312//ESTs//0.83:253:59//Hs.121898:AI336314
 F-HEMBA1004321//Zinc finger protein 136 (clone pHZ-20)//2.3e-40:452:65//
 Hs.69740:U09367
 F-HEMBA1004323//EST//0.44:134:64//Hs.145464:AI204532
 F-HEMBA1004327//Homo sapiens SOX22 protein (SOX22) mRNA, complete cds//0.
 .017:209:64//Hs.43627:U35612
 F-HEMBA1004330//ESTs//4.5e-27:171:91//Hs.112838:AA614062
 F-HEMBA1004334//EST//2.4e-53:556:75//Hs.139093:AA166888
 F-HEMBA1004335//Homo sapiens mRNA for KIAA0706 protein, complete cds//0.
 49:80:73//Hs.139648:AB014606
 F-HEMBA1004341
 F-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cd
 s//2.7e-39:270:86//Hs.80686:D89667
 F-HEMBA1004354//Human CHL1 potential helicase (CHLR1), complete cds//1.3
 e-46:190:92//Hs.27424:U75968
 F-HEMBA1004356//Thyrotropin-releasing hormone receptor//0.15:296:62//Hs.
 3022:D85376
 F-HEMBA1004366//ESTs, Weakly similar to transposon LRE2 reverse transcri
 ptase homolog [H.sapiens]//7.8e-10:396:61//Hs.33688:AA020928
 F-HEMBA1004372//ESTs//0.90:172:62//Hs.145611:R68800
 F-HEMBA1004389//Zinc finger protein 148 (pHZ-52)//8.0e-28:359:67//Hs.112
 180:AF039019
 F-HEMBA1004394//ESTs//0.023:357:58//Hs.47212:N51250
 F-HEMBA1004396//EST//3.4e-22:244:74//Hs.162554:AA584818
 F-HEMBA1004405//EST//4.0e-43:214:100//Hs.33100:H42199
 F-HEMBA1004408//ESTs, Weakly similar to The ha1539 protein is related to
 cyclophilin. [H.sapiens]//1.4e-20:144:88//Hs.121076:AI246426
 F-HEMBA1004429//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltrans

ferase, Bombay phenotype included)//4.8e-18:248:72//Hs.69747:M35531
 F-HEMBA1004433//Small inducible cytokine A5 (RANTES)//8.2e-39:248:81//Hs.
 .155464:AF088219
 F-HEMBA1004460//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.6e-87:65
 0:81//Hs.113283:AF018080
 F-HEMBA1004461//ESTs//0.057:217:61//Hs.26989:Z41606
 F-HEMBA1004479//Homo sapiens clone 23698 mRNA sequence//4.9e-17:223:71//
 Hs.8136:U81984
 F-HEMBA1004482//EST//0.0056:261:59//Hs.45012:N39450
 F-HEMBA1004499//ESTs//4.1e-68:340:97//Hs.134266:AA992600
 F-HEMBA1004502//ESTs//7.7e-32:195:91//Hs.134906:H93431
 F-HEMBA1004506//Human Line-1 repeat mRNA with 2 open reading frames//9.0
 e-89:758:76//Hs.23094:M19503
 F-HEMBA1004507//ESTs, Weakly similar to T19B10.6 [C.elegans]//1.4e-61:29
 6:99//Hs.114622:AA693492
 F-HEMBA1004509//Homo sapiens suppressor of white apricot homolog 2 (SWAP
 2) mRNA, complete cds//0.014:265:61//Hs.43543:AF042800
 F-HEMBA1004534//Filamin 1 (actin-binding protein-280)//5.0e-74:678:74//H
 s.76279:X53416
 F-HEMBA1004538//EST//0.00047:268:58//Hs.136870:AA805381
 F-HEMBA1004542//Human butyrophilin protein (BT3.3) mRNA, partial cds//0.
 74:74:75//Hs.87497:U90552
 F-HEMBA1004554
 F-HEMBA1004560//ESTs//3.1e-19:240:73//Hs.112637:AA805331
 F-HEMBA1004573//EST//2.4e-59:290:99//Hs.112908:AA620802
 F-HEMBA1004577//ESTs, Weakly similar to UTR1 PROTEIN [S.cerevisiae]//1.2
 e-17:334:67//Hs.24536:AA479825
 F-HEMBA1004586//Von Hippel-Lindau syndrome//5.1e-35:337:78//Hs.78160:AF0
 10238

F-HEMBA1004596//ESTs//3.3e-32:189:94//Hs.42530:N41661
 F-HEMBA1004604//Human hindlimb expressed homeobox protein backfoot (Bft)
 mRNA, complete cds//0.42:186:66//Hs.84136:U70370
 F-HEMBA1004610//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING
 ENTRY !!!! [H.sapiens]//2.3e-16:297:68//Hs.106008:AA147606
 F-HEMBA1004617//EST//0.027:188:61//Hs.159094:AI383198
 F-HEMBA1004629//ESTs//7.8e-09:348:63//Hs.138358:T66178
 F-HEMBA1004631//EST//0.0012:268:60//Hs.150685:AA923416
 F-HEMBA1004632//ESTs//0.82:125:67//Hs.143619:AI360891
 F-HEMBA1004637//ESTs//0.0034:229:64//Hs.157178:AI346780
 F-HEMBA1004638//ESTs//2.0e-11:166:71//Hs.128657:AI017522
 F-HEMBA1004666//EST//0.44:294:58//Hs.44780:N36083
 F-HEMBA1004669//ESTs//1.7e-28:200:86//Hs.8084:W22796
 F-HEMBA1004670//Mucin 1, transmembrane//0.060:416:57//Hs.89603:J05582
 F-HEMBA1004672//ESTs//0.27:44:95//Hs.86237:AA206141
 F-HEMBA1004693//ESTs//5.3e-55:301:95//Hs.159066:AI093252
 F-HEMBA1004697//H.sapiens mRNA for ribosomal protein L18a homologue//0.6
 4:313:61//Hs.118578:X80821
 F-HEMBA1004705//Homo sapiens KIAA0432 mRNA, complete cds//4.5e-19:230:73
 //Hs.155174:AB007892
 F-HEMBA1004709//ESTs//3.1e-31:176:88//Hs.152413:AA780515
 F-HEMBA1004711//Cholinergic receptor, nicotinic, delta polypeptide//1.0:
 244:57//Hs.99975:X55019
 F-HEMBA1004725//Homo sapiens agrin precursor mRNA, partial cds//0.24:328
 :60//Hs.68900:AF016903
 F-HEMBA1004730//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//5
 .9e-32:476:70//Hs.116874:AA524909
 F-HEMBA1004733//ESTs//3.8e-16:96:79//Hs.152413:AA780515
 F-HEMBA1004734//Human epidermoid carcinoma mRNA for ubiquitin-conjugatin

g enzyme E2 similar to Drosophila bendless gene product, complete cds//0.16:329:58//Hs.75355:D83004

F-HEMBA1004736//Human Line-1 repeat mRNA with 2 open reading frames//2.0e-61:663:71//Hs.23094:M19503

F-HEMBA1004748//ESTs//1.5e-05:343:63//Hs.42241:H96813

F-HEMBA1004751//ESTs//3.7e-32:147:80//Hs.138788:N54504

F-HEMBA1004752//Homo sapiens mRNA for KIAA0288 gene, complete cds//0.00020:521:59//Hs.91400:AB006626

F-HEMBA1004753//Homo sapiens DEC-205 mRNA, complete cds//5.1e-46:337:84//Hs.153563:AF011333

F-HEMBA1004756//Human transporter protein (gl7) mRNA, complete cds//3.1e-24:416:65//Hs.76460:U49082

F-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds//1.2e-136:769:91//Hs.153088:L39060

F-HEMBA1004763//Loricrin//0.0018:227:62//Hs.155657:M61120

F-HEMBA1004768//Human Line-1 repeat mRNA with 2 open reading frames//4.5e-115:909:78//Hs.23094:M19503

F-HEMBA1004770//Human Rad50 (Rad50) mRNA, complete cds//0.020:728:57//Hs.41587:U63139

F-HEMBA1004771

F-HEMBA1004776//ESTs, Weakly similar to progesterone receptor-related protein p23 [H.sapiens]//1.0:158:63//Hs.62004:AF039235

F-HEMBA1004778//ESTs//1.2e-70:336:99//Hs.113052:AI222106

F-HEMBA1004795

F-HEMBA1004803//ESTs//5.0e-75:454:88//Hs.138632:H97952

F-HEMBA1004806//EST//0.080:142:65//Hs.160268:AI148971

F-HEMBA1004807//Human HIV1 tata element modulatory factor mRNA sequence from chromosome 3//4.5e-48:171:92//Hs.134510:L01042

F-HEMBA1004816//EST//1.0e-17:175:71//Hs.140680:AA873646

F-HEMBA1004820//ESTs//1.3e-136:629:99//Hs.160726:AI300481
 F-HEMBA1004847//ESTs//2.1e-09:66:98//Hs.158161:AA312511
 F-HEMBA1004850//EST//0.033:253:64//Hs.158782:AI376601
 F-HEMBA1004863//Homo sapiens mRNA for KIAA0578 protein, partial cds//0.8
 3:179:62//Hs.22998:AB011150
 F-HEMBA1004864//ESTs, Weakly similar to ANON-66Db [D.melanogaster]//1.7e
 -13:81:100//Hs.75884:AA446987
 F-HEMBA1004865//ESTs//0.92:148:65//Hs.126980:AA934077
 F-HEMBA1004880//H.sapiens mRNA for retrotransposon//1.2e-30:264:79//Hs.6
 940:Z48633
 F-HEMBA1004889//Growth arrest-specific 1//0.20:146:68//Hs.65029:L13698
 F-HEMBA1004900//ESTs//1.6e-32:196:93//Hs.132032:R85304
 F-HEMBA1004909//ESTs//3.4e-13:154:75//Hs.151467:N51106
 F-HEMBA1004918//EST//0.78:122:61//Hs.145491:AI254348
 F-HEMBA1004923//ELK1, member of ETS oncogene family//1.6e-40:340:79//Hs.
 116549:AL009172
 F-HEMBA1004929//Cardiac gap junction protein//0.0048:588:57//Hs.74471:X5
 2947
 F-HEMBA1004930//ESTs//1.5e-17:227:74//Hs.148739:AI224959
 F-HEMBA1004933//Human pseudoautosomal homeodomain-containing protein (PH
 OG) mRNA, complete cds//0.11:182:65//Hs.105932:U89331
 F-HEMBA1004934
 F-HEMBA1004944//EST//1.2e-67:349:96//Hs.162281:AA553981
 F-HEMBA1004954//ESTs//0.014:404:60//Hs.11177:AA417813
 F-HEMBA1004956//EST//2.3e-05:208:64//Hs.146958:AI174478
 F-HEMBA1004960//ESTs//0.79:169:62//Hs.11637:W03274
 F-HEMBA1004972
 F-HEMBA1004973//Homo sapiens mRNA for KIAA0445 protein, complete cds//0.
 073:574:58//Hs.154139:AB007914

F-HEMBA1004977//EST//4.4e-12:86:94//Hs.157819:AI361946
 F-HEMBA1004978//ESTs//0.097:337:60//Hs.114157:AA703013
 F-HEMBA1004980//EST//3.2e-10:169:65//Hs.149123:AI244750
 F-HEMBA1004983//EST//0.93:85:71//Hs.162267:AA553589
 F-HEMBA1004995//ESTs//0.46:296:61//Hs.135168:AI394026
 F-HEMBA1005008//ESTs//1.5e-20:156:85//Hs.114140:U35429
 F-HEMBA1005009//Homo sapiens chromosome 7q22 sequence//1.5e-52:379:72//Hs.151887:AF053356
 F-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds//4.5e-148:693:98//Hs.31921:AB014548
 F-HEMBA1005029//Homo sapiens mRNA for KIAA0660 protein, complete cds//1.0:215:65//Hs.6727:AB014560
 F-HEMBA1005035//ESTs, Weakly similar to HYPOTHETICAL 82.8 KD PROTEIN B0303.4 IN CHROMOSOME III [C.elegans]//9.4e-106:503:98//Hs.21362:AF039237
 F-HEMBA1005039//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//5.8e-60:272:89//Hs.103948:K00627
 F-HEMBA1005047//Homo sapiens MAD-related gene SMAD7 (SMAD7) mRNA, complete cds//0.078:442:59//Hs.100602:AF010193
 F-HEMBA1005050//H. sapiens ERF-2 mRNA//0.0025:251:63//Hs.78909:U07802
 F-HEMBA1005062//ESTs//0.020:268:59//Hs.146181:AI264462
 F-HEMBA1005066//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//1.5e-59:411:85//Hs.129727:AF035587
 F-HEMBA1005075//Human mRNA for KIAA0383 gene, partial cds//0.00010:395:57//Hs.27590:AB002381
 F-HEMBA1005079//Dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex)//3.5e-26:344:72//Hs.89479:X66785
 F-HEMBA1005083//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.59:631:59//Hs.27910:AF049105

F-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete
 cds//4.1e-163:762:98//Hs.11170:AF080561
 F-HEMBA1005113//ESTs//0.52:109:68//Hs.106330:AI031916
 F-HEMBA1005123//Homo sapiens mRNA for KIAA0761 protein, partial cds//1.3
 e-52:468:78//Hs.93121:AB018304
 F-HEMBA1005133//ESTs//1.6e-27:366:73//Hs.151467:N51106
 F-HEMBA1005149//EST//3.3e-37:304:80//Hs.132635:AI032875
 F-HEMBA1005152//ESTs//3.9e-09:285:62//Hs.155876:AA593021
 F-HEMBA1005159//EST//8.4e-05:289:64//Hs.125563:AA884216
 F-HEMBA1005185//ESTs//1.4e-22:129:96//Hs.14920:AA910914
 F-HEMBA1005201//EST//4.0e-16:96:98//Hs.89002:AA282197
 F-HEMBA1005202
 F-HEMBA1005206//Homo sapiens sox1 gene//0.0079:431:58//Hs.144029:Y13436
 F-HEMBA1005219//ESTs//4.3e-47:299:88//Hs.5019:W26547
 F-HEMBA1005223//ESTs//0.00030:168:66//Hs.76487:N37081
 F-HEMBA1005232//EST//0.0078:209:61//Hs.46852:N48302
 F-HEMBA1005241//Homo sapiens neuronal thread protein AD7c-NTP mRNA, comp
 lete cds//6.0e-54:399:79//Hs.129735:AF010144
 F-HEMBA1005244//ESTs//2.5e-14:85:100//Hs.128744:AI191922
 F-HEMBA1005251//ESTs//0.012:49:95//Hs.161554:AA393896
 F-HEMBA1005252//Homo sapiens mRNA for KIAA0585 protein, partial cds//4.7
 e-151:705:98//Hs.72660:AB011157
 F-HEMBA1005274//ESTs//7.1e-09:298:64//Hs.145522:AI261380
 F-HEMBA1005275//ESTs//7.9e-13:375:63//Hs.148974:AA001777
 F-HEMBA1005293//Homo sapiens clone 23662 mRNA sequence//7.7e-22:338:65//
 Hs.12451:U97018
 F-HEMBA1005296//ESTs//0.055:299:60//Hs.86320:AI149232
 F-HEMBA1005304//Small inducible cytokine A5 (RANTES)//1.7e-45:322:85//Hs
 .155464:AF088219

F-HEMBA1005311
 F-HEMBA1005314//ESTs//8.1e-39:199:98//Hs.119974:AI279516
 F-HEMBA1005315//ESTs//1.9e-07:266:64//Hs.141440:N21615
 F-HEMBA1005318//ESTs//5.3e-06:161:72//Hs.119411:AA937117
 F-HEMBA1005331//Human checkpoint suppressor 1 mRNA, complete cds//0.0007
 5:310:63//Hs.111597:U68723
 F-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial//4.4e-153:740:
 97//Hs.129361:AJ007581
 F-HEMBA1005353//EST//5.4e-09:222:68//Hs.119508:AA485732
 F-HEMBA1005359//Zinc finger protein 137 (clone pHZ-30)//5.7e-100:500:88/
 /Hs.151689:U09414
 F-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1) mRNA, complete cds//2.
 5e-70:572:73//Hs.43265:AF071787
 F-HEMBA1005372//ESTs//0.00045:163:66//Hs.164058:AI417905
 F-HEMBA1005374//Human melanoma antigen recognized by T-cells (MART-1) mR
 NA//6.1e-43:341:81//Hs.154069:U06452
 F-HEMBA1005382//EST//2.4e-32:167:99//Hs.147186:AI193053
 F-HEMBA1005389//ESTs//0.0021:245:59//Hs.104463:AA804448
 F-HEMBA1005394//ESTs, Weakly similar to No definition line found [C.eleg
 ans]//1.0e-130:620:98//Hs.108990:N25951
 F-HEMBA1005403//ESTs, Weakly similar to No definition line found [C.eleg
 ans]//7.7e-151:727:97//Hs.17118:AI033807
 F-HEMBA1005408//ESTs//3.2e-70:426:89//Hs.158078:H24513
 F-HEMBA1005410//EST//2.5e-25:460:67//Hs.138765:N70347
 F-HEMBA1005411
 F-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C)
 mRNA, complete cds//3.3e-171:537:99//Hs.4854:AF041248
 F-HEMBA1005426//EST//1.0:148:64//Hs.44469:N33323
 F-HEMBA1005443//Zinc finger protein 157 (HZF22)//9.0e-34:259:72//Hs.8989

7:U28687

F-HEMBA1005447//EST//3.9e-10:211:70//Hs.145960:AI276783

F-HEMBA1005468//ESTs//8.4e-53:390:81//Hs.152395:AA533107

F-HEMBA1005469//Human (clone E5.1) RNA-binding protein mRNA, complete cd
s//3.1e-29:155:99//Hs.75104:L37368

F-HEMBA1005472//Human Line-1 repeat mRNA with 2 open reading frames//1.4
e-88:481:92//Hs.23094:M19503

F-HEMBA1005474//Small inducible cytokine A5 (RANTES)//4.2e-29:257:78//Hs
.155464:AF088219

F-HEMBA1005475//Homo sapiens antigen NY-CO-16 mRNA, complete cds//5.3e-0
9:414:60//Hs.132206:AF039694

F-HEMBA1005497//Glucocorticoid receptor alpha [alternative products]//8.
7e-41:588:69//Hs.102761:U25029

F-HEMBA1005500//Homo sapiens PAC clone DJ1093017 from 7q11.23-q21//1.1e-
28:318:73//Hs.159530:AC004957

F-HEMBA1005506//Human mRNA for KIAA0010 gene, complete cds//0.67:351:58/
/Hs.155287:D13635

F-HEMBA1005508//ESTs//0.45:326:59//Hs.102756:AA526911

F-HEMBA1005511//Human mRNA for KIAA0355 gene, complete cds//4.2e-49:400:
79//Hs.153014:AB002353

F-HEMBA1005513//ESTs, Weakly similar to males-absent on the first [D.mel
anogaster]//5.3e-76:378:97//Hs.22767:N99220

F-HEMBA1005517//Homo sapiens transcription factor forkhead-like 7 (FKHL7
) gene, complete cds//0.54:623:56//Hs.143551:AF048693

F-HEMBA1005518//ESTs//0.10:207:60//Hs.72447:AA160575

F-HEMBA1005520//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//3.
1e-55:288:85//Hs.144563:AF057280

F-HEMBA1005526//Small inducible cytokine A5 (RANTES)//5.4e-48:176:76//Hs
.155464:AF088219

F-HEMBA1005528//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae] //1.2e-30:166:96//Hs.17035:AI080471

F-HEMBA1005530

F-HEMBA1005548//Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds//4.6e-18:391:64//Hs.30250:AF055376

F-HEMBA1005552//ESTs//1.8e-46:238:88//Hs.138856:H47461

F-HEMBA1005558//Human involucrin mRNA//3.0e-07:501:60//Hs.157091:M13903

F-HEMBA1005568//ESTs//0.013:259:63//Hs.13669:H47257

F-HEMBA1005570//ESTs//0.0084:442:59//Hs.125384:AI346507

F-HEMBA1005576//Homo sapiens mRNA for KIAA0463 protein, partial cds//1.9e-128:610:98//Hs.77738:AB007932

F-HEMBA1005577//ESTs//0.98:199:61//Hs.146226:AI312873

F-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//9.1e-53:830:64//Hs.57929:AB011538

F-HEMBA1005582

F-HEMBA1005583

F-HEMBA1005588//ESTs//1.3e-35:386:70//Hs.55855:AA621381

F-HEMBA1005593//S-ADENOSYLMETHIONINE SYNTHETASE ALPHA AND BETA FORMS//0.54:439:59//Hs.2137:D49357

F-HEMBA1005595//Human mRNA for KIAA0325 gene, partial cds//5.5e-06:378:57//Hs.7720:AB002323

F-HEMBA1005606//EST//2.0e-60:324:94//Hs.5062:D19609

F-HEMBA1005609//ESTs//6.0e-39:378:76//Hs.142242:H06982

F-HEMBA1005616//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//8.2e-22:721:61//Hs.144563:AF057280

F-HEMBA1005621//ESTs, Weakly similar to MITOTIC MAD2 PROTEIN [Saccharomyces cerevisiae] //1.8e-89:454:96//Hs.19400:AA662845

F-HEMBA1005627//EST//1.0:161:60//Hs.162765:AA622535

F-HEMBA1005631//EST//0.74:124:62//Hs.156185:AA723734

F-HEMBA1005632//ESTs//1.0:96:70//Hs.141321:N70199
 F-HEMBA1005634//EST//6.6e-10:105:73//Hs.159692:AI416956
 F-HEMBA1005666
 F-HEMBA1005670//Homo sapiens mRNA for KIAA0570 protein, complete cds//2.
 7e-45:255:79//Hs.114293:AB011142
 F-HEMBA1005679//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//
 1.2e-37:356:77//Hs.139107:K00629
 F-HEMBA1005680
 F-HEMBA1005685
 F-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (E
 plg8) mRNA, complete cds//3.3e-71:497:85//Hs.26988:U66406
 F-HEMBA1005705//ESTs//0.00093:149:65//Hs.163564:R43678
 F-HEMBA1005717//EST//0.018:115:66//Hs.160541:AI270143
 F-HEMBA1005732//Farnesyl diphosphate synthase (farnesyl pyrophosphate sy
 nthetase, dimethylallyltranstransferase, geranyltranstransferase)//2.6e-
 20:151:88//Hs.77393:D14697
 F-HEMBA1005737//ESTs//9.5e-34:235:88//Hs.160197:AA393754
 F-HEMBA1005746//ESTs//0.20:260:59//Hs.112451:AI264024
 F-HEMBA1005755//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//
 1.8e-48:425:78//Hs.103948:K00627
 F-HEMBA1005765//Small inducible cytokine A5 (RANTES)//1.3e-36:280:81//Hs
 .155464:AF088219
 F-HEMBA1005780//ESTs//1.0:139:67//Hs.88684:AA885141
 F-HEMBA1005813//ESTs//0.012:209:63//Hs.113365:R77747
 F-HEMBA1005815//Human calpain-like protease (htra-3) mRNA, complete cds/
 /2.0e-07:439:62//Hs.6133:U94346
 F-HEMBA1005822//ESTs//9.3e-06:444:59//Hs.124344:T10577
 F-HEMBA1005829//ESTs//1.1e-47:394:80//Hs.146811:AA410788
 F-HEMBA1005834//Human Line-1 repeat mRNA with 2 open reading frames//7.9

e-42:690:66//Hs.23094:M19503
 F-HEMBA1005852//Human plectin (PLEC1) mRNA, complete cds//0.17:470:56//H
 s.79706:U53204
 F-HEMBA1005853//EST//0.013:211:60//Hs.162604:AA595150
 F-HEMBA1005884//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
 0484//1.4e-53:332:83//Hs.158095:AB007953
 F-HEMBA1005891//ESTs//1.1e-77:393:97//Hs.28545:AI268097
 F-HEMBA1005894//Human G protein-coupled receptor (STRL22) mRNA, complete
 cds//7.2e-45:411:77//Hs.46468:U45984
 F-HEMBA1005909//Human neuropeptide y2 receptor mRNA, complete cds//0.000
 54:477:59//Hs.37125:U42766
 F-HEMBA1005911//Thromboxane A2 receptor//4.1e-45:419:75//Hs.89887:D38081
 F-HEMBA1005921//Homo sapiens haemopoietic progenitor homeobox HPX42B (HP
 X42B) mRNA, complete cds//2.0e-46:434:78//Hs.125231:AF068006
 F-HEMBA1005931//ESTs, Weakly similar to kruppel-related zinc finger prot
 ein [H.sapiens]//1.2e-46:228:100//Hs.152178:AI224880
 F-HEMBA1005934//EST//3.1e-14:121:85//Hs.150003:AI291588
 F-HEMBA1005962//EST//0.0010:212:62//Hs.163197:AA767883
 F-HEMBA1005963
 F-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, comple
 te cds//4.2e-151:697:99//Hs.26285:AF082516
 F-HEMBA1005991//EST//3.0e-07:361:59//Hs.146442:AI127530
 F-HEMBA1005999//EST//1.2e-14:350:66//Hs.122326:AA782526
 F-HEMBA1006002
 F-HEMBA1006005//ESTs, Weakly similar to TH1 protein [D.melanogaster]//0.
 98:197:61//Hs.5184:AA709151
 F-HEMBA1006031
 F-HEMBA1006035
 F-HEMBA1006036//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.4e-92:61

7:84//Hs.113283:AF018080
 F-HEMBA1006042//ESTs//6.3e-41:161:81//Hs.141186:R99609
 F-HEMBA1006067//ESTs//2.0e-74:354:99//Hs.143321:AI139422
 F-HEMBA1006081
 F-HEMBA1006090//EST//1.2e-12:340:62//Hs.161195:AI418788
 F-HEMBA1006091//ESTs//4.7e-98:473:98//Hs.9658:AA506313
 F-HEMBA1006100//ESTs//7.1e-22:273:73//Hs.144407:AA737799
 F-HEMBA1006108//ESTs, Weakly similar to ZK792.1 [C.elegans]//2.1e-26:273
 :66//Hs.8763:W30741
 F-HEMBA1006121//EST//0.00012:232:59//Hs.117096:AA677968
 F-HEMBA1006124//EST//0.047:251:62//Hs.132257:AI027222
 F-HEMBA1006130//Human HOX4C mRNA for a homeobox protein//1.0:150:62//Hs.
 74061:X59372
 F-HEMBA1006138//ESTs//1.8e-27:132:84//Hs.141575:AA211734
 F-HEMBA1006142//EST//2.5e-47:310:87//Hs.149580:AI281881
 F-HEMBA1006155
 F-HEMBA1006158//ESTs//5.1e-105:506:98//Hs.93468:N40575
 F-HEMBA1006173//ESTs//2.5e-24:195:84//Hs.79092:H29627
 F-HEMBA1006182//ESTs//2.5e-19:237:72//Hs.141840:AA028117
 F-HEMBA1006198//ESTs//0.017:133:67//Hs.142168:AA292540
 F-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//8.6e-177:836:98/
 /Hs.109268:AF070557
 F-HEMBA1006248//Human zinc finger protein (MAZ) mRNA//0.0014:221:67//Hs.
 7647:M94046
 F-HEMBA1006252
 F-HEMBA1006253//EST//1.3e-100:467:100//Hs.146619:AI140706
 F-HEMBA1006259//Homo sapiens mRNA for KIAA0798 protein, complete cds//0.
 00037:158:69//Hs.159277:AB018341
 F-HEMBA1006268//ESTs//1.1e-20:376:67//Hs.72814:AA706631

F-HEMBA1006272//EST//4.8e-20:252:69//Hs.162992:AA688140
 F-HEMBA1006278//H.sapiens PAP mRNA//6.5e-57:610:71//Hs.49007:X76770
 F-HEMBA1006283
 F-HEMBA1006284//ESTs//0.00017:248:63//Hs.143840:AI189964
 F-HEMBA1006291
 F-HEMBA1006293
 F-HEMBA1006309//Homo sapiens T cell immune response cDNA7 (TIRC7) mRNA,
 complete cds//0.76:416:58//Hs.46465:U45285
 F-HEMBA1006310//Homo sapiens mRNA for KIAA0602 protein, partial cds//9.3
 e-49:637:68//Hs.37656:AB011174
 F-HEMBA1006328//ESTs//1.8e-71:429:88//Hs.139922:AA281350
 F-HEMBA1006334//EST//0.082:267:57//Hs.136449:AA572789
 F-HEMBA1006344//ESTs//6.2e-08:67:94//Hs.42302:AI032142
 F-HEMBA1006347//ESTs, Weakly similar to males-absent on the first [D.mel
 anogaster] //5.3e-76:378:97//Hs.22767:N99220
 F-HEMBA1006349//ESTs//0.87:276:60//Hs.23628:H03287
 F-HEMBA1006359//Zinc finger protein 43 (HTF6)//4.4e-117:823:81//Hs.74107
 :X59244
 F-HEMBA1006364//EST//0.0012:168:66//Hs.156756:AI351026
 F-HEMBA1006377//Homo sapiens RalBP1-interacting protein (POB1) mRNA, com
 plete cds//0.0028:422:59//Hs.80667:AF010233
 F-HEMBA1006380//Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c
) mRNA, complete cds//0.41:265:61//Hs.8813:AF032922
 F-HEMBA1006381//ESTs//3.8e-78:382:98//Hs.132171:AI042531
 F-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frames//2.1
 e-49:395:80//Hs.23094:M19503
 F-HEMBA1006416//EST//7.3e-12:154:77//Hs.134086:AI077477
 F-HEMBA1006419//EST//4.6e-51:179:86//Hs.149580:AI281881
 F-HEMBA1006421//ISLET AMYLOID POLYPEPTIDE PRECURSOR//4.9e-46:517:72//Hs.

51048:X68830

F-HEMBA1006424//ESTs//2.7e-08:380:60//Hs.44369:AI206835

F-HEMBA1006426//ESTs//3.0e-98:465:99//Hs.129251:AA993264

F-HEMBA1006438//EST//1.3e-29:183:93//Hs.147412:AI209194

F-HEMBA1006445

F-HEMBA1006446//EST//0.14:200:59//Hs.160695:AI282889

F-HEMBA1006461//Thiopurine S-methyltransferase//1.4e-29:210:72//Hs.51124

:AF019369

F-HEMBA1006467

F-HEMBA1006471//ESTs//1.4e-05:391:60//Hs.121282:AI091453

F-HEMBA1006474//ESTs, Highly similar to 40 KD PROTEIN [Borna disease virus]//1.1e-13:346:63//Hs.31257:AA875998

F-HEMBA1006483//Thromboxane A2 receptor//2.2e-51:386:82//Hs.89887:D38081

F-HEMBA1006485//EST//5.4e-111:516:99//Hs.61925:AA039532

F-HEMBA1006486//EST//4.7e-23:286:72//Hs.137800:AA886897

F-HEMBA1006489//ESTs//2.5e-06:137:71//Hs.128621:AA910431

F-HEMBA1006492

F-HEMBA1006494//ESTs//8.5e-24:299:72//Hs.153413:AI248625

F-HEMBA1006497//EST//0.00034:431:61//Hs.130057:AA903389

F-HEMBA1006502//ESTs//2.6e-11:131:80//Hs.141267:H22072

F-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//7.3e-141:470:98//Hs.153858:AB014566

F-HEMBA1006521//ESTs, Weakly similar to 3-oxoacyl-[acyl-carrier protein] reductase [E.coli]//3.9e-98:483:97//Hs.94811:AA011185

F-HEMBA1006530//EST//1.7e-42:530:71//Hs.163207:AA808002

F-HEMBA1006535//ESTs//2.9e-84:404:98//Hs.128679:AI160081

F-HEMBA1006540//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//4.4e-173:654:98//Hs.21301:AF093419

F-HEMBA1006546//ESTs//2.8e-45:391:78//Hs.146307:AA584638

F-HEMBA1006559//Homo sapiens KIAA0438 mRNA, complete cds//2.1e-47:363:79
 //Hs.21490:AB007898

F-HEMBA1006562//ESTs//4.5e-09:116:75//Hs.142368:AI198425

F-HEMBA1006566//EST//0.85:100:68//Hs.13052:T67136

F-HEMBA1006569//ESTs//2.7e-06:213:64//Hs.144372:AI346522

F-HEMBA1006579//EST//0.064:160:62//Hs.126244:AA873479

F-HEMBA1006583//Homo sapiens Jagged 2 mRNA, complete cds//1.7e-07:533:60
 //Hs.106387:AF029778

F-HEMBA1006595//Small inducible cytokine A5 (RANTES)//6.8e-69:328:81//Hs.
 .155464:AF088219

F-HEMBA1006597//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.6
 e-38:441:69//Hs.23711:AB018295

F-HEMBA1006612//ESTs//8.8e-135:668:97//Hs.7942:AA205862

F-HEMBA1006617//EST//4.6e-31:254:81//Hs.132635:AI032875

F-HEMBA1006624//ESTs, Weakly similar to HYPOTHETICAL 41.9 KD PROTEIN IN
 SDS3-THS1 INTERGENIC REGION [S.cerevisiae]//2.5e-75:379:97//Hs.40911:AI3
 91502

F-HEMBA1006631//ESTs//1.4e-126:612:98//Hs.131737:AI343331

F-HEMBA1006635//EST//0.65:145:63//Hs.104560:AA340589

F-HEMBA1006639//ESTs, Highly similar to POLYADENYLATE-BINDING PROTEIN [
 Homo sapiens]//9.1e-27:170:92//Hs.109818:AA411185

F-HEMBA1006643//ESTs, Moderately similar to putative p150 [H.sapiens]//9
 .7e-05:259:65//Hs.105747:AA505003

F-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete
 cds//3.9e-28:108:93//Hs.6196:U40282

F-HEMBA1006652//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L7 [Droso
 phila melanogaster]//3.0e-87:452:96//Hs.159574:AA190615

F-HEMBA1006653

F-HEMBA1006659//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//2.9e-92:

438:98//Hs.8173:AC005189
 F-HEMBA1006665//Homo sapiens clone 23892 mRNA sequence//2.8e-18:180:80//
 Hs.91916:AF035317
 F-HEMBA1006674//Homo sapiens mRNA for nucleolar protein hNop56//1.6e-16:
 122:90//Hs.5092:Y12065
 F-HEMBA1006676
 F-HEMBA1006682//EST//0.12:193:61//Hs.128367:AA974575
 F-HEMBA1006695//ESTs//5.6e-27:110:80//Hs.159510:AA297145
 F-HEMBA1006696//EST//3.2e-12:160:75//Hs.146472:AI128198
 F-HEMBA1006708
 F-HEMBA1006709//ESTs//0.69:60:80//Hs.152752:AA643545
 F-HEMBA1006717//ESTs//2.6e-31:286:78//Hs.55573:W37226
 F-HEMBA1006737//ESTs//1.6e-37:189:99//Hs.97490:AA394105
 F-HEMBA1006744//Human mRNA for KIAA0118 gene, partial cds//1.9e-52:360:8
 4//Hs.154326:D42087
 F-HEMBA1006754//Homo sapiens X-ray repair cross-complementing protein 2
 (XRCC2) mRNA, complete cds//2.0e-92:817:78//Hs.129727:AF035587
 F-HEMBA1006758//Human mRNA for KIAA0327 protein, complete cds//4.0e-10:5
 76:56//Hs.149323:AB002325
 F-HEMBA1006767//ESTs//1.7e-18:252:72//Hs.141073:W72720
 F-HEMBA1006779//EST//9.1e-26:395:69//Hs.145366:AI252657
 F-HEMBA1006780//EST//1.0:93:69//Hs.116946:AA680250
 F-HEMBA1006789//ESTs//0.0060:276:59//Hs.144121:AI369798
 F-HEMBA1006795//Human Line-1 repeat mRNA with 2 open reading frames//4.1
 e-37:781:64//Hs.23094:M19503
 F-HEMBA1006796//Human clone 23803 mRNA, partial cds//1.4e-07:202:68//Hs.
 34054:U79298
 F-HEMBA1006807//ESTs, Moderately similar to HYPOTHETICAL 46.4 KD PROTEIN
 T16H12.5 IN CHROMOSOME III [C.elegans]//4.8e-110:523:98//Hs.125790:AA28

7723

F-HEMBA1006821//EST//5.1e-11:246:66//Hs.150542:AI051551

F-HEMBA1006824//ESTs//1.4e-29:158:98//Hs.127712:AA961624

F-HEMBA1006832//EST//3.1e-24:277:74//Hs.139357:AA420970

F-HEMBA1006849//ESTs//0.99:332:57//Hs.128993:AA985327

F-HEMBA1006865

F-HEMBA1006877//ESTs, Highly similar to HYPOTHETICAL 113.8 KD PROTEIN I
N ERG7-NMD2 INTERGENIC REGION [Saccharomyces cerevisiae]//2.4e-61:311:97
//Hs.127793:W25938

F-HEMBA1006885//ESTs, Highly similar to HYPOTHETICAL 29.1 KD PROTEIN IN
URA7-POL12 INTERGENIC REGION [Saccharomyces cerevisiae]//9.1e-128:805:8
7//Hs.32376:AA758214

F-HEMBA1006900//EST//6.8e-05:255:63//Hs.163173:AA781592

F-HEMBA1006914//EST//0.065:366:62//Hs.162914:AA666199

F-HEMBA1006921//ESTs//2.9e-42:347:82//Hs.159266:AI376989

F-HEMBA1006926//Human I kappa BR mRNA, complete cds//0.90:545:59//Hs.154
764:U16258

F-HEMBA1006929//EST//0.00013:403:61//Hs.162642:AA602539

F-HEMBA1006936//ESTs//0.00014:60:93//Hs.8737:W22712

F-HEMBA1006938//ESTs//4.7e-51:256:98//Hs.143651:AI150382

F-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein/
/4.4e-92:437:98//Hs.42644:AJ010841

F-HEMBA1006949//H.sapiens mRNA for retrotransposon//6.9e-43:385:76//Hs.6
940:Z48633

F-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete c
ds//1.8e-144:740:94//Hs.14934:AF004828

F-HEMBA1006976//H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2.3-sia
lyltransferase//1.9e-79:447:89//Hs.75268:X74570

F-HEMBA1006993//ESTs//5.4e-19:380:66//Hs.152635:AA600968

F-HEMBA1006996//ESTs//0.17:242:59//Hs.106879:AA054723
 F-HEMBA1007002
 F-HEMBA1007017//EST//1.0:59:72//Hs.113400:R39282
 F-HEMBA1007018//Homo sapiens dynein light intermediate chain 2 (LIC2) mRNA, complete cds//2.5e-78:827:70//Hs.43003:AF035812
 F-HEMBA1007045
 F-HEMBA1007051//EST//0.85:65:73//Hs.158641:AI370659
 F-HEMBA1007052
 F-HEMBA1007062
 F-HEMBA1007066//ESTs//0.94:160:63//Hs.56071:W52212
 F-HEMBA1007073//ESTs//3.6e-50:246:80//Hs.142678:H37845
 F-HEMBA1007078//Human arginine-rich nuclear protein mRNA, complete cds//6.7e-75:417:91//Hs.80510:M74002
 F-HEMBA1007080
 F-HEMBA1007085//Guanylate cyclase 2D, membrane (retina-specific)//1.3e-06:568:61//Hs.1974:M92432
 F-HEMBA1007087//Human mevalonate pyrophosphate decarboxylase (MPD) mRNA, complete cds//0.95:541:57//Hs.3828:U49260
 F-HEMBA1007112//ESTs//3.4e-104:494:98//Hs.19207:AA039595
 F-HEMBA1007113//ESTs//0.71:246:62//Hs.96235:AA196354
 F-HEMBA1007121//ESTs//3.5e-69:335:98//Hs.140519:AA643182
 F-HEMBA1007129
 F-HEMBA1007147//ESTs//3.2e-07:235:64//Hs.124813:W46172
 F-HEMBA1007149//ESTs//7.2e-08:161:68//Hs.121179:AA757136
 F-HEMBA1007151
 F-HEMBA1007174//Homo sapiens epsin 2b mRNA, complete cds//6.6e-64:318:97//Hs.22396:AF062085
 F-HEMBA1007178//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.2e-39:248:90//Hs.157148:AA311921

F-HEMBA1007194//ESTs//2.3e-107:503:99//Hs.100605:AA305965
 F-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//5.
 6e-158:478:98//Hs.3363:D86987
 F-HEMBA1007206//EST//0.23:119:66//Hs.144402:AA609252
 F-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//1.6
 e-177:839:98//Hs.27197:AB018340
 F-HEMBA1007243//Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan sy
 ndrome)//2.7e-56:647:69//Hs.82314:M31642
 F-HEMBA1007251//Human plectin (PLEC1) mRNA, complete cds//0.19:210:67//H
 s.79706:U53204
 F-HEMBA1007256//Homo sapiens clone 24407 mRNA sequence//1.0:144:64//Hs.1
 2432:AF070575
 F-HEMBA1007267//Human homolog of yeast mutL (hPMS1) gene, complete cds//
 0.99:239:60//Hs.111749:U13695
 F-HEMBA1007273//ESTs//5.6e-24:271:73//Hs.144951:N34836
 F-HEMBA1007279//ESTs//6.1e-36:185:78//Hs.141022:H06475
 F-HEMBA1007281//ESTs//0.74:94:65//Hs.162533:AA584529
 F-HEMBA1007288//EST//0.83:99:67//Hs.127878:AA968637
 F-HEMBA1007300//EST//3.6e-62:355:91//Hs.150139:AI300062
 F-HEMBA1007301//Collagen, type I, alpha 1//1.5e-09:406:61//Hs.111913:Z74
 615
 F-HEMBA1007319//EST//0.0068:50:96//Hs.163362:AA890506
 F-HEMBA1007320//ESTs//1.0:133:66//Hs.38032:N63634
 F-HEMBA1007322//ESTs//0.0077:187:66//Hs.4852:R84241
 F-HEMBA1007327//ESTs, Weakly similar to HOST CELL FACTOR C1 [H.sapiens] /
 /3.5e-09:144:76//Hs.20597:W58370
 F-HEMBA1007341//ESTs//7.5e-61:302:98//Hs.154944:AA494130
 F-HEMBA1007342//ESTs//2.9e-12:289:64//Hs.135555:AA911006
 F-HEMBA1007347//EST//0.44:89:70//Hs.65949:Z40561

F-HEMBB1000005//ESTs//1.6e-07:337:60//Hs.126718:AA916568
 F-HEMBB1000008//H.sapiens mRNA for translin associated protein X//1.1e-4
 3:370:78//Hs.96247:X95073
 F-HEMBB1000018//Nuclear factor of kappa light polypeptide gene enhancer
 in B-cells 1 (p105)//1.0:108:70//Hs.83428:M58603
 F-HEMBB1000024//EST//5.4e-07:137:70//Hs.125389:AA878307
 F-HEMBB1000025//EST//0.99:362:58//Hs.121221:AA757392
 F-HEMBB1000030//H.sapiens mRNA for cyclin II//1.3e-10:525:62//Hs.3232:Z
 46788
 F-HEMBB1000036
 F-HEMBB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, c
 omplete cds//6.2e-102:450:98//Hs.20815:AF084928
 F-HEMBB1000039//EST//0.0034:97:73//Hs.141684:W35358
 F-HEMBB1000044//ESTs//0.0048:218:63//Hs.123161:AA807319
 F-HEMBB1000048//EST//0.00025:222:62//Hs.122474:AA765131
 F-HEMBB1000050//ESTs//5.6e-28:293:75//Hs.136839:H93717
 F-HEMBB1000054//Human Line-1 repeat mRNA with 2 open reading frames//3.3
 e-54:259:88//Hs.23094:M19503
 F-HEMBB1000055//ESTs//0.0017:289:62//Hs.125755:AA286923
 F-HEMBB1000059//Homo sapiens mRNA for KIAA0761 protein, partial cds//5.9
 e-59:286:84//Hs.93121:AB018304
 F-HEMBB1000083
 F-HEMBB1000089//EST//0.0016:192:66//Hs.137093:AA917621
 F-HEMBB1000099//ESTs//5.7e-20:213:76//Hs.57883:AA218645
 F-HEMBB1000103//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//
 4.9e-43:418:74//Hs.103948:K00627
 F-HEMBB1000113//EST//4.6e-23:221:76//Hs.142065:AA173763
 F-HEMBB1000119//Homo sapiens ASMTL gene//2.5e-132:621:98//Hs.6315:Y15521
 F-HEMBB1000136//ESTs//2.3e-101:507:96//Hs.12659:AA195207

F-HEMBB1000141//ESTs//2.1e-15:283:69//Hs.126257:AI279044
 F-HEMBB1000144//EST//4.5e-52:298:91//Hs.149580:AI281881
 F-HEMBB1000173//Zinc finger protein 74 (Cos52)//2.4e-63:285:82//Hs.3057:
 X92715
 F-HEMBB1000175//EST//1.0:101:65//Hs.162898:AA659646
 F-HEMBB1000198//EST//0.99:179:56//Hs.116880:AA662457
 F-HEMBB1000215//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.4
 e-15:139:82//Hs.101414:AB011129
 F-HEMBB1000217//ESTs//3.4e-06:81:88//Hs.121151:T66277
 F-HEMBB1000218//EST//0.11:136:63//Hs.134683:AI092013
 F-HEMBB1000226//Fragile X mental retardation 1//0.99:126:65//Hs.89764:X6
 9962
 F-HEMBB1000240//H.sapiens mRNA for Nup88 protein//1.0:334:57//Hs.90734:Y
 08612
 F-HEMBB1000244//ESTs//3.2e-15:139:81//Hs.134549:AI078483
 F-HEMBB1000250//Homo sapiens protein associated with Myc mRNA, complete
 cds//2.1e-156:735:98//Hs.151411:AF075587
 F-HEMBB1000258//EST//0.0091:325:60//Hs.97533:AA435884
 F-HEMBB1000264//Human CHL1 potential helicase (CHLR1), complete cds//1.4
 e-33:100:100//Hs.27424:U75968
 F-HEMBB1000266//Homo sapiens mRNA for myosin phosphatase target subunit
 1 (MYPT1)//0.0019:373:60//Hs.16533:D87930
 F-HEMBB1000272//ESTs//1.3e-93:440:99//Hs.109224:N46684
 F-HEMBB1000274//ESTs//0.41:221:65//Hs.71990:AA151796
 F-HEMBB1000284//EST//0.00024:108:73//Hs.100725:F13689
 F-HEMBB1000307//EST//3.6e-10:149:73//Hs.140415:AA778574
 F-HEMBB1000312//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.
 00092:252:65//Hs.41153:AB018326
 F-HEMBB1000317//Thrombospondin 1//7.1e-05:342:59//Hs.87409:X14787

F-HEMBB1000318//EST//0.014:184:61//Hs.155758:AI311870
 F-HEMBB1000335//EST//0.99:187:63//Hs.137424:AA243729
 F-HEMBB1000336//EST//1.0:209:63//Hs.150410:AI003611
 F-HEMBB1000337//EST//0.086:133:66//Hs.128207:AA972330
 F-HEMBB1000338//EST//7.1e-07:129:72//Hs.140488:AA767127
 F-HEMBB1000339//Small inducible cytokine A5 (RANTES)//1.2e-36:336:76//Hs
 .155464:AF088219
 F-HEMBB1000341
 F-HEMBB1000343//EST//0.66:163:63//Hs.150822:AI302729
 F-HEMBB1000354//ESTs//7.1e-61:292:100//Hs.152266:AA926874
 F-HEMBB1000369//ESTs, Highly similar to t-BOP [M.musculus]//0.013:157:64
 //Hs.129982:AI420970
 F-HEMBB1000374//ESTs//8.7e-53:454:79//Hs.133518:R69934
 F-HEMBB1000376//ESTs//5.9e-14:87:97//Hs.163973:AA744348
 F-HEMBB1000391//ESTs//0.033:237:64//Hs.135289:AI092963
 F-HEMBB1000399//Homo sapiens mRNA for cell cycle checkpoint protein//9.4
 e-165:762:98//Hs.16184:AJ001642
 F-HEMBB1000402//EST//0.013:291:59//Hs.149191:AI246155
 F-HEMBB1000404//ESTs//3.0e-69:353:96//Hs.135857:AA947194
 F-HEMBB1000420//EST//6.3e-52:258:98//Hs.136434:AA557925
 F-HEMBB1000434//Homo sapiens neuronal thread protein AD7c-NTP mRNA, comp
 lete cds//9.4e-73:364:83//Hs.129735:AF010144
 F-HEMBB1000438//ESTs//0.073:446:58//Hs.134632:AI223429
 F-HEMBB1000441//Interleukin 10//1.7e-38:336:77//Hs.2180:M57627
 F-HEMBB1000449//EST//5.5e-21:356:67//Hs.157848:AI362501
 F-HEMBB1000455//ESTs//0.092:147:65//Hs.106446:N93227
 F-HEMBB1000472
 F-HEMBB1000480//EST//0.98:83:71//Hs.146462:AI124898
 F-HEMBB1000487//ESTs//1.4e-59:341:92//Hs.48561:N79206

F-HEM BB1000490//ESTs//2.5e-27:200:79//Hs.56825:AI057560
 F-HEM BB1000491
 F-HEM BB1000493//ESTs//0.019:103:69//Hs.138358:T66178
 F-HEM BB1000510//Glucocorticoid receptor alpha {alternative products} //1.
 6e-46:409:77//Hs.102761:U25029
 F-HEM BB1000518//ESTs//3.7e-06:187:64//Hs.140989:R68413
 F-HEM BB1000523//ESTs//0.69:332:59//Hs.106845:W19543
 F-HEM BB1000530//H.sapiens mRNA for extracellular matrix protein collagen
 type XIV, C-terminus//2.1e-38:138:96//Hs.36131:Y11710
 F-HEM BB1000550//ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING EN
 TRY !!!! [H.sapiens] //7.7e-31:554:67//Hs.157142:U85996
 F-HEM BB1000554//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
 0484//4.0e-27:282:75//Hs.158095:AB007953
 F-HEM BB1000556//Homo sapiens mRNA for KIAA0750 protein, complete cds//2.
 0e-33:537:65//Hs.5444:AB018293
 F-HEM BB1000564
 F-HEM BB1000573//H.sapiens HCG II mRNA//7.5e-27:197:76//Hs.146333:X81001
 F-HEM BB1000575//Von Hippel-Lindau syndrome//2.7e-72:255:79//Hs.78160:AF0
 10238
 F-HEM BB1000586//Dystrophin (muscular dystrophy, Duchenne and Becker type
 s), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS
 270, DXS272//0.011:338:59//Hs.79012:M18533
 F-HEM BB1000589//PLATELET GLYCOPROTEIN V PRECURSOR//2.4e-22:228:79//Hs.73
 734:Z23091
 F-HEM BB1000591//ESTs//1.0e-17:370:64//Hs.58156:W71990
 F-HEM BB1000592//EST//0.0038:51:88//Hs.148022:AI269323
 F-HEM BB1000593//Homo sapiens chromosome 7q22 sequence//4.7e-109:503:99//
 Hs.3386:AF053356
 F-HEM BB1000598//Ribosomal protein L5//3.5e-29:537:66//Hs.118781:U66589

F-HEMBB1000623//H.sapiens mRNA for GAIP protein//0.89:376:59//Hs.22698:X
91809

F-HEMBB1000630//Homo sapiens KIAA0404 mRNA, partial cds//0.074:168:61//H
s.105850:AB007864

F-HEMBB1000631//ESTs//1.7e-06:247:64//Hs.156864:AI346481

F-HEMBB1000632//Human mRNA for KIAA0351 gene, complete cds//5.1e-50:811:
65//Hs.29963:AB002349

F-HEMBB1000637//Sialophorin (gpL115, leukosialin, CD43)//2.4e-79:304:85/
/Hs.80738:X52075

F-HEMBB1000638//EST//0.0076:92:75//Hs.125496:AA883735

F-HEMBB1000643//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.5e-45:477:74//Hs.
51048:X68830

F-HEMBB1000649//Homo sapiens histone H2A.1b mRNA, complete cds//7.4e-52:
533:75//Hs.51011:L19778

F-HEMBB1000652//ESTs//1.6e-49:345:84//Hs.132722:AA618531

F-HEMBB1000665//EST//0.44:152:63//Hs.149534:AI280924

F-HEMBB1000671//Human Line-1 repeat mRNA with 2 open reading frames//2.2
e-79:280:85//Hs.23094:M19503

F-HEMBB1000673//ESTs//0.99:177:59//Hs.149864:N80474

F-HEMBB1000684//Protein kinase, interferon-inducible double stranded RNA
dependent//2.6e-31:220:87//Hs.73821:M35663

F-HEMBB1000693//Homo sapiens neuroan1 mRNA, complete cds//5.3e-120:575:9
7//Hs.158300:AF040723

F-HEMBB1000705//ESTs//4.7e-65:350:94//Hs.24610:R33125

F-HEMBB1000706//EST//8.6e-14:373:61//Hs.138281:R55703

F-HEMBB1000709//EST//0.99:110:65//Hs.162437:AA577510

F-HEMBB1000725//RAS-RELATED PROTEIN RAB-8//1.7e-77:635:77//Hs.123109:X56
741

F-HEMBB1000726//EST//1.3e-43:257:84//Hs.162197:AA535216

F-HEMBB1000738//EST//5.9e-13:259:64//Hs.159699:AI417328
 F-HEMBB1000749//EST//3.1e-42:271:87//Hs.162197:AA535216
 F-HEMBB1000763
 F-HEMBB1000770//ESTs, Weakly similar to MOESIN/EZRIN/RADIXIN HOMOLOG [D.
 melanogaster] //0.021:111:72//Hs.38178:AA921830
 F-HEMBB1000774//ESTs, Weakly similar to mTERF [H.sapiens] //2.5e-116:580:
 97//Hs.5009:AA081390
 F-HEMBB1000781//Human MEK kinase 3 mRNA, complete cds//5.3e-47:426:74//H
 s.86201:U78876
 F-HEMBB1000789//Homo sapiens mRNA for KIAA0677 protein, complete cds//3.
 0e-65:672:71//Hs.155983:AB014577
 F-HEMBB1000790//ESTs//1.2e-52:344:86//Hs.35254:AI133727
 F-HEMBB1000794//ESTs//0.00098:289:59//Hs.138782:N73572
 F-HEMBB1000807//ESTs//2.1e-91:434:99//Hs.61334:AI298375
 F-HEMBB1000810//ESTs//0.038:92:71//Hs.148763:AA668871
 F-HEMBB1000821//EST//0.94:129:62//Hs.162299:AA555154
 F-HEMBB1000822//ESTs//7.5e-05:199:63//Hs.117018:AA832421
 F-HEMBB1000826//ESTs//4.8e-13:343:65//Hs.153429:AI283069
 F-HEMBB1000827
 F-HEMBB1000831
 F-HEMBB1000835//EST//4.3e-27:201:85//Hs.141451:N29915
 F-HEMBB1000840//EST//6.3e-75:380:96//Hs.142557:AA464948
 F-HEMBB1000848//Human Line-1 repeat mRNA with 2 open reading frames//1.4
 e-135:875:85//Hs.23094:M19503
 F-HEMBB1000852//Phosphoribosyl pyrophosphate amidotransferase//0.12:292:
 61//Hs.311:U00238
 F-HEMBB1000870//EST//0.00091:246:62//Hs.126502:AA913831
 F-HEMBB1000876//Homo sapiens ELISC-1 mRNA, partial cds//4.9e-34:200:94//
 Hs.128434:AF085351

F-HEMBB1000883//ESTs//0.42:107:67//Hs.154173:AI379823
 F-HEMBB1000887
 F-HEMBB1000888//ESTs//1.0:137:67//Hs.8121:AA521290
 F-HEMBB1000890//ESTs//1.0:116:65//Hs.7105:T23433
 F-HEMBB1000893//EST//0.0079:408:58//Hs.146504:AI129834
 F-HEMBB1000908//EST//9.2e-21:205:79//Hs.132635:AI032875
 F-HEMBB1000910//Human mRNA for KIAA0231 gene, partial cds//0.16:327:60//
 Hs.7938:D86984
 F-HEMBB1000913//ESTs//1.0e-12:233:68//Hs.137545:AA487049
 F-HEMBB1000915//ESTs//2.5e-90:423:99//Hs.135254:AI095468
 F-HEMBB1000917//EST//2.8e-49:241:100//Hs.162216:AA548089
 F-HEMBB1000927//Hippocalcin//1.2e-31:528:65//Hs.89692:D16593
 F-HEMBB1000947
 F-HEMBB1000959//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//9
 .3e-48:572:72//Hs.2379:U23942
 F-HEMBB1000973//ESTs//4.5e-26:286:76//Hs.137393:AA142938
 F-HEMBB1000975//ESTs//0.78:180:66//Hs.104789:AA417124
 F-HEMBB1000981
 F-HEMBB1000985//Homo sapiens actin binding protein MAYVEN mRNA, complete
 cds//6.7e-07:308:62//Hs.122967:AF059569
 F-HEMBB1000991//EST//0.12:125:66//Hs.22945:R43713
 F-HEMBB1000996//ESTs//6.9e-05:273:63//Hs.133116:AI054055
 F-HEMBB1001004//Homo sapiens mRNA for KIAA0665 protein, complete cds//0.
 62:193:62//Hs.119004:AB014565
 F-HEMBB1001008//EST//4.7e-09:203:65//Hs.105221:AA489025
 F-HEMBB1001011//Human Chromosome 16 BAC clone CIT987SK-A-635H12//2.4e-17
 :384:67//Hs.108604:AC002310
 F-HEMBB1001014//EST, Weakly similar to putative p150 [H.sapiens]//0.21:2
 84:60//Hs.161547:W04991

F-HEMBB1001020//ESTs//9.7e-37:186:76//Hs.138852:AA284247
 F-HEMBB1001024//ESTs, Highly similar to t-BOP [M.musculus]//0.11:242:61/
 /Hs.129982:AI420970
 F-HEMBB1001037//EST//0.0057:192:66//Hs.149987:AI291177
 F-HEMBB1001047//ESTs//1.6e-22:360:70//Hs.120734:W58721
 F-HEMBB1001051//H.sapiens mRNA for FAN protein//3.8e-29:160:98//Hs.78687
 :X96586
 F-HEMBB1001056//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.
 0e-42:149:96//Hs.15832:AB014518
 F-HEMBB1001058//Small inducible cytokine A5 (RANTES)//1.1e-45:349:82//Hs
 .155464:AF088219
 F-HEMBB1001060//ESTs//1.6e-62:464:81//Hs.138663:N24942
 F-HEMBB1001063
 F-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds//9.9e-148:73
 6:95//Hs.12953:AF034803
 F-HEMBB1001096//EST//0.017:154:66//Hs.130403:AA909272
 F-HEMBB1001102//ESTs//2.1e-18:120:95//Hs.163767:R06293
 F-HEMBB1001105//Human BRCA2 region, mRNA sequence CG016//0.30:84:75//Hs.
 112434:U50529
 F-HEMBB1001112//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61
 ALPHA SUBUNIT [Canis familiaris]//9.3e-38:341:77//Hs.14038:R06800
 F-HEMBB1001114//EST//6.4e-07:296:62//Hs.128420:AA975062
 F-HEMBB1001117//EST//1.6e-99:464:99//Hs.130493:AA928139
 F-HEMBB1001119
 F-HEMBB1001126
 F-HEMBB1001133//H.sapiens mRNA for translin associated protein X//1.2e-2
 8:739:61//Hs.96247:X95073
 F-HEMBB1001137
 F-HEMBB1001142//Human mRNA for KIAA0331 gene, complete cds//2.1e-23:340:

69//Hs.146395:AB002329
 F-HEMBB1001151//ESTs//2.6e-30:252:79//Hs.6880:W26854
 F-HEMBB1001153//ESTs//7.6e-16:97:96//Hs.113307:H16716
 F-HEMBB1001169//ESTs//1.4e-32:374:71//Hs.161682:AA206863
 F-HEMBB1001175//Human mRNA for ankyrin motif, complete cds//7.1e-36:509:66//Hs.73073:D78334
 F-HEMBB1001177//ESTs, Weakly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN HXT14-PHA2. INTERGENIC REGION [S.cerevisiae]//1.5e-65:312:100//Hs.86878:AA599183
 F-HEMBB1001182//Electron-transfer-flavoprotein, beta polypeptide//0.94:199:64//Hs.74047:X71129
 F-HEMBB1001199
 F-HEMBB1001208//ESTs//0.12:120:69//Hs.130093:AA928802
 F-HEMBB1001209//EST//0.00028:215:65//Hs.118276:W15258
 F-HEMBB1001210//EST//2.9e-05:297:60//Hs.88840:AA281452
 F-HEMBB1001218//Homo sapiens mRNA for KIAA0585 protein, partial cds//8.5e-37:260:76//Hs.72660:AB011157
 F-HEMBB1001221//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//0.00046:650:58//Hs.158241:AB007976
 F-HEMBB1001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Mus musculus]//6.7e-103:477:100//Hs.127835:AI378790
 F-HEMBB1001242//Homo sapiens mRNA for LAK-1, complete cds//1.2e-31:458:67//Hs.129918:AB005754
 F-HEMBB1001249//EST//0.26:203:63//Hs.140791:AA935909
 F-HEMBB1001253//ESTs//4.0e-91:433:98//Hs.120636:AA325219
 F-HEMBB1001254//ESTs//2.0e-24:180:85//Hs.136391:H04977
 F-HEMBB1001267//Ataxia telangiectasia mutated (includes complementation groups A, C and D)//6.1e-24:146:78//Hs.51187:U82828
 F-HEMBB1001271//ESTs//2.5e-05:686:58//Hs.115423:AI359248

F-HEMBB1001282//GA-binding protein transcription factor, beta subunit 2 (47kd)//0.39:531:57//Hs.78915:U13045

F-HEMBB1001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK 353.7 IN CHROMOSOME III [Caenorhabditis elegans]//4.9e-10:91:89//Hs.16606:W81021

F-HEMBB1001289//ESTs//6.4e-100:467:99//Hs.151720:AI287890

F-HEMBB1001294//ESTs, Highly similar to RAS-LIKE PROTEIN TC10 [Homo sapiens]//1.3e-135:654:98//Hs.124217:AA020848

F-HEMBB1001302

F-HEMBB1001304//ESTs//0.98:109:68//Hs.138972:AA047725

F-HEMBB1001314//ESTs//7.4e-39:285:77//Hs.144749:AI217339

F-HEMBB1001315//Small inducible cytokine A5 (RANTES)//1.9e-40:355:78//Hs.155464:AF088219

F-HEMBB1001317//Human Line-1 repeat mRNA with 2 open reading frames//4.7e-98:625:85//Hs.23094:M19503

F-HEMBB1001326//ESTs//0.00030:257:63//Hs.62208:H12380

F-HEMBB1001331//ESTs, Weakly similar to DFS70 [H.sapiens]//1.0e-48:332:87//Hs.43071:AA206222

F-HEMBB1001335

F-HEMBB1001337//Homo sapiens mRNA for KIAA0563 protein, complete cds//8.5e-56:282:87//Hs.15731:AB011135

F-HEMBB1001339//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.039:161:65//Hs.132206:AF039694

F-HEMBB1001346//Oxytocin receptor//4.2e-42:456:73//Hs.2820:X64878

F-HEMBB1001348//Homo sapiens mRNA for KIAA0570 protein, complete cds//1.2e-45:176:77//Hs.114293:AB011142

F-HEMBB1001356//EST//0.32:292:59//Hs.135771:AI005648

F-HEMBB1001364

F-HEMBB1001366//EST//7.8e-24:367:69//Hs.138765:N70347

F-HEMBB1001367//Small inducible cytokine A5 (RANTES)//8.7e-50:326:86//Hs.155464:AF088219

F-HEMBB1001369//EST//0.17:211:63//Hs.120066:AA707973

F-HEMBB1001380//Homo sapiens mRNA for KIAA0527 protein, partial cds//8.2e-36:225:79//Hs.129748:AB011099

F-HEMBB1001384

F-HEMBB1001387//ESTs//0.61:215:60//Hs.145915:AI342230

F-HEMBB1001394//Human Line-1 repeat mRNA with 2 open reading frames//3.8e-94:568:83//Hs.23094:M19503

F-HEMBB1001410//Homo sapiens keratan sulfate proteoglycan mRNA, complete cds//0.021:373:58//Hs.125750:AF065988

F-HEMBB1001424//EST//0.20:307:58//Hs.135336:AI049827

F-HEMBB1001426//Homo sapiens clone 23579 mRNA sequence//8.3e-17:205:72//Hs.83466:AF038174

F-HEMBB1001429//ESTs, Highly similar to CYTOSOL AMINOPEPTIDASE [Bos tau rus] //5.5e-153:729:96//Hs.21679:AF034175

F-HEMBB1001436//Human mRNA for KIAA0347 gene, complete cds//1.2e-44:316:85//Hs.101996:AB002345

F-HEMBB1001443

F-HEMBB1001449//Homo sapiens sodium bicarbonate cotransporter (HNBC1) mRNA, complete cds//0.033:478:58//Hs.5462:AF007216

F-HEMBB1001454//ESTs//1.4e-46:279:93//Hs.104866:AA426038

F-HEMBB1001458//EST//1.7e-09:106:83//Hs.141422:N20920

F-HEMBB1001463//Homo sapiens mRNA for semaphorin E, complete cds//0.18:387:59//Hs.62705:AB000220

F-HEMBB1001464//Homo sapiens Coch-5B2 mRNA, complete cds//0.26:189:67//Hs.21016:AF006740

F-HEMBB1001482//Homo sapiens mRNA for KIAA0760 protein, partial cds//1.2e-27:292:74//Hs.137168:AB018303

F-HEM BB1001500//ESTs//8.1e-28:312:74//Hs.18498:N52088
 F-HEM BB1001521//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//8.8e-54:359:74//Hs.46328:D87942
 F-HEM BB1001527//Protein tyrosine phosphatase, receptor type, f polypeptide//1.0:198:63//Hs.75216:Y00815
 F-HEM BB1001531//ESTs//4.3e-33:403:75//Hs.44862:N38735
 F-HEM BB1001535//ESTs//0.0029:47:93//Hs.124864:AA663093
 F-HEM BB1001536//ESTs//0.0047:120:68//Hs.144858:R67748
 F-HEM BB1001537//ESTs, Weakly similar to eukaryotic initiation factor eIF-2 alpha kinase [D.melanogaster]//3.7e-20:297:73//Hs.42457:AA523306
 F-HEM BB1001555//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//1.1e-35:188:77//Hs.102877:U41315
 F-HEM BB1001562//ESTs//0.95:161:61//Hs.145075:AI208240
 F-HEM BB1001564//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//3.4e-49:526:73//Hs.158095:AB007953
 F-HEM BB1001565//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.9e-44:324:84//Hs.113283:AF018080
 F-HEM BB1001585
 F-HEM BB1001586//EST//0.84:132:64//Hs.145264:AI218708
 F-HEM BB1001588//Human clone 23695 mRNA sequence//6.6e-20:327:67//Hs.90798:U79289
 F-HEM BB1001603//ESTs//1.3e-12:84:96//Hs.13380:R60414
 F-HEM BB1001618//ESTs//4.4e-11:349:63//Hs.132046:AA693680
 F-HEM BB1001619//ESTs//2.1e-06:246:63//Hs.63428:AA058314
 F-HEM BB1001630//EST//1.4e-07:334:62//Hs.145698:AI266713
 F-HEM BB1001635//ESTs//0.92:282:60//Hs.126980:AA934077
 F-HEM BB1001637//ELK1, member of ETS oncogene family//1.1e-27:395:64//Hs.116549:AL009172
 F-HEM BB1001641//EST//0.11:53:81//Hs.112445:AA594279

F-HEM BB1001653//EST//0.91:124:64//Hs.144213:T40480
 F-HEM BB1001665//Human mRNA for apolipoprotein E receptor 2, complete cds
 //7.0e-13:473:63//Hs.54481:D86407
 F-HEM BB1001668//ESTs//0.94:83:69//Hs.146202:AI252519
 F-HEM BB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//2.
 3e-172:803:98//Hs.24439:AB014546
 F-HEM BB1001684//ESTs, Highly similar to Tbc1 [M.musculus]//5.4e-20:110:1
 00//Hs.106104:AA599496
 F-HEM BB1001685//EST//2.2e-05:112:73//Hs.130984:AI015430
 F-HEM BB1001695//Human novel homeobox mRNA for a DNA binding protein//1.6
 e-08:425:62//Hs.37035:U07664
 F-HEM BB1001704//EST//5.8e-20:295:69//Hs.140231:AI054398
 F-HEM BB1001706
 F-HEM BB1001707//EST//0.091:241:60//Hs.136830:AA769219
 F-HEM BB1001717//ESTs//2.9e-06:325:60//Hs.150063:AI298064
 F-HEM BB1001735//Small inducible cytokine A5 (RANTES)//3.2e-46:326:83//Hs
 .155464:AF088219
 F-HEM BB1001736//ESTs, Weakly similar to E04D5.1 [C.elegans]//5.4e-99:485
 :97//Hs.120581:W25578
 F-HEM BB1001747//ESTs//8.3e-87:421:98//Hs.137051:AA884244
 F-HEM BB1001749//Homo sapiens neuronal thread protein AD7c-NTP mRNA, comp
 lete cds//3.5e-75:315:83//Hs.129735:AF010144
 F-HEM BB1001753//ESTs//0.00013:35:100//Hs.139643:H06263
 F-HEM BB1001756//ESTs//2.3e-89:433:98//Hs.128868:AA931077
 F-HEM BB1001760//ESTs//6.5e-06:503:58//Hs.21766:AI357639
 F-HEM BB1001762//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
 0507//2.9e-13:498:60//Hs.158241:AB007976
 F-HEM BB1001785//EST//0.16:262:60//Hs.162526:AA584102
 F-HEM BB1001797//ESTs//0.37:201:63//Hs.91559:AA806370

F-HEM BB1001802//ESTs//1.6e-06:447:58//Hs.134672:AI087951
 F-HEM BB1001812//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
 0487//1.3e-54:311:81//Hs.92381:AB007956
 F-HEM BB1001816//ESTs//2.2e-39:302:84//Hs.35985:AA783017
 F-HEM BB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCI
 P1) mRNA, complete cds//7.6e-164:763:98//Hs.159396:AF056209
 F-HEM BB1001834//TRICHOHYALIN//7.1e-05:548:60//Hs.82276:L09190
 F-HEM BB1001836//Human mRNA for KIAA0033 gene, partial cds//4.0e-34:272:8
 6//Hs.22271:D26067
 F-HEM BB1001839//Pyruvate carboxylase//0.050:686:59//Hs.89890:S72370
 F-HEM BB1001850//EST//0.0035:204:61//Hs.7311:T23858
 F-HEM BB1001863//Small inducible cytokine A5 (RANTES)//3.0e-48:357:82//Hs
 .155464:AF088219
 F-HEM BB1001867//ESTs//2.2e-40:265:88//Hs.146323:AI251752
 F-HEM BB1001868//ESTs//5.2e-06:131:73//Hs.123362:AA811371
 F-HEM BB1001869//ESTs//1.0e-86:429:96//Hs.141208:AA825503
 F-HEM BB1001872
 F-HEM BB1001874//H.sapiens mRNA for CHD5 protein//0.0033:388:60//Hs.19923
 :Y12478
 F-HEM BB1001875//H.sapiens mRNA for RNA helicase (Myc-regulated dead box
 protein)//0.32:346:60//Hs.100555:X98743
 F-HEM BB1001880//EST//4.0e-28:171:92//Hs.151194:AI125868
 F-HEM BB1001899//ESTs//0.17:242:62//Hs.136969:AA830918
 F-HEM BB1001905
 F-HEM BB1001906//ESTs//5.6e-49:290:92//Hs.127298:H09155
 F-HEM BB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA
 , complete cds//1.2e-83:672:81//Hs.82210:U47742
 F-HEM BB1001910//EST, Weakly similar to albumin [H.sapiens]//0.047:206:62
 //Hs.159777:Z19955

F-HEMBB1001911

F-HEMBB1001915//ESTs//0.92:136:71//Hs.144465:R68882

F-HEMBB1001921//EST//2.0e-19:398:67//Hs.44789:N36113

F-HEMBB1001922//ESTs//4.3e-05:370:59//Hs.123669:AA805245

F-HEMBB1001925//ESTs//5.7e-27:329:71//Hs.141071:H16398

F-HEMBB1001930//EST//0.043:157:63//Hs.161927:AA483904

F-HEMBB1001944//Human mRNA for KIAA0118 gene, partial cds//5.7e-55:444:80//Hs.154326:D42087

F-HEMBB1001945//ESTs//1.1e-19:142:88//Hs.7341:N57875

F-HEMBB1001947//Human mRNA for KIAA0392 gene, partial cds//1.8e-21:333:66//Hs.40100:AB002390

F-HEMBB1001950//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.020:384:60//Hs.8546:U97669

F-HEMBB1001952//EST//7.0e-13:302:63//Hs.120089:AA708101

F-HEMBB1001953//ATL-derived PMA-responsive (APR) peptide//0.97:252:60//Hs.96:D90070

F-HEMBB1001957//ESTs//6.1e-32:446:67//Hs.51305:T47418

F-HEMBB1001962//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//2.3e-31:390:70//Hs.1361:M55053

F-HEMBB1001967//H.sapiens mRNA for urea transporter//9.7e-52:322:88//Hs.66710:X96969

F-HEMBB1001973//Myelin oligodendrocyte glycoprotein (alternative products) //2.1e-48:426:78//Hs.53217:Z48051

F-HEMBB1001983

F-HEMBB1001988//ESTs//6.5e-05:237:63//Hs.49760:AA741051

F-HEMBB1001990//ESTs//0.25:171:64//Hs.7961:AA401205

F-HEMBB1001996//ESTs//1.8e-19:436:65//Hs.125539:AI339103

F-HEMBB1001997//EST//5.3e-33:294:76//Hs.161041:H82636

F-HEMBB1002002//ESTs//1.9e-06:224:67//Hs.110915:AA132964

F-HEMBB1002005//ESTs//5.8e-17:170:78//Hs.141825:AA017093
 F-HEMBB1002009//ESTs//0.066:441:58//Hs.125313:AI201685
 F-HEMBB1002015//EST//2.3e-18:310:68//Hs.145899:AI274951
 F-HEMBB1002042//CYTOCHROME P450 IVB1//2.9e-11:446:62//Hs.687:X16699
 F-HEMBB1002043//ESTs, Weakly similar to T06E6.d [C.elegans]//1.0:217:60/
 /Hs.3487:AA425553
 F-HEMBB1002044
 F-HEMBB1002045
 F-HEMBB1002049//Homo sapiens mRNA for KIAA0713 protein, partial cds//0.0
 82:201:61//Hs.88756:AB018256
 F-HEMBB1002050//Breakpoint cluster region protein BCR//0.84:267:59//Hs.2
 557:Y00661
 F-HEMBB1002068//Homo sapiens mRNA for KIAA0612 protein, partial cds//8.1
 e-07:402:61//Hs.112499:AB014512
 F-HEMBB1002069
 F-HEMBB1002092//EST//5.1e-15:180:75//Hs.127928:AA969239
 F-HEMBB1002094//EST//2.0e-52:264:98//Hs.71763:AA146625
 F-HEMBB1002115//EST//0.0083:244:64//Hs.125353:AA877080
 F-HEMBB1002134//ESTs//1.7e-69:398:91//Hs.157492:AI361027
 F-HEMBB1002139//ESTs//0.64:145:71//Hs.157821:AI362013
 F-HEMBB1002142//ESTs//0.013:311:59//Hs.150037:AI292214
 F-HEMBB1002152//ESTs//8.4e-12:121:82//Hs.119540:T95254
 F-HEMBB1002189//EST//0.26:81:70//Hs.147726:AI220208
 F-HEMBB1002190//Alcohol dehydrogenase 2 (class I), beta polypeptide//0.1
 6:608:58//Hs.4:X03350
 F-HEMBB1002193//Human sky mRNA for Sky, complete cds//6.6e-35:179:100//H
 s.301:U18934
 F-HEMBB1002217//Homo sapiens mRNA for zinc finger protein 10//3.7e-25:40
 5:67//Hs.104115:X52332

F-HEMBB1002218//EST//0.015:241:61//Hs.105298:AA489813

F-HEMBB1002232//Small inducible cytokine A5 (RANTES)//9.0e-31:365:71//Hs.155464:AF088219

F-HEMBB1002247

F-HEMBB1002249//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//6.8e-47:418:77//Hs.125231:AF068006

F-HEMBB1002254//Homo sapiens mRNA for KIAA0594 protein, partial cds//5.0e-47:437:77//Hs.154872:AB011166

F-HEMBB1002255//ESTs//0.017:255:61//Hs.126786:U74314

F-HEMBB1002266//Homo sapiens retinoblastoma-associated protein HEC mRNA, complete cds//0.17:511:57//Hs.58169:AF017790

F-HEMBB1002280//EST//4.0e-35:182:98//Hs.127701:AA864998

F-HEMBB1002300

F-HEMBB1002306//Human G protein-coupled receptor (STRL22) mRNA, complete cds//6.3e-14:228:72//Hs.46468:U45984

F-HEMBB1002327//EST//4.3e-21:242:75//Hs.72377:AA161083

F-HEMBB1002329//ESTs, Weakly similar to C17G10.1 [C.elegans]//1.7e-77:399:96//Hs.105837:AA536054

F-HEMBB1002340//INSULIN-DEGRADING ENZYME//1.0:319:60//Hs.1508:M21188

F-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein//1.4e-155:724:98//Hs.42644:AJ010841

F-HEMBB1002358//Deoxythymidylate kinase//1.1e-37:192:98//Hs.79006:L16991

F-HEMBB1002359//Human Rev interacting protein Rip-1 mRNA, complete cds//1.7e-06:66:96//Hs.154762:U00943

F-HEMBB1002364//EST//4.7e-16:201:73//Hs.149925:AI288838

F-HEMBB1002371//EST//2.4e-07:319:61//Hs.136459:AA577796

F-HEMBB1002381

F-HEMBB1002383//vasoactive intestinal peptide receptor 2//0.98:190:63//Hs.2126:L36566

F-HEMBB1002387//EST//2.1e-07:253:61//Hs.145993:AI277784
F-HEMBB1002409//ESTs//1.4e-11:94:91//Hs.125958:AI206456
F-HEMBB1002415//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0501//2.0e-32:371:73//Hs.159897:AB007970
F-HEMBB1002425//Fc fragment of IgA, receptor for//2.7e-32:156:82//Hs.544
86:X54150
F-HEMBB1002442
F-HEMBB1002453//Human mRNA for KIAA0118 gene, partial cds//5.6e-53:461:7
7//Hs.154326:D42087
F-HEMBB1002457//ESTs//3.4e-25:184:70//Hs.140225:AA704101
F-HEMBB1002458//ESTs//7.0e-10:343:62//Hs.163816:N76274
F-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds//6.0e-
89:493:92//Hs.159605:U43885
F-HEMBB1002489//Homo sapiens 195 kDa cornified envelope precursor mRNA,
complete cds//0.019:228:63//Hs.74304:AF001691
F-HEMBB1002492//EST//0.24:149:62//Hs.146790:AI149051
F-HEMBB1002495//Fc fragment of IgE, high affinity I, receptor for; beta
polypeptide//1.3e-22:331:71//Hs.30:M89796
F-HEMBB1002502//ESTs//1.3e-41:380:78//Hs.61199:AA024494
F-HEMBB1002509//ESTs//0.017:220:63//Hs.155263:AI273725
F-HEMBB1002510//ESTs//6.4e-102:476:99//Hs.152289:AI247354
F-HEMBB1002520//Human Line-1 repeat mRNA with 2 open reading frames//2.4
e-50:580:72//Hs.23094:M19503
F-HEMBB1002522//EST//0.010:172:62//Hs.147224:AI205719
F-HEMBB1002531
F-HEMBB1002534//Small inducible cytokine A5 (RANTES)//3.7e-59:258:88//Hs
.155464:AF088219
F-HEMBB1002545//ESTs//3.9e-24:181:86//Hs.13753:AI088102
F-HEMBB1002550//Syntaxin 5A//0.27:354:59//Hs.154546:U26648

F-HEMBB1002556//ESTs//1.7e-33:286:79//Hs.146173:AA906191
 F-HEMBB1002579//EST//1.0:77:68//Hs.147935:AI250286
 F-HEMBB1002582//ESTs//0.00032:178:68//Hs.139163:AA226095
 F-HEMBB1002590//ESTs//0.64:132:63//Hs.155688:AI003657
 F-HEMBB1002596//ESTs//3.4e-19:462:64//Hs.124399:AA832336
 F-HEMBB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds//3.0e-15
 2:710:98//Hs.129826:AF089749
 F-HEMBB1002601//EST//9.6e-13:368:62//Hs.137080:AA894817
 F-HEMBB1002603//EST//0.10:144:63//Hs.158180:AI367945
 F-HEMBB1002607//ESTs//0.024:345:62//Hs.143304:AI084058
 F-HEMBB1002610//EST//2.1e-14:291:64//Hs.140573:AA826323
 F-HEMBB1002613//ESTs//1.9e-17:192:75//Hs.141161:AA210711
 F-HEMBB1002614//ESTs//0.0048:136:71//Hs.106280:R13901
 F-HEMBB1002617//EST//0.034:320:59//Hs.41223:H89127
 F-HEMBB1002623//ESTs//0.88:222:60//Hs.129920:AA167217
 F-HEMBB1002635//Human MAP kinase mRNA, complete cds//3.1e-23:127:100//Hs
 .151051:U07620
 F-HEMBB1002664//EST//0.00013:203:61//Hs.117141:AA678811
 F-HEMBB1002677//ESTs//2.4e-22:439:66//Hs.132046:AA693680
 F-HEMBB1002683//ESTs//0.23:224:61//Hs.128883:AI026679
 F-HEMBB1002684//ESTs//7.2e-09:82:87//Hs.140457:H05124
 F-HEMBB1002686//EST//0.25:189:62//Hs.132431:AA909674
 F-HEMBB1002692//ESTs//0.00020:162:66//Hs.118180:N68504
 F-HEMBB1002697//EST//7.2e-17:219:74//Hs.100459:T61992
 F-HEMBB1002699//Homo sapiens transmembrane activator and CAML interactor
 (TACI) mRNA, complete cds//0.059:297:62//Hs.158341:AF023614
 F-HEMBB1002702//ESTs//0.26:284:61//Hs.41250:H89588
 F-HEMBB1002705//ESTs, Weakly similar to HYPOTHETICAL 38.5 KD PROTEIN IN
 SUI2-TDH2 INTERGENIC REGION [Saccharomyces cerevisiae]//0.0048:84:83//Hs

.20814:AI242922
 F-HEMBB1002712//ESTs//0.0025:317:58//Hs.7344:AA972729
 F-MAMMA1000009//Human c-yes-1 mRNA//1.0e-48:447:77//Hs.75680:M15990
 F-MAMMA1000019
 F-MAMMA1000020//EST//2.6e-84:431:95//Hs.143333:H51750
 F-MAMMA1000025//EST//1.0:169:59//Hs.130165:AA906945
 F-MAMMA1000043//Human NSCL-1 mRNA sequence//0.94:262:60//Hs.30956:M96739
 F-MAMMA1000045//ESTs//1.7e-48:499:75//Hs.158469:AA897461
 F-MAMMA1000055//ESTs, Highly similar to TESTIN 2 PRECURSOR [Mus musculus]//2.7e-18:330:63//Hs.59906:AA001281
 F-MAMMA1000057//Homo sapiens DNA fragmentation factor 40 kDa subunit (DF F40) mRNA, complete cds//1.2e-50:367:75//Hs.133089:AF064019
 F-MAMMA1000069//ESTs//0.58:286:60//Hs.134417:AI336840
 F-MAMMA1000084//Human mRNA for KIAA0033 gene, partial cds//1.1e-48:641:70//Hs.22271:D26067
 F-MAMMA1000085//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.00013:199:69//Hs.37656:AB011174
 F-MAMMA1000092//Homo sapiens telomeric repeat binding factor (TRF1) mRNA, complete cds//1.2e-52:346:77//Hs.90357:U40705
 F-MAMMA1000103//Homo sapiens mRNA for extracellular matrix protein, complete cds//1.0:151:64//Hs.35094:AB011792
 F-MAMMA1000117
 F-MAMMA1000129//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.0015:492:60//Hs.89631:U48508
 F-MAMMA1000133//ESTs//1.0:125:67//Hs.118309:AA653402
 F-MAMMA1000134//EST//1.2e-08:75:92//Hs.160674:AI248319
 F-MAMMA1000139//EST//5.5e-10:139:76//Hs.159121:AI383843
 F-MAMMA1000143//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.2e-26:148:97//Hs.153121:AB014585

F-MAMMA1000155//Homo sapiens homeobox transcription factor barx2 (BARX2)
 mRNA, complete cds//3.3e-31:219:87//Hs.129724:AF031924
 F-MAMMA1000163//ESTs//1.2e-59:317:94//Hs.49559:AA401050
 F-MAMMA1000171//ESTs//1.7e-09:161:69//Hs.119070:AA629695
 F-MAMMA1000173//Human drebrin E2 mRNA (DBN1), complete cds//9.2e-40:686:
 65//Hs.89434:D17530
 F-MAMMA1000175//ESTs//0.65:141:68//Hs.133152:H91657
 F-MAMMA1000183//Human mRNA for KIAA0065 gene, partial cds//1.0e-92:904:7
 2//Hs.70617:D31763
 F-MAMMA1000198//ESTs//0.0092:235:62//Hs.98783:AI091739
 F-MAMMA1000221//EST//3.3e-16:95:98//Hs.128271:AA973035
 F-MAMMA1000227//ESTs//0.010:268:60//Hs.116412:AA506926
 F-MAMMA1000241//ESTs//0.13:140:67//Hs.12328:AI377913
 F-MAMMA1000251//EST//3.7e-07:118:73//Hs.153116:AA856873
 F-MAMMA1000254//ESTs//0.00023:245:59//Hs.150513:AI247587
 F-MAMMA1000257//EST//4.2e-10:155:74//Hs.150409:AI003543
 F-MAMMA1000264//ESTs//2.0e-18:217:75//Hs.152748:N53015
 F-MAMMA1000266//EST//0.14:270:60//Hs.132593:AI031874
 F-MAMMA1000270//Human mRNA for KIAA0118 gene, partial cds//2.5e-54:354:8
 7//Hs.154326:D42087
 F-MAMMA1000277//Hydroxysteroid (11-beta) dehydrogenase 2//1.0e-07:306:65
 //Hs.1376:U26726
 F-MAMMA1000278//ESTs//4.0e-09:197:67//Hs.157034:AI347361
 F-MAMMA1000279//Complement component 5 receptor 1 (C5a ligand)//8.4e-34:
 341:68//Hs.2161:M62505
 F-MAMMA1000284
 F-MAMMA1000287//Human mRNA for KIAA0118 gene, partial cds//5.4e-50:245:8
 4//Hs.154326:D42087
 F-MAMMA1000302//EST//5.3e-40:213:98//Hs.122363:AA788641

F-MAMMA1000307//Polycystic kidney disease 1 (autosomal dominant)//0.55:5
10:57//Hs.75813:L33243

F-MAMMA1000309//Apolipoprotein E//9.7e-06:691:58//Hs.76260:M12529

F-MAMMA1000312//EST//0.042:183:63//Hs.158928:A1379519

F-MAMMA1000313

F-MAMMA1000331

F-MAMMA1000339

F-MAMMA1000340//ESTs, Highly similar to HYPOTHETICAL 29.4 KD PROTEIN IN
STE6-LOS1 INTERGENIC REGION [Saccharomyces cerevisiae]//2.9e-11:87:93//
Hs.13096:AA180963

F-MAMMA1000348//Homo sapiens KIAA0432 mRNA, complete cds//3.6e-23:270:72
//Hs.155174:AB007892

F-MAMMA1000356//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0484//3.7e-24:233:72//Hs.158095:AB007953

F-MAMMA1000360//Human Line-1 repeat mRNA with 2 open reading frames//9.0
e-75:498:85//Hs.23094:M19503

F-MAMMA1000361//Human mRNA for KIAA0118 gene, partial cds//9.1e-50:304:8
5//Hs.154326:D42087

F-MAMMA1000372//EST//1.2e-53:376:86//Hs.144295:AA136569

F-MAMMA1000385//ESTs//1.4e-22:220:76//Hs.142552:AA235344

F-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like facto
r, complete cds//1.2e-149:710:98//Hs.32170:AB015132

F-MAMMA1000395//Acyl-Coenzyme A dehydrogenase, very long chain//0.74:330
:60//Hs.82208:L46590

F-MAMMA1000402//Human Line-1 repeat mRNA with 2 open reading frames//2.4
e-58:834:68//Hs.23094:M19503

F-MAMMA1000410//Human NADH:ubiquinone oxidoreductase subunit B13 (B13) m
RNA, complete cds//1.2e-08:117:84//Hs.83916:U53468

F-MAMMA1000413//ESTs//3.3e-31:209:88//Hs.146154:A1200725

F-MAMMA1000414//ESTs//0.82:132:62//Hs.124857:AA687092
 F-MAMMA1000416//ESTs, Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN C09
 F5.2 IN CHROMOSOME III [C.elegans]//9.8e-33:267:81//Hs.32370:AA521111
 F-MAMMA1000421//ESTs//7.3e-33:320:75//Hs.121659:H02532
 F-MAMMA1000422//Homo sapiens protocadherin (PCDH8) mRNA, complete cds//0
 .98:553:56//Hs.19492:AF061573
 F-MAMMA1000423//EST//0.0075:179:63//Hs.162974:AA678459
 F-MAMMA1000424//ESTs//1.3e-17:313:67//Hs.139858:A1377641
 F-MAMMA1000429//Homo sapiens sorting nexin 3 (SNX3) mRNA, complete cds//
 5.1e-48:491:72//Hs.12102:AF034546
 F-MAMMA1000431//ISLET AMYLOID POLYPEPTIDE PRECURSOR//5.1e-39:320:81//Hs.
 51048:X68830
 F-MAMMA1000444//Homo sapiens mRNA for KIAA0594 protein, partial cds//9.1
 e-39:342:78//Hs.154872:AB011166
 F-MAMMA1000446
 F-MAMMA1000458//ESTs, Weakly similar to similar to CCAAT/enhancer-bindin
 g protein [C.elegans]//5.1e-08:58:93//Hs.9043:W21827
 F-MAMMA1000468//Homo sapiens mRNA for 6-phosphofructo-2-kinase/fructose-
 2, 6-bisphosphatase, complete cds//0.58:311:63//Hs.66721:D49818
 F-MAMMA1000472//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.1e-44:346:80//Hs.
 51048:X68830
 F-MAMMA1000478//Homo sapiens PYRIN (MEFV) mRNA, complete cds//0.0017:157
 :73//Hs.113283:AF018080
 F-MAMMA1000483//ISLET AMYLOID POLYPEPTIDE PRECURSOR//4.5e-39:400:75//Hs.
 51048:X68830
 F-MAMMA1000490//ESTs//3.6e-52:331:88//Hs.163686:AA291948
 F-MAMMA1000500//EST//9.7e-73:346:99//Hs.98812:AA434482
 F-MAMMA1000501//Small inducible cytokine A5 (RANTES)//2.3e-50:325:86//Hs
 .155464:AF088219

F-MAMMA1000516//Oxytocin receptor//1.6e-29:660:64//Hs.2820:X64878
 F-MAMMA1000522//ESTs//2.9e-23:328:70//Hs.125142:AA421352
 F-MAMMA1000524//ESTs//1.1e-08:211:65//Hs.33467:R85497
 F-MAMMA1000559//EST//4.7e-17:207:71//Hs.162733:AA614352
 F-MAMMA1000565
 F-MAMMA1000567//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//5.8e-51:404:80//Hs.125231:AF068006
 F-MAMMA1000576//ESTs//3.8e-32:236:74//Hs.140039:AA047045
 F-MAMMA1000583//ESTs//0.00099:123:70//Hs.135173:AI276780
 F-MAMMA1000585//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//8.8e-45:390:78//Hs.159523:AF001622
 F-MAMMA1000594//ESTs//8.3e-42:322:81//Hs.161660:AA167744
 F-MAMMA1000597//Homo sapiens KIAA0426 mRNA, complete cds//2.6e-37:592:68//Hs.97476:AB007886
 F-MAMMA1000605//Homo sapiens 4F5S mRNA, complete cds//5.1e-26:228:73//Hs.32567:AF073519
 F-MAMMA1000612//Homo sapiens Gx protein (GX) mRNA, complete cds//0.00091:300:60//Hs.29207:AF071494
 F-MAMMA1000616//ESTs//0.41:373:59//Hs.130699:AA621478
 F-MAMMA1000621//EST//0.027:146:62//Hs.148305:AA909605
 F-MAMMA1000623
 F-MAMMA1000625//Homo sapiens ES/130 mRNA, complete cds//0.89:428:56//Hs.98614:AF006751
 F-MAMMA1000643//Homo sapiens nephrocystin (NPHP1) mRNA, partial cds//0.092:365:59//Hs.75474:AF023674
 F-MAMMA1000664//ESTs//7.6e-07:259:64//Hs.140622:AA844353
 F-MAMMA1000669//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//9.0e-30:531:64//Hs.139107:K00629
 F-MAMMA1000670//ESTs//6.6e-83:389:100//Hs.148595:AI244490

F-MAMMA1000672//Homo sapiens CAGH32 mRNA, partial cds//0.17:109:73//Hs.4316:U80743

F-MAMMA1000684//Homo sapiens forkhead protein FREAC-2 mRNA, complete cds//3.3e-07:249:62//Hs.44481:U13220

F-MAMMA1000696//Interleukin 10//5.6e-47:355:82//Hs.2180:M57627

F-MAMMA1000707//ESTs//1.4e-09:225:65//Hs.138722:N51081

F-MAMMA1000713//Acetylcholinesterase {I4-E5 doman} [human, tumor cell lines, Genomic, 847 nt]//0.16:84:72//Hs.157124:S71129

F-MAMMA1000714//Human clone 23947 mRNA, partial cds//0.97:263:61//Hs.27414:U79275

F-MAMMA1000718//ESTs, Weakly similar to putative p150 [H.sapiens]//5.0e-07:210:66//Hs.71148:AA854648

F-MAMMA1000720//ESTs//1.4e-50:301:83//Hs.138852:AA284247

F-MAMMA1000723//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//8.1e-22:288:72//Hs.114685:AA700024

F-MAMMA1000731//Homo sapiens CHD1 mRNA, complete cds//1.5e-23:292:66//Hs.22670:AF006513

F-MAMMA1000732//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.8e-40:288:78//Hs.158095:AB007953

F-MAMMA1000733//RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1//0.25:467:58//Hs.1742:L33075

F-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.3e-169:802:98//Hs.31575:AF100141

F-MAMMA1000738//EST//1.0:149:63//Hs.136928:AA812580

F-MAMMA1000744//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.3e-51:323:88//Hs.153468:AB011147

F-MAMMA1000746//ESTs//2.3e-42:409:76//Hs.61199:AA024494

F-MAMMA1000752//EST, Weakly similar to putative p150 [H.sapiens]//1.1e-14:285:68//Hs.162011:AA513663

F-MAMMA1000760//Myelin oligodendrocyte glycoprotein {alternative products} //6.2e-47:341:82//Hs.53217:Z48051

F-MAMMA1000761//ESTs, Moderately similar to '!!!! ALU SUBFAMILY SX WARNIN G ENTRY '!!!! [H.sapiens] //9.8e-19:131:76//Hs.118972:AA761369

F-MAMMA1000775//EST//6.9e-32:424:69//Hs.44554:N34288

F-MAMMA1000776//ESTs//5.5e-43:154:84//Hs.141581:AA315361

F-MAMMA1000778//EST//4.4e-28:226:80//Hs.128952:AA984114

F-MAMMA1000782//ESTs//0.35:270:60//Hs.29153:AA551137

F-MAMMA1000798//Homo sapiens clone 24407 mRNA sequence//1.6e-23:531:65//Hs.12432:AF070575

F-MAMMA1000802//ESTs//3.1e-67:340:97//Hs.126081:AA459849

F-MAMMA1000824//ESTs//0.98:44:90//Hs.42802:N20130

F-MAMMA1000831//ESTs//0.0081:194:60//Hs.150400:AI298089

F-MAMMA1000839//Small inducible cytokine A5 (RANTES)//4.7e-48:241:74//Hs.155464:AF088219

F-MAMMA1000841

F-MAMMA1000842//Human monocytic leukaemia zinc finger protein (MOZ) mRNA , complete cds//0.18:483:59//Hs.82210:U47742

F-MAMMA1000843//EST//0.34:113:68//Hs.58415:W74696

F-MAMMA1000845//EST//2.9e-06:56:80//Hs.123243:AA804877

F-MAMMA1000851//EST//0.78:103:65//Hs.135656:AA907022

F-MAMMA1000855

F-MAMMA1000856//Homo sapiens preprocathepsin P mRNA, partial cds//0.14:320:59//Hs.71388:AF032906

F-MAMMA1000859//SOX-3 PROTEIN//0.014:474:57//Hs.157429:X71135

F-MAMMA1000862//EST//1.0:92:66//Hs.157599:AI357342

F-MAMMA1000863//ELK1, member of ETS oncogene family//1.2e-30:214:75//Hs.116549:AL009172

F-MAMMA1000865//ESTs//0.99:127:66//Hs.125230:AA873812

F-MAMMA1000867//EST//0.027:236:60//Hs.147156:AI191777
 F-MAMMA1000875//Human mRNA for KIAA0269 gene, complete cds//0.96:245:59/
 /Hs.75850:D87459
 F-MAMMA1000876//ESTs//1.5e-39:192:90//Hs.132020:AA704147
 F-MAMMA1000877//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
 RY !!!! [H.sapiens]//1.4e-91:484:94//Hs.138938:AA012894
 F-MAMMA1000880//EST//0.014:142:66//Hs.137044:AA878812
 F-MAMMA1000883//EST//1.0:166:62//Hs.126352:AA894465
 F-MAMMA1000897//H.sapiens mRNA for inter-alpha-trypsin inhibitor heavy c
 hain H3//2.6e-06:211:63//Hs.76716:X67055
 F-MAMMA1000905//Cartilage matrix protein//0.97:190:64//Hs.150366:M55683
 F-MAMMA1000906//ESTs//3.0e-07:145:72//Hs.133556:AA702506
 F-MAMMA1000908//ESTs//1.1e-70:484:84//Hs.142497:AA189081
 F-MAMMA1000914//Angiopoietin 1//0.14:450:59//Hs.2463:D13628
 F-MAMMA1000921//ESTs//6.8e-96:448:99//Hs.135721:AI125239
 F-MAMMA1000931//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA,
 3429 nt]//1.0e-25:312:66//Hs.116007:S79267
 F-MAMMA1000940//EST//2.9e-42:209:76//Hs.140567:AA825968
 F-MAMMA1000941//Dihydrolipoamide branched chain transacylase (E2 compone
 nt of branched chain keto acid dehydrogenase complex)//1.8e-38:395:71//H
 s.89479:X66785
 F-MAMMA1000942//ESTs//1.9e-19:252:71//Hs.141575:AA211734
 F-MAMMA1000943//Human mRNA for KIAA0305 gene, complete cds//0.077:236:63
 //Hs.83790:AB002303
 F-MAMMA1000956//Homo sapiens hRVP1 mRNA for RVP1, complete cds//8.8e-33:
 566:64//Hs.25640:AB000714
 F-MAMMA1000957//ESTs//1.0:177:59//Hs.149864:N80474
 F-MAMMA1000962//Homo sapiens neuronal thread protein AD7c-NTP mRNA, comp
 lete cds//1.1e-56:310:85//Hs.129735:AF010144

F-MAMMA1000968//ESTs//9.2e-18:128:89//Hs.163980:AA715814
 F-MAMMA1000975//ESTs//3.8e-08:219:66//Hs.110937:AA137096
 F-MAMMA1000979//EST//0.00022:155:65//Hs.101379:Z39802
 F-MAMMA1000987//EST//1.1e-48:373:81//Hs.139034:W27062
 F-MAMMA1000998//EST//2.0e-07:356:62//Hs.132467:AA922007
 F-MAMMA1001003//ESTs//0.47:129:67//Hs.164016:AI003724
 F-MAMMA1001008//ESTs//1.9e-17:153:82//Hs.141161:AA210711
 F-MAMMA1001021//Homo sapiens beta-dystrobrevin (BDTN) mRNA, complete cds
 //4.7e-17:100:100//Hs.13451:Y15718
 F-MAMMA1001024//ESTs//0.97:251:62//Hs.59389:R93968
 F-MAMMA1001030//Homo sapiens orphan G protein-coupled receptor HC38 mRNA
 , complete cds//3.6e-32:753:61//Hs.98384:AF062006
 F-MAMMA1001035//ESTs//6.9e-28:268:77//Hs.139536:AA180857
 F-MAMMA1001038
 F-MAMMA1001041//ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM//2.7e-10:357:65//H
 s.119000:M95178
 F-MAMMA1001050//EST//1.8e-29:321:74//Hs.161240:AI419882
 F-MAMMA1001059//ESTs, Weakly similar to protein synthesis initiation fac
 tor 4A-II homolog//7.9e-87:415:99//Hs.135623:AA134719
 F-MAMMA1001067//EST//0.30:166:60//Hs.148441:AI198503
 F-MAMMA1001073//ESTs//1.0e-98:476:98//Hs.98321:AA455585
 F-MAMMA1001074//ESTs//1.6e-82:396:98//Hs.118923:AA252116
 F-MAMMA1001075//Homo sapiens (clone F4) transmembrane protein mRNA seque
 nce//3.7e-29:559:65//Hs.135251:L09749
 F-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frames//2.7
 e-99:689:83//Hs.23094:M19503
 F-MAMMA1001080//IG ALPHA-2 CHAIN C REGION//5.8e-43:319:81//Hs.32225:AF06
 7420
 F-MAMMA1001082//ESTs//6.2e-28:275:77//Hs.152685:AA613896

F-MAMMA1001091//Homo sapiens mRNA for KIAA0711 protein, complete cds//0.0081:586:57//Hs.5333:AB018254

F-MAMMA1001092//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//5.1e-24:328:72//Hs.103948:K00627

F-MAMMA1001105//Homo sapiens OVO-like 1 binding protein (OVOL1) mRNA, complete cds//2.1e-24:507:66//Hs.97905:AF016045

F-MAMMA1001110//Human mRNA for KIAA0125 gene, complete cds//0.94:448:57//Hs.38365:D50915

F-MAMMA1001126//Small inducible cytokine A5 (RANTES)//4.6e-18:123:85//Hs.155464:AF088219

F-MAMMA1001133

F-MAMMA1001139

F-MAMMA1001143//ESTs//2.6e-18:121:82//Hs.135117:AI091534

F-MAMMA1001145//ESTs//1.5e-36:442:69//Hs.124712:H90217

F-MAMMA1001154//EST//0.054:208:61//Hs.162088:AA505741

F-MAMMA1001161//Homo sapiens mRNA for KIAA0575 protein, complete cds//6.6e-38:337:77//Hs.153468:AB011147

F-MAMMA1001162//EST//4.7e-16:117:90//Hs.130894:AI014299

F-MAMMA1001181

F-MAMMA1001186//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//6.5e-47:313:81//Hs.97203:U83171

F-MAMMA1001191//ESTs//5.8e-34:197:94//Hs.121575:AA758083

F-MAMMA1001198

F-MAMMA1001202//ESTs//1.5e-37:210:83//Hs.79788:AA527348

F-MAMMA1001203//ESTs//1.2e-29:199:76//Hs.141605:H92974

F-MAMMA1001206//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.5e-25:275:75//Hs.105292:AA504776

F-MAMMA1001215//ESTs//1.9e-06:300:63//Hs.113566:T03200

F-MAMMA1001220//Human mRNA for KIAA0118 gene, partial cds//2.7e-53:367:8

4//Hs.154326:D42087

F-MAMMA1001222//Homo sapiens mRNA for KIAA0634 protein, partial cds//1.8e-05:435:59//Hs.30898:AB014534

F-MAMMA1001243//ESTs//5.2e-19:118:94//Hs.122830:AA765587

F-MAMMA1001244

F-MAMMA1001249//ESTs//1.3e-89:420:99//Hs.147744:AI220476

F-MAMMA1001256//ESTs//2.1e-34:282:80//Hs.46158:AI160121

F-MAMMA1001259//ESTs//2.9e-07:68:95//Hs.6193:AA045149

F-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//2.8e-41:659:64//Hs.65238:AB014561

F-MAMMA1001268//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-33:336:74//Hs.23094:M19503

F-MAMMA1001271//Homo sapiens CAGH3 mRNA, complete cds//3.4e-06:487:59//Hs.21858:U80747

F-MAMMA1001274//Human mRNA for KIAA0080 gene, partial cds//5.1e-62:396:76//Hs.74554:D38522

F-MAMMA1001280//ESTs//7.3e-14:273:67//Hs.126503:AA913832

F-MAMMA1001292//Human mRNA for KIAA0176 gene, partial cds//5.6e-54:616:71//Hs.4935:D79998

F-MAMMA1001296//ESTs//4.8e-34:136:85//Hs.70279:AA757426

F-MAMMA1001298//ESTs//0.021:73:80//Hs.114233:N91305

F-MAMMA1001305//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein. ribosomal protein L6 pseudogene, ESTs and CA repeat//1.9e-58:295:97//Hs.102336:Z83838

F-MAMMA1001322//ESTs//9.4e-18:221:74//Hs.139132:AA211087

F-MAMMA1001324//Human endogenous retrovirus pHE.1 (ERV9)//6.7e-75:745:73//Hs.93174:X57147

F-MAMMA1001330//ESTs//2.6e-26:169:91//Hs.4209:AA205806

F-MAMMA1001341//ESTs//0.10:267:62//Hs.155922:AI147197
 F-MAMMA1001343//ESTs//0.0024:323:62//Hs.119238:AA476267
 F-MAMMA1001346//Homo sapiens mRNA for KIAA0715 protein, partial cds//0.9
 4:89:75//Hs.109358:AB018258
 F-MAMMA1001383//Putative mismatch repair/binding protein hMSH3//7.3e-49:
 273:80//Hs.42674:U61981
 F-MAMMA1001388//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID
 LABILE CHAIN PRECURSOR//4.6e-09:415:58//Hs.839:M86826
 F-MAMMA1001397//Prostaglandin I2 (prostacyclin) synthase //1.3e-26:358:6
 7//Hs.61333:D83402
 F-MAMMA1001408//ESTs//7.2e-06:123:72//Hs.26753:R60763
 F-MAMMA1001411//Autosomal dominant polycystic kidney disease type II//1.
 0:176:64//Hs.82001:U50928
 F-MAMMA1001419//Homo sapiens KIAA0395 mRNA, partial cds//4.1e-45:409:80/
 /Hs.43681:AL022394
 F-MAMMA1001420//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, comp
 lete cds//0.00042:125:75//Hs.46328:D87942
 F-MAMMA1001435//Human HsLIM15 mRNA for HsLim15, complete cds//8.2e-43:54
 3:71//Hs.37181:D64108
 F-MAMMA1001442//ESTs//7.9e-15:103:92//Hs.25780:R51321
 F-MAMMA1001446//ESTs//3.5e-44:292:73//Hs.111583:AA463590
 F-MAMMA1001452//ESTs//0.73:152:65//Hs.163766:AI424040
 F-MAMMA1001465//ESTs//1.0e-15:201:75//Hs.8836:AA181053
 F-MAMMA1001476//Human mRNA for 5'-terminal region of UMK, complete cds//
 2.0e-24:273:72//Hs.75939:D78335
 F-MAMMA1001487//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//3
 .2e-25:397:68//Hs.116874:AA524909
 F-MAMMA1001501//CALPAIN 1, LARGE//3.1e-53:438:81//Hs.2575:X04366
 F-MAMMA1001502//Human p120E4F transcription factor mRNA, complete cds//0

.99:258:61//Hs.154196:U87269

F-MAMMA1001510//ESTs//8.7e-09:380:61//Hs.118701:AA420795

F-MAMMA1001522//ESTs//7.1e-44:321:80//Hs.120170:AI018506

F-MAMMA1001547

F-MAMMA1001551//Homo sapiens mRNA for KIAA0462 protein, partial cds//7.5e-130:614:98//Hs.129937:AB007931

F-MAMMA1001575//ESTs, Weakly similar to zinc finger protein C2H2-171 [H. sapiens] //0.71:181:62//Hs.118866:AI017072

F-MAMMA1001576//Tubulin, gamma polypeptide//5.7e-97:529:91//Hs.150785:M61764

F-MAMMA1001590//EST//1.7e-13:94:92//Hs.95900:AA160339

F-MAMMA1001600//EST//1.0e-08:81:87//Hs.149220:AI247132

F-MAMMA1001604//EST//0.0070:157:62//Hs.162516:AA583375

F-MAMMA1001606//Human clone 23627 mRNA, complete cds//0.64:336:58//Hs.23642:U79266

F-MAMMA1001620//ESTs//6.8e-16:99:79//Hs.164052:AA836152

F-MAMMA1001627//Pregnancy-associated plasma protein A//0.27:379:58//Hs.158229:U28727

F-MAMMA1001630//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo)gene, an unknown putative gene, a pseudogene with high similarity to part of antigen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and DXS1055//1.4e-40:447:73//Hs.154353:AL022165

F-MAMMA1001633//Human zinc finger protein (LD5-1) mRNA, complete cds//3.6e-44:611:67//Hs.57679:U57796

F-MAMMA1001635

F-MAMMA1001649//ESTs//1.4e-47:238:99//Hs.124063:T75524

F-MAMMA1001654//Homo sapiens retinal rod Na-Ca+K exchanger (NCKX1) mRNA,
complete cds//0.00069:140:68//Hs.59829:AB014602

F-MAMMA1001663//Homo sapiens mRNA for KIAA0448 protein, complete cds//0.
015:135:71//Hs.27349:AB007917

F-MAMMA1001670//ESTs, Highly similar to 52 KD RO PROTEIN [Homo sapiens]
//0.064:472:60//Hs.110819:AI027548

F-MAMMA1001671

F-MAMMA1001679//ESTs//0.94:55:83//Hs.152506:AA573317

F-MAMMA1001683//ESTs//1.6e-92:480:96//Hs.118496:AA036889

F-MAMMA1001686//ESTs//0.00019:171:66//Hs.140402:AI138765

F-MAMMA1001692//ESTs//0.97:104:70//Hs.27596:AI188549

F-MAMMA1001711//Human G protein-coupled receptor (STRL22) mRNA, complete
cds//8.0e-45:323:83//Hs.46468:U45984

F-MAMMA1001715//ESTs//1.3e-14:188:72//Hs.130815:AA936548

F-MAMMA1001730//ESTs//0.048:198:65//Hs.116412:AA506926

F-MAMMA1001735//Human beta-tubulin class III isotype (beta-3) mRNA, comp
lete cds//1.5e-111:725:84//Hs.159154:U47634

F-MAMMA1001740//EST//0.77:119:65//Hs.148140:AA887098

F-MAMMA1001743//ESTs//6.5e-27:195:72//Hs.163688:H48768

F-MAMMA1001744//EST//0.00019:134:70//Hs.146863:AI161245

F-MAMMA1001745//Human Line-1 repeat mRNA with 2 open reading frames//4.7
e-67:822:69//Hs.23094:M19503

F-MAMMA1001751//Homo sapiens two P domain potassium channel subunit (HOH
01) mRNA, complete cds//1.0e-36:583:65//Hs.79351:U33632

F-MAMMA1001754//ESTs//5.1e-97:456:99//Hs.157928:AA775822

F-MAMMA1001757//EST//0.042:177:63//Hs.144436:R07109

F-MAMMA1001760//Homo sapiens RET finger protein-like 1 antisense transcr
ipt, partial//6.6e-41:309:84//Hs.102576:AJ010230

F-MAMMA1001764//ESTs//0.057:290:60//Hs.68647:AA524072

F-MAMMA1001768//Human transcription factor, forkhead related activator 4
(FREAC-4) mRNA, complete cds//2.2e-05:504:60//Hs.96028:AF042832

F-MAMMA1001769//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-85:68
6:79//Hs.113283:AF018080

F-MAMMA1001771//Human semaphorin III family homolog mRNA, complete cds//
0.00071:392:60//Hs.32981:U38276

F-MAMMA1001783//ESTs//8.8e-23:206:79//Hs.142524:H02940

F-MAMMA1001785//ESTs//1.3e-52:270:97//Hs.61809:AA503549

F-MAMMA1001788//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//
6.7e-21:212:77//Hs.103948:K00627

F-MAMMA1001790//Homo sapiens KIAA0409 mRNA, partial cds//2.2e-06:139:72/
/Hs.5158:AB007869

F-MAMMA1001806//ESTs//6.4e-44:373:79//Hs.105665:H78987

F-MAMMA1001812//ESTs//4.8e-83:407:97//Hs.98613:D83884

F-MAMMA1001815//EST//2.1e-56:374:85//Hs.141488:N47096

F-MAMMA1001817//EST//8.6e-39:336:78//Hs.162236:AA551582

F-MAMMA1001818//EST//0.32:375:58//Hs.72729:AA167589

F-MAMMA1001820//Homo sapiens cytokine-like factor-1 precursor (CLF-1) mR
NA, complete cds//0.082:153:66//Hs.114948:AF059293

F-MAMMA1001824//EST//0.0013:195:63//Hs.129275:AA992742

F-MAMMA1001836//ESTs//7.4e-52:283:95//Hs.92290:R78691

F-MAMMA1001837//Homo sapiens mRNA for zinc finger protein FPM315, comple
te cds//2.0e-29:641:62//Hs.56808:D88827

F-MAMMA1001848//ESTs//3.5e-53:264:99//Hs.116430:AA644665

F-MAMMA1001851//ESTs//0.00050:251:64//Hs.163776:AI393028

F-MAMMA1001854

F-MAMMA1001858//EST//1.0:113:68//Hs.132482:AA922218

F-MAMMA1001864//EST//1.3e-06:399:60//Hs.161500:N68060

F-MAMMA1001868//Homo sapiens nuclear receptor co-repressor N-CoR mRNA, c

omplete cds//0.084:672:58//Hs.152455:AF044209
 F-MAMMA1001874//ESTs//0.97:292:58//Hs.24553:AI150687
 F-MAMMA1001878
 F-MAMMA1001880//ESTs//9.2e-09:277:62//Hs.15776:T91944
 F-MAMMA1001890//EST//1.7e-85:440:97//Hs.128842:AA977576
 F-MAMMA1001907//EST//2.7e-26:294:74//Hs.98794:AA434078
 F-MAMMA1001908//ESTs//3.2e-109:505:100//Hs.146145:AI391521
 F-MAMMA1001931//ESTs//1.0:108:67//Hs.126624:AA768874
 F-MAMMA1001956//Apolipoprotein E//1.0:322:59//Hs.76260:M12529
 F-MAMMA1001963//ESTs//0.84:320:60//Hs.6523:AA218859
 F-MAMMA1001969//Homo sapiens clone 23892 mRNA sequence//3.6e-79:423:81//
 Hs.91916:AF035317
 F-MAMMA1001970//Oxytocin receptor//9.7e-31:626:64//Hs.2820:X64878
 F-MAMMA1001992//EST, Weakly similar to reverse transcriptase [H.sapiens]
 //7.9e-09:150:72//Hs.118222:N91115
 F-MAMMA1002009//ESTs//2.2e-18:234:69//Hs.21978:AA009633
 F-MAMMA1002011//ESTs//0.91:276:59//Hs.141196:AA704826
 F-MAMMA1002032//ESTs//7.8e-40:344:77//Hs.141658:N77915
 F-MAMMA1002033//ESTs//2.5e-30:293:76//Hs.139158:AA226159
 F-MAMMA1002041//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
 0484//1.2e-54:455:70//Hs.158095:AB007953
 F-MAMMA1002042//ESTs//1.4e-20:199:79//Hs.140913:R44580
 F-MAMMA1002047//EST//4.2e-14:170:75//Hs.124348:AA830225
 F-MAMMA1002056//EST//2.1e-49:414:80//Hs.162335:AA564256
 F-MAMMA1002058//EST//4.7e-26:268:78//Hs.140520:AA809305
 F-MAMMA1002068//Human Line-1 repeat mRNA with 2 open reading frames//8.5
 e-36:382:75//Hs.23094:M19503
 F-MAMMA1002078
 F-MAMMA1002082

F-MAMMA1002084//EST//0.37:351:59//Hs.46576:N46012
 F-MAMMA1002093//Homo sapiens mRNA for ATP-dependent RNA helicase, partia
 l//0.54:388:57//Hs.99423:AJ010840
 F-MAMMA1002108//Loricrin//0.00066:410:56//Hs.155657:M61120
 F-MAMMA1002118//EST//0.50:202:64//Hs.126872:AA932932
 F-MAMMA1002125//Small inducible cytokine A5 (RANTES)//2.4e-39:272:86//Hs
 .155464:AF088219
 F-MAMMA1002132//EST//6.4e-05:245:60//Hs.149361:AI272963
 F-MAMMA1002140//ESTs//5.8e-33:212:77//Hs.141203:H52638
 F-MAMMA1002143//SERUM PROTEIN MSE55//1.9e-12:192:70//Hs.148101:M88338
 F-MAMMA1002145//EST//0.12:204:60//Hs.160983:AI392837
 F-MAMMA1002153
 F-MAMMA1002155//ESTs, Weakly similar to p40 [H.sapiens]//3.6e-67:335:97/
 /Hs.88424:AA281385
 F-MAMMA1002156//Integrin, beta 3 (platelet glycoprotein IIIa, antigen CD
 61)//0.99:310:58//Hs.87149:M35999
 F-MAMMA1002158//EST//0.015:278:58//Hs.162666:AA605196
 F-MAMMA1002170//40S RIBOSOMAL PROTEIN S2//6.9e-82:573:82//Hs.119389:X172
 06
 F-MAMMA1002174//Human NOF1 mRNA, complete cds//2.2e-42:375:78//Hs.75859:
 U39400
 F-MAMMA1002198//H.sapiens mRNA for thiol-specific antioxidant//3.3e-36:1
 21:98//Hs.146354:Z22548
 F-MAMMA1002209//ESTs//1.1e-84:409:98//Hs.139235:AA278362
 F-MAMMA1002215//Loricrin//0.0024:369:57//Hs.155657:M61120
 F-MAMMA1002219//ESTs, Weakly similar to coded for by C. elegans cDNA yk5
 2b10.3 [C.elegans]//9.5e-41:202:100//Hs.118849:AA215645
 F-MAMMA1002230//ESTs//0.92:253:60//Hs.4222:AI024063
 F-MAMMA1002236//ESTs, Moderately similar to initiation factor eIF-2B gam

ma subunit [R.norvegicus] //4.6e-69:344:90//Hs.76822:AI359536
 F-MAMMA1002243//Homo sapiens serine threonine kinase 11 (STK11) mRNA, complete cds//0.99:454:56//Hs.122755:AF032986
 F-MAMMA1002250//Human involucrin mRNA//0.0037:396:62//Hs.157091:M13903
 F-MAMMA1002267//ESTs//2.0e-12:296:62//Hs.155686:AI308841
 F-MAMMA1002268//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//1.2e-06:427:61//Hs.69949:M94172
 F-MAMMA1002269
 F-MAMMA1002282//ESTs//5.9e-65:342:95//Hs.13962:T72715
 F-MAMMA1002292//EST//0.0050:346:58//Hs.97639:AA398440
 F-MAMMA1002293//Homo sapiens DNA fragmentation factor 40 kDa subunit (DF F40) mRNA, complete cds//2.8e-60:387:75//Hs.133089:AF064019
 F-MAMMA1002294//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//4.3e-07:349:64//Hs.92614:M62302
 F-MAMMA1002297//EST//0.98:98:68//Hs.148207:AA897460
 F-MAMMA1002298//Paired basic amino acid cleaving system 4//0.0061:471:57//Hs.77234:AB001914
 F-MAMMA1002299//ESTs//1.0:162:68//Hs.134132:AA205935
 F-MAMMA1002308//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] //6.9e-41:293:83//Hs.105292:AA504776
 F-MAMMA1002310//Homo sapiens serine protease-like protease (nes1) mRNA, complete cds//0.0037:173:67//Hs.69423:AF055481
 F-MAMMA1002311//Homo sapiens mRNA, chromosome 1 specific transcript KIAA 0487//1.8e-41:473:65//Hs.92381:AB007956
 F-MAMMA1002312//ESTs//0.0017:279:60//Hs.163773:AA806291
 F-MAMMA1002317//ESTs//1.0:131:64//Hs.66075:F08908
 F-MAMMA1002319//Homo sapiens clone 24566 mRNA sequence//1.2e-28:410:68//Hs.133342:AF070536
 F-MAMMA1002322//ESTs//1.2e-47:356:82//Hs.152413:AA780515

F-MAMMA1002329//Homo sapiens clone 24444 RaP2 interacting protein 8 (RPI
P8) mRNA, complete cds//0.0079:143:67//Hs.6755:AF055026

F-MAMMA1002332//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//
1.2e-26:342:72//Hs.103948:K00627

F-MAMMA1002333//Homo sapiens mRNA for KIAA0711 protein, complete cds//6.
8e-07:669:58//Hs.5333:AB018254

F-MAMMA1002339//H.sapiens mRNA for retrotransposon//3.2e-40:348:73//Hs.6
940:Z48633

F-MAMMA1002347//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING
ENTRY !!!! [H.sapiens]//3.9e-14:146:81//Hs.163073:R02591

F-MAMMA1002351//ESTs//1.2e-74:371:96//Hs.111429:W28907

F-MAMMA1002352//EST//1.7e-09:198:68//Hs.149218:AI247086

F-MAMMA1002353//ESTs//7.4e-15:163:77//Hs.157253:AI357539

F-MAMMA1002355//Homo sapiens KIAA0441 mRNA, complete cds//7.7e-47:307:78
//Hs.32511:AB007901

F-MAMMA1002356//ESTs//0.012:380:58//Hs.105349:AA779733

F-MAMMA1002359//EST//1.1e-44:264:77//Hs.141095:H23818

F-MAMMA1002360//ESTs//7.6e-15:200:70//Hs.19770:AA447830

F-MAMMA1002361//ESTs//2.5e-29:277:79//Hs.155115:AA669923

F-MAMMA1002362//EST//0.25:304:58//Hs.162427:AA576345

F-MAMMA1002380//FACTOR VIII INTRON 22 PROTEIN//0.29:485:59//Hs.83363:M34
677

F-MAMMA1002384//ESTs//1.1e-05:220:65//Hs.141388:R52022

F-MAMMA1002385//ESTs, Moderately similar to T11G6.8 [C.elegans]//8.4e-11
8:578:97//Hs.25516:AI086362

F-MAMMA1002392//EST//0.85:319:57//Hs.126484:AA913624

F-MAMMA1002411//ESTs//0.00044:89:76//Hs.141685:AI142632

F-MAMMA1002413//ESTs//0.0020:303:61//Hs.94903:W85737

F-MAMMA1002417//ESTs//1.4e-06:223:65//Hs.143695:AA662745

F-MAMMA1002427//ESTs//5.4e-48:356:82//Hs.146811:AA410788
 F-MAMMA1002428//EST//1.0:96:71//Hs.105130:AA482030
 F-MAMMA1002434//Human mRNA for KIAA0118 gene, partial cds//2.2e-52:370:83//Hs.154326:D42087
 F-MAMMA1002446
 F-MAMMA1002454//ESTs//9.1e-50:163:100//Hs.80162:AA534809
 F-MAMMA1002461//Human diacylglycerol kinase (DAGK) mRNA, complete cds//6.3e-06:595:59//Hs.99932:L38707
 F-MAMMA1002470
 F-MAMMA1002475//Human MAP kinase activated protein kinase 2 mRNA, complete cds//0.018:417:58//Hs.75074:U12779
 F-MAMMA1002480//ESTs//0.0015:258:62//Hs.132082:N67059
 F-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//9.4e-120:560:98//Hs.155223:AF055460
 F-MAMMA1002494//ESTs//2.4e-68:359:95//Hs.124652:AA857628
 F-MAMMA1002498//ESTs, Weakly similar to hypothetical protein [H.sapiens]//4.0e-07:257:63//Hs.133013:AA604920
 F-MAMMA1002524//Huntingtin (Huntington disease)//0.0085:215:65//Hs.79391:L12392
 F-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds//4.5e-162:775:97//Hs.18858:AF065214
 F-MAMMA1002545//ESTs//6.4e-46:351:81//Hs.146811:AA410788
 F-MAMMA1002554
 F-MAMMA1002556//Human beige-like protein (BGL) mRNA, partial cds//0.96:187:62//Hs.62354:M83822
 F-MAMMA1002566//ESTs//0.0033:130:68//Hs.117018:AA832421
 F-MAMMA1002571//EST//0.28:115:66//Hs.156768:AI351368
 F-MAMMA1002573//ESTs//2.1e-48:265:94//Hs.155128:AI224516
 F-MAMMA1002585

F-MAMMA1002590//ESTs//3.2e-11:280:63//Hs.36049:AA436831
 F-MAMMA1002597//ESTs//4.8e-10:118:77//Hs.156166:AI334107
 F-MAMMA1002598//Ribosomal protein L7//3.6e-23:123:100//Hs.153:X57958
 F-MAMMA1002603//EST//0.070:99:71//Hs.122387:AA789220
 F-MAMMA1002612//ESTs, Moderately similar to hCDC10 protein [H.sapiens]//
 8.3e-18:353:65//Hs.60895:AA428463
 F-MAMMA1002617//B94 PROTEIN//0.0097:229:62//Hs.75522:M92357
 F-MAMMA1002618
 F-MAMMA1002619
 F-MAMMA1002622//Homo sapiens advillin mRNA, complete cds//4.7e-22:157:90
 //Hs.47344:AF041449
 F-MAMMA1002623//EST//1.5e-33:168:81//Hs.141526:N52300
 F-MAMMA1002625
 F-MAMMA1002629//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
 0507//1.1e-35:355:76//Hs.158241:AB007976
 F-MAMMA1002636//Homo sapiens mRNA for KIAA0288 gene, complete cds//1.9e-
 05:439:61//Hs.91400:AB006626
 F-MAMMA1002637//KINESIN LIGHT CHAIN//2.0e-47:367:72//Hs.117977:L04733
 F-MAMMA1002646//EST//1.2e-32:302:78//Hs.112540:AA601385
 F-MAMMA1002650//TRICHOHYALIN//1.2e-08:570:63//Hs.82276:L09190
 F-MAMMA1002655//EST//8.8e-40:198:100//Hs.159724:AI393335
 F-MAMMA1002662//EST//0.99:95:63//Hs.144074:AI005489
 F-MAMMA1002665//Lysosomal-associated membrane protein 2//1.8e-35:722:64/
 /Hs.8262:U36336
 F-MAMMA1002671//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//8.6e-0
 6:272:64//Hs.106070:U22398
 F-MAMMA1002673
 F-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.
 2e-162:752:99//Hs.3363:D86987

F-MAMMA1002685//ESTs//7.5e-40:373:78//Hs.163937:N69915
 F-MAMMA1002698//ESTs//2.5e-09:190:68//Hs.138292:AI220397
 F-MAMMA1002699//Homo sapiens epsin 2b mRNA, complete cds//4.7e-56:398:81
 //Hs.22396:AF062085
 F-MAMMA1002701//ESTs//4.3e-10:110:80//Hs.156041:AI274697
 F-MAMMA1002708//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//1.1e-51:307:79//Hs.46328:D87942
 F-MAMMA1002711//EST//3.6e-38:186:77//Hs.139715:N25041
 F-MAMMA1002721//EST//3.9e-06:110:71//Hs.136758:AA714692
 F-MAMMA1002727//EST//0.97:137:63//Hs.145153:AI150165
 F-MAMMA1002728//ESTs, Highly similar to PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE [Saccharomyces cerevisiae]//2.6e-12:129:81//Hs.154181:AA193
 502
 F-MAMMA1002744//ESTs//0.0026:420:58//Hs.95793:AA617853
 F-MAMMA1002746//ESTs//0.28:117:69//Hs.12925:T66312
 F-MAMMA1002748
 F-MAMMA1002754//ESTs//1.1e-34:340:77//Hs.163641:R61848
 F-MAMMA1002758//Homo sapiens KIAA0442 mRNA, partial cds//1.1e-27:151:98/
 /Hs.32168:AB007902
 F-MAMMA1002764//ESTs//1.7e-45:323:84//Hs.155243:N70293
 F-MAMMA1002765//EST//3.2e-11:145:73//Hs.162551:AA584782
 F-MAMMA1002769
 F-MAMMA1002775//Human ABL gene, exon 1b and intron 1b, and putative M860
 4 Met protein (M8604 Met) gene//7.6e-84:417:97//Hs.77705:U07563
 F-MAMMA1002780//EST//0.78:210:63//Hs.149413:AI273988
 F-MAMMA1002782
 F-MAMMA1002796//ESTs//0.021:122:65//Hs.132221:AI380710
 F-MAMMA1002807//EST//1.0e-31:184:71//Hs.161497:N66919
 F-MAMMA1002820//ESTs//0.21:292:59//Hs.132513:AI378514

F-MAMMA1002830//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.4e-57:286:88//Hs.15731:AB011135

F-MAMMA1002833//Human mRNA for KIAA0033 gene, partial cds//9.1e-52:583:72//Hs.22271:D26067

F-MAMMA1002835

F-MAMMA1002838//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE C HAIN 1 [Locusta migratoria]//7.7e-38:179:78//Hs.141344:H29951

F-MAMMA1002842//ESTs//1.7e-19:134:89//Hs.111583:AA463590

F-MAMMA1002843//Homo sapiens mRNA for KIAA0810 protein, partial cds//5.4e-137:635:99//Hs.7531:AB018353

F-MAMMA1002844//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//1.6e-07:329:58//Hs.107747:AI357868

F-MAMMA1002858

F-MAMMA1002868//EST//4.1e-23:180:77//Hs.163196:AA767643

F-MAMMA1002869//Human PINCH protein mRNA, complete cds//7.0e-88:696:78//Hs.83987:U09284

F-MAMMA1002871//ESTs//3.4e-93:466:96//Hs.11873:T68423

F-MAMMA1002880//EST//2.0e-09:364:59//Hs.145181:AI183632

F-MAMMA1002881//Homo sapiens mRNA for 25 kDa trypsin inhibitor, complete cds//3.8e-30:680:61//Hs.129732:D45027

F-MAMMA1002886//Long (electrocardiographic) QT syndrome 2//0.00075:504:60//Hs.19944:U04270

F-MAMMA1002887//ESTs//0.044:144:68//Hs.133152:H91657

F-MAMMA1002890//EST//1.7e-05:74:86//Hs.116013:AA612666

F-MAMMA1002892//EST//2.1e-67:383:93//Hs.22815:R44265

F-MAMMA1002895//Human transcription factor ERF-1 mRNA, complete cds//0.00053:382:57//Hs.61796:U85658

F-MAMMA1002908//EST//0.0022:132:68//Hs.161697:AA224952

F-MAMMA1002909//ESTs//9.1e-21:343:70//Hs.142068:AA176125

F-MAMMA1002930//ESTs//0.55:72:72//Hs.132440:AA923730
 F-MAMMA1002937//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapien
 s]//7.9e-103:485:99//Hs.102928:AI346344
 F-MAMMA1002938//Homo sapiens mRNA for KIAA0698 protein, complete cds//1.
 6e-194:910:98//Hs.31720:AB014598
 F-MAMMA1002941//ESTs//9.5e-19:196:67//Hs.137945:AI423389
 F-MAMMA1002947//ESTs//1.2e-96:460:99//Hs.156001:AI313418
 F-MAMMA1002964//Homo sapiens KIAA0424 mRNA, partial cds//0.48:250:60//Hs
 .54697:AB007884
 F-MAMMA1002970//EST//2.0e-16:132:84//Hs.136518:AA601400
 F-MAMMA1002972
 F-MAMMA1002973//ESTs//3.2e-43:225:74//Hs.155179:AA223932
 F-MAMMA1002982//ESTs//0.0017:162:66//Hs.152669:AA604944
 F-MAMMA1002987//EST//0.044:254:59//Hs.135014:AI095645
 F-MAMMA1003003//Coagulation factor III (thromboplastin, tissue factor)//
 3.9e-22:185:83//Hs.62192:J02931
 F-MAMMA1003004//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
 0501//1.0e-16:343:61//Hs.159897:AB007970
 F-MAMMA1003007//EST//6.6e-10:265:66//Hs.144389:AA530979
 F-MAMMA1003011//Homo sapiens histone macroH2A1.2 mRNA, complete cds//6.2
 e-51:620:69//Hs.75258:AF054174
 F-MAMMA1003013//Human HOX4C mRNA for a homeobox protein//0.73:347:58//Hs
 .74061:X59372
 F-MAMMA1003015//EST//2.5e-11:137:77//Hs.141312:H73062
 F-MAMMA1003019//ESTs//0.0099:182:65//Hs.60787:AI374951
 F-MAMMA1003026//EST//1.0:136:67//Hs.9123:T50137
 F-MAMMA1003031//EST//1.3e-11:244:67//Hs.136611:AA669549
 F-MAMMA1003035
 F-MAMMA1003039//ESTs//1.4e-23:265:74//Hs.33393:R83391

F-MAMMA1003040//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.5e-9
3:339:85//Hs.5247:AF029750

F-MAMMA1003044//Cyclin D2//1.0:234:61//Hs.75586:D13639

F-MAMMA1003047//H.sapiens mRNA for F25B3.3 kinase like protein from C.elegans//1.0:209:60//Hs.99491:Y12336

F-MAMMA1003049//EST//0.99:126:67//Hs.162634:AA601742

F-MAMMA1003055//ESTs//0.00011:130:70//Hs.130539:R68518

F-MAMMA1003056

F-MAMMA1003057//ESTs, Moderately similar to hypothetical protein MD6 [M.musculus] //1.3e-88:334:97//Hs.96500:AI206781

F-MAMMA1003066//ESTs//0.77:88:71//Hs.143618:AI022618

F-MAMMA1003089//Homo sapiens mRNA for KIAA0631 protein, partial cds//4.5e-51:329:71//Hs.75154:AB014531

F-MAMMA1003099//Homo sapiens actin-binding protein homolog ABP-278 mRNA, complete cds//8.5e-44:288:88//Hs.81008:AF043045

F-MAMMA1003104//H.sapiens mRNA for ASM-like phosphodiesterase 3a//1.0:213:60//Hs.42945:Y08136

F-MAMMA1003113//Homo sapiens mRNA for hair keratin acidic 3-II//0.99:200:64//Hs.32950:X82634

F-MAMMA1003127//Homo sapiens brush border myosin I (BBMI) mRNA, complete cds//5.4e-27:421:66//Hs.5394:AF105424

F-MAMMA1003135//Envoplakin//0.56:250:62//Hs.25482:U53786

F-MAMMA1003140

F-MAMMA1003146//Homo sapiens mRNA for GalT3 protein//7.2e-82:397:97//Hs.151344:Y15062

F-MAMMA1003150//Homo sapiens mRNA for KIAA0515 protein, partial cds//0.00019:297:61//Hs.108945:AB011087

F-MAMMA1003166//Glycoprotein Ib (platelet), beta polypeptide//1.2e-31:487:65//Hs.3847:U59632

F-NT2RM1000001//Human plectin (PLEC1) mRNA, complete cds//0.16:244:63//Hs.79706:U53204

F-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds//1.5e-66:385:92//Hs.82510:D31886

F-NT2RM1000032

F-NT2RM1000035//Human mRNA for KIAA0199 gene, partial cds//4.1e-110:849:81//Hs.78442:D83782

F-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds//3.5e-108:542:95//Hs.60103:AB014590

F-NT2RM1000039//Human plectin (PLEC1) mRNA, complete cds//0.11:545:57//Hs.79706:U53204

F-NT2RM1000055//ESTs, Highly similar to TIP120 [R.norvegicus]//3.2e-69:53:96//Hs.154980:AA948067

F-NT2RM1000059//Homo sapiens T cell immune response cDNA7 (TIRC7) mRNA, complete cds//0.029:281:59//Hs.46465:U45285

F-NT2RM1000062//ESTs//0.30:368:59//Hs.131675:AA843210

F-NT2RM1000080//Homo sapiens chromosome 9, P1 clone 11659//2.8e-102:493:97//Hs.3439:AC004472

F-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds//5.8e-116:550:97//Hs.65238:AB014561

F-NT2RM1000092//Murine leukemia viral (bmi-1) oncogene homolog//0.42:190:63//Hs.431:L13689

F-NT2RM1000118//Homo sapiens clone 23763 unknown mRNA, partial cds//0.00086:126:70//Hs.92693:AF007155

F-NT2RM1000119//Peroxisome receptor 1//0.00055:458:58//Hs.158084:Z48054

F-NT2RM1000127

F-NT2RM1000131

F-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUF56 subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds//3.7e

-92:448:97//Hs.49767:AF044959
 F-NT2RM1000153//Homo sapiens mRNA for MTG8-related protein MTG16a, complete cds//1.0:546:58//Hs.110099:AB010419
 F-NT2RM1000186//Homo sapiens clone 23763 unknown mRNA, partial cds//0.0081:126:70//Hs.92693:AF007155
 F-NT2RM1000187//ESTs//3.4e-79:400:96//Hs.54971:AI424382
 F-NT2RM1000199//Homo sapiens mRNA for KIAA0722 protein, complete cds//0.87:454:59//Hs.47061:AF045458
 F-NT2RM1000242
 F-NT2RM1000244//Homo sapiens centrosomal Nek2-associated protein 1 (C-NA P1) mRNA, complete cds//0.97:135:66//Hs.27910:AF049105
 F-NT2RM1000252//TRICHOHYALIN//0.030:273:58//Hs.82276:L09190
 F-NT2RM1000256//Glutamine-fructose-6-phosphate transaminase//1.5e-13:248:69//Hs.1674:M90516
 F-NT2RM1000257//ESTs, Highly similar to similar to mago nashi [H.sapiens]//2.9e-98:530:93//Hs.104650:AI037879
 F-NT2RM1000260//Human mRNA for KIAA0130 gene, complete cds//2.1e-58:460:80//Hs.23106:D50920
 F-NT2RM1000271//ESTs//0.93:224:60//Hs.91226:AA649047
 F-NT2RM1000272
 F-NT2RM1000280//ESTs, Highly similar to VACUOLAR ATP SYNTHASE SUBUNIT D [Bos taurus]//1.3e-21:308:73//Hs.15071:AA781144
 F-NT2RM1000300
 F-NT2RM1000314//Human mRNA for KIAA0159 gene, complete cds//2.6e-128:708:92//Hs.5719:D63880
 F-NT2RM1000318//Human mRNA for ribosomal protein L39, complete cds//1.8e-35:182:99//Hs.9837:D79205
 F-NT2RM1000341//ESTs//2.3e-72:381:95//Hs.23070:AA631976
 F-NT2RM1000354//EST//5.2e-27:202:84//Hs.151186:AI125798

F-NT2RM1000355//ESTs, Weakly similar to putative [M.musculus]//7.7e-75:3
87:95//Hs.108619:W28608

F-NT2RM1000365//ESTs//1.7e-99:495:97//Hs.103926:AA165691

F-NT2RM1000377//ESTs, Weakly similar to protein-tyrosine-phosphatase [H.
sapiens]//7.4e-91:481:95//Hs.163707:AA137181

F-NT2RM1000388//65 KD YES-ASSOCIATED PROTEIN//0.36:340:57//Hs.8939:X8050
7

F-NT2RM1000394//HISTONE H3.3//8.5e-91:474:93//Hs.118838:M11353

F-NT2RM1000399

F-NT2RM1000421

F-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, c
omplete cds//1.2e-85:418:97//Hs.20815:AF084928

F-NT2RM1000499//ESTs, Weakly similar to KIAA0167 protein [H.sapiens]//1.
6e-38:201:97//Hs.106262:AI052382

F-NT2RM1000539//EST//0.070:145:62//Hs.149711:AI284660

F-NT2RM1000553//EST//2.2e-48:265:95//Hs.99230:AA449847

F-NT2RM1000555//ESTs//0.82:193:61//Hs.96944:AI359957

F-NT2RM1000563//Human plectin (PLEC1) mRNA, complete cds//1.0:336:58//Hs.
.79706:U53204

F-NT2RM1000623//Homo sapiens mRNA for KIAA0287 gene, partial cds//0.98:2
26:61//Hs.17931:AB006625

F-NT2RM1000648//ESTs, Weakly similar to similar to M. musculus MER5 and
other AHPC/TSA proteins [C.elegans]//6.2e-51:254:98//Hs.132096:AA314601

F-NT2RM1000661//Homo sapiens translation initiation factor 4e mRNA, comp
lete cds//8.5e-55:276:97//Hs.19122:AF038957.

F-NT2RM1000666//Homo sapiens BAI 1 mRNA, complete cds//0.87:274:60//Hs.1
13936:AB005297

F-NT2RM1000669//ESTs//5.5e-63:481:85//Hs.90527:AI188279

F-NT2RM1000672

F-NT2RM1000691//Homo sapiens mRNA for HRIHFB2060, partial cds//7.0e-121:
582:98//Hs.146282:AB015348

F-NT2RM1000699//ESTs//1.1e-89:435:97//Hs.28964:AA715101

F-NT2RM1000702//ESTs//5.4e-90:429:99//Hs.151001:AA564706

F-NT2RM1000725//Homo sapiens mRNA for neuropathy target esterase//1.5e-6
6:435:85//Hs.5038:AJ004832

F-NT2RM1000741//Homo sapiens mRNA for KIAA0567 protein, partial cds//2.6
e-127:690:92//Hs.147946:AB011139

F-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds//8.2e-68:5
24:83//Hs.112360:AF027208

F-NT2RM1000746//ESTs//2.6e-37:231:89//Hs.94446:AA845465

F-NT2RM1000770//Homo sapiens KIAA0425 mRNA, complete cds//3.3e-09:321:63
//Hs.150390:AB007885

F-NT2RM1000772//Eukaryotic translation initiation factor 3 (eIF-3) p36 s
ubunit//0.053:271:60//Hs.139745:U39067

F-NT2RM1000780//Human Line-1 repeat mRNA with 2 open reading frames//6.9
e-20:128:94//Hs.23094:M19503

F-NT2RM1000781//ESTs//4.4e-60:346:92//Hs.35089:N50845

F-NT2RM1000800

F-NT2RM1000802

F-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds//1.2e-64:4
90:84//Hs.112360:AF027208

F-NT2RM1000826//ESTs//0.82:193:61//Hs.96944:AI359957

F-NT2RM1000829//Mannose-binding lectin, soluble (opsonic defect)//0.92:2
83:58//Hs.2314:X15422

F-NT2RM1000833//Hydroxysteroid (11-beta) dehydrogenase 2//0.022:178:67//
Hs.1376:U26726

F-NT2RM1000850//Human protein tyrosine kinase related mRNA sequence//3.8
e-06:384:59//Hs.90314:L05148

F-NT2RM1000852//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//3.0e-149:726:97//Hs.99423:AJ010840

F-NT2RM1000857//ESTs//0.52:274:60//Hs.112095:AA447643

F-NT2RM1000867//ESTs, Highly similar to signal peptidase:SUBUNIT//5.3e-54:277:96//Hs.11125:AI015619

F-NT2RM1000874//ESTs//0.032:185:64//Hs.97713:AA442239

F-NT2RM1000882//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//4.0e-155:750:97//Hs.132898:AC004770

F-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//8.8e-158:762:97//Hs.26285:AF082516

F-NT2RM1000885//Homo sapiens mRNA for KIAA0661 protein, complete cds//6.3e-19:310:67//Hs.65238:AB014561

F-NT2RM1000894

F-NT2RM1000898

F-NT2RM1000905//EST//4.8e-07:77:84//Hs.148017:AI268701

F-NT2RM1000924//HOMEODOMAIN PROTEIN HOX-A5//0.00051:458:59//Hs.37034:M26679

F-NT2RM1000927//Homo sapiens mRNA for KIAA0807 protein, partial cds//0.084:386:58//Hs.101474:AB018350

F-NT2RM1000962//Human mRNA for KIAA0252 gene, partial cds//0.98:299:59//Hs.83419:D87440

F-NT2RM1000978

F-NT2RM1001003//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.3e-161:760:98//Hs.58488:U97067

F-NT2RM1001008//ESTs//1.3e-12:144:75//Hs.133122:AI025200

F-NT2RM1001043//EST//0.24:117:64//Hs.161536:N80395

F-NT2RM1001044//ESTs, Weakly similar to C43E11.9 [C.elegans]//3.0e-98:491:96//Hs.102173:AA045270

F-NT2RM1001059//Human plectin (PLEC1) mRNA, complete cds//0.52:533:57//Hs.79706:U53204

F-NT2RM1001066//ESTs//1.2e-114:538:99//Hs.129020:AI380703
 F-NT2RM1001072//Human beige-like protein (BGL) mRNA, partial cds//0.69:5
 86:56//Hs.62354:M83822
 F-NT2RM1001074//Macrophage stimulating 1 (hepatocyte growth factor-like)
 //0.0019:294:64//Hs.30223:X90846
 F-NT2RM1001082//Archain//3.9e-37:290:81//Hs.33642:X81198
 F-NT2RM1001085
 F-NT2RM1001092//Zinc finger protein 43 (HTF6)//1.9e-57:770:68//Hs.74107:
 X59244
 F-NT2RM1001102//ESTs//1.2e-35:638:63//Hs.131737:AI343331
 F-NT2RM1001105//WEE1-LIKE PROTEIN KINASE//0.0024:246:63//Hs.75188:U10564
 F-NT2RM1001112//ESTs//8.9e-82:437:93//Hs.6330:H38495
 F-NT2RM1001115
 F-NT2RM1001139//Keratin 9//1.5e-05:518:59//Hs.2783:Z29074
 F-NT2RM2000006//ESTs//3.9e-16:96:98//Hs.101117:AA576113
 F-NT2RM2000013//RNA polymerase II polypeptide B (140 kD)//6.3e-13:640:59
 //Hs.148027:X63563
 F-NT2RM2000030
 F-NT2RM2000032//ESTs//7.1e-18:138:68//Hs.114031:AA700958
 F-NT2RM2000042//ESTs//0.0091:241:61//Hs.147895:AI286243
 F-NT2RM2000092
 F-NT2RM2000093//ESTs//2.6e-40:226:94//Hs.163521:H42085
 F-NT2RM2000101//ESTs//1.0:235:61//Hs.48860:N27428
 F-NT2RM2000124//Protein kinase, cAMP-dependent, catalytic, alpha//5.8e-4
 6:287:88//Hs.77271:X07767
 F-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, com
 plete cds//3.0e-139:566:97//Hs.18953:AF067223
 F-NT2RM2000192//EST//3.5e-07:168:65//Hs.163122:AA756999
 F-NT2RM2000239//ESTs, Weakly similar to K04G2.6 [C.elegans]//3.6e-93:489

:95//Hs.143499:R72672

F-NT2RM2000240//ESTs//1.0e-70:269:97//Hs.156175:AI334328

F-NT2RM2000250//Homo sapiens mRNA for KIAA0590 protein, complete cds//1.0e-129:615:98//Hs.111862:AB011162

F-NT2RM2000259//ESTs//6.1e-30:172:85//Hs.116406:AA209520

F-NT2RM2000260//ESTs//2.5e-25:133:93//Hs.14169:AA203500

F-NT2RM2000287//ESTs//6.2e-13:97:83//Hs.118523:H98981

F-NT2RM2000322//Interferon regulatory factor 5//0.84:208:61//Hs.54434:U51127

F-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds//2.8e-176:805:99//Hs.129952:AB011132

F-NT2RM2000363//ESTs//1.2e-24:139:96//Hs.48818:N63543

F-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds//3.7e-96:599:86//Hs.75871:U48251

F-NT2RM2000371

F-NT2RM2000374//ESTs//3.2e-13:98:91//Hs.65853:AI050866

F-NT2RM2000395//Growth arrest-specific 1//0.80:129:67//Hs.65029:L13698

F-NT2RM2000402//Human p76 mRNA, complete cds//7.2e-23:714:59//Hs.28757:U81006

F-NT2RM2000407//ESTs//9.4e-92:458:96//Hs.148873:T33582

F-NT2RM2000420//EST//1.8e-61:296:99//Hs.147186:AI193053

F-NT2RM2000422//Solute carrier family 6 (neurotransmitter transporter, serotonin), member 4//1.5e-06:260:61//Hs.553:L05568

F-NT2RM2000452//ESTs//1.0:132:62//Hs.110004:AI097379

F-NT2RM2000469//ESTs//0.34:249:60//Hs.149575:AI281807

F-NT2RM2000490//Homo sapiens mRNA for KIAA0747 protein, partial cds//2.4e-16:386:63//Hs.8309:AB018290

F-NT2RM2000502//Human nicotinamide N-methyltransferase (NNMT) mRNA, complete cds//0.99:272:61//Hs.76669:U08021

F-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds/
/1.6e-172:824:97//Hs.4812:AF061243
F-NT2RM2000522//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.18:313:6
0//Hs.129725:AF047487
F-NT2RM2000540//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]
//2.7e-41:231:94//Hs.7049:AI141736
F-NT2RM2000556//ESTs//3.1e-33:183:96//Hs.136990:AA769220
F-NT2RM2000566//Integrin, alpha 7B//2.0e-155:751:97//Hs.74369:AF032108
F-NT2RM2000567//RYANODINE RECEPTOR, SKELETAL MUSCLE//6.3e-09:689:59//Hs.
89631:U48508
F-NT2RM2000569//ESTs//5.4e-17:170:77//Hs.158277:H09128
F-NT2RM2000577//ESTs, Highly similar to ISOLEUCYL-TRNA SYNTHETASE, MITO
CHONDRIAL [Saccharomyces cerevisiae]//1.4e-33:214:92//Hs.55609:W37993
F-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.
8e-175:820:98//Hs.3363:D86987
F-NT2RM2000588//ESTs//1.5e-33:183:97//Hs.136990:AA769220
F-NT2RM2000594
F-NT2RM2000599//Homo sapiens Mad4 homolog (Mad4) mRNA, complete cds//0.0
17:253:65//Hs.102402:AF040963
F-NT2RM2000609//ESTs//1.0:220:59//Hs.110155:AA007313
F-NT2RM2000612//ESTs//0.97:208:59//Hs.73217:AA846548
F-NT2RM2000623//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.0
24:326:59//Hs.6150:AB011093
F-NT2RM2000624//ESTs//2.3e-118:557:99//Hs.145904:AA203258
F-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds//2.0
e-143:664:98//Hs.19542:AB018272
F-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds//2.4
e-139:664:98//Hs.7278:AB014558
F-NT2RM2000639//ESTs//0.98:144:65//Hs.154364:AI189702

F-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds//3.4
e-169:518:99//Hs.115763:AB014576

F-NT2RM2000669//ESTs//1.3e-56:283:98//Hs.156342:AI337371

F-NT2RM2000691//Homo sapiens actin-related protein Arp3 (ARP3) mRNA, com
plete cds//6.7e-86:746:74//Hs.5321:AF006083

F-NT2RM2000714//Human mRNA for KIAA0231 gene, partial cds//2.2e-50:748:6
4//Hs.7938:D86984

F-NT2RM2000718//Homa sapiens mRNA for HRIHFB2436, partial cds//7.6e-126:
594:98//Hs.136058:AB015342

F-NT2RM2000735//Zinc finger protein 43 (HTF6)//2.7e-112:756:82//Hs.74107
:X59244

F-NT2RM2000740//ESTs, Highly similar to HYPOTHETICAL 132.7 KD HELICASE
IN ALG7-ENP1 INTERGENIC REGION [Saccharomyces cerevisiae]//4.2e-85:464:9
1//Hs.161551:W24286

F-NT2RM2000795//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.0e-8
2:640:81//Hs.5247:AF029750

F-NT2RM2000821//Human mRNA for KIAA0340 gene, partial cds//0.32:679:59//
Hs.105919:AB002338

F-NT2RM2000837//ESTs//2.3e-105:501:98//Hs.101514:AI346701

F-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds//2
.8e-185:847:99//Hs.137580:AB015046

F-NT2RM2000952//ESTs, Weakly similar to lethal(2)denticleless [D.melanog
aster]//6.2e-94:441:99//Hs.59075:AI023761

F-NT2RM2000984//Human mRNA for KIAA0246 gene, partial cds//0.94:351:62//
Hs.84753:D87433

F-NT2RM2001004//ESTs//5.0e-10:247:64//Hs.36049:AA436831

F-NT2RM2001035//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cer
evisiae]//2.9e-48:282:93//Hs.17035:AI080471

F-NT2RM2001065

F-NT2RM2001100//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//1.7e-08:449:62//Hs.75111:D87258
F-NT2RM2001105//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.00079:274:59//Hs.102732:U88153
F-NT2RM2001131//TRICHOHYALIN//2.5e-20:684:62//Hs.82276:L09190
F-NT2RM2001141
F-NT2RM2001152//ESTs//0.53:333:58//Hs.153087:AA649042
F-NT2RM2001177
F-NT2RM2001194//ESTs, Weakly similar to T28H10.2 [C.elegans]//2.4e-23:149:93//Hs.10618:AI288739
F-NT2RM2001196//ESTs//4.0e-98:486:97//Hs.59628:W91959
F-NT2RM2001201//Human mRNA for KIAA0005 gene, complete cds//2.8e-44:554:69//Hs.155291:D13630
F-NT2RM2001221//Homo sapiens mRNA for KIAA0806 protein, complete cds//0.97:165:64//Hs.24279:AB018349
F-NT2RM2001238//EST//6.8e-67:420:89//Hs.130586:AI004766
F-NT2RM2001243//V-jun avian sarcoma virus 17 oncogene homolog//0.87:125:64//Hs.75889:U65928
F-NT2RM2001247//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.0066:321:61//Hs.132206:AF039694
F-NT2RM2001256
F-NT2RM2001291//ESTs//1.1e-86:459:93//Hs.10267:W27845
F-NT2RM2001306//Homo sapiens paraoxonase (PON2) mRNA, complete cds//1.0:182:65//Hs.75221:AF001601
F-NT2RM2001312//ESTs//2.0e-35:338:70//Hs.141440:N21615
F-NT2RM2001319//ESTs, Weakly similar to No definition line found [C.elegans]//5.2e-30:277:77//Hs.25347:AI138605
F-NT2RM2001324//Homo sapiens mRNA for beta-spectrin III, complete cds//0.031:245:62//Hs.26915:AB008567

F-NT2RM2001345//ESTs//9.2e-91:428:99//Hs.151001:AA564706
 F-NT2RM2001360//ESTs//0.98:45:80//Hs.133520:AA878905
 F-NT2RM2001370//Human transportin (TRN) mRNA, complete cds//0.72:224:61/
 /Hs.82925:U70322
 F-NT2RM2001393//Mannosidase, alpha B, lysosomal//0.42:383:57//Hs.108969:
 U68382
 F-NT2RM2001420//EST//1.0:287:62//Hs.125285:AA830378
 F-NT2RM2001424//Homo sapiens mRNA for E1B-55kDa-associated protein//2.3e
 -97:453:99//Hs.155218:AJ007509
 F-NT2RM2001499//Ecotropic retroviral receptor//5.4e-47:589:68//Hs.2928:X
 57303
 F-NT2RM2001504//Homo sapiens agrin precursor mRNA, partial cds//0.25:328
 :60//Hs.68900:AF016903
 F-NT2RM2001524//ESTs//1.0e-11:93:90//Hs.33687:R85969
 F-NT2RM2001544//ESTs//1.0e-25:157:92//Hs.137451:AA351459
 F-NT2RM2001547//ESTs//2.0e-29:168:96//Hs.116392:AA936262
 F-NT2RM2001575//Sjogren syndrome antigen A1 (52kD, ribonucleoprotein aut
 oantigen SS-A/Ro)//6.9e-28:582:64//Hs.1042:M62800
 F-NT2RM2001582//ESTs, Moderately similar to red-1 [M.musculus]//0.0032:5
 7:89//Hs.114722:AA448077
 F-NT2RM2001588//Homo sapiens KIAA0442 mRNA, partial cds//2.3e-11:282:65/
 /Hs.32168:AB007902
 F-NT2RM2001592//ESTs//4.8e-73:372:95//Hs.163801:AI391729
 F-NT2RM2001605//Homo sapiens clone 23592 mRNA sequence//7.3e-87:749:75//
 Hs.76272:S66431
 F-NT2RM2001613//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61
 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:AI016073
 F-NT2RM2001632//EST//8.7e-18:222:76//Hs.160402:AI393918
 F-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds//3.

0e-154:740:98//Hs.15832:AB014518
 F-NT2RM2001637//ESTs//2.2e-06:386:61//Hs.145198:AI276952
 F-NT2RM2001641//ESTs, Highly similar to NADH-CYTOCHROME B5 REDUCTASE [Bos taurus] //3.5e-13:94:92//Hs.22142:AA814725
 F-NT2RM2001648//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris] //1.3e-17:181:75//Hs.131840:AI016073
 F-NT2RM2001652//ESTs//2.5e-06:82:80//Hs.128203:AA972301
 F-NT2RM2001659//ESTs//2.8e-15:92:98//Hs.123321:AA810287
 F-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//1.2e-173:802:99//Hs.31323:AF044195
 F-NT2RM2001668//ESTs, Weakly similar to DNA MISMATCH REPAIR PROTEIN MSH 6 [H.sapiens] //1.1e-136:671:97//Hs.27721:U17907
 F-NT2RM2001670//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.1e-25:352:70//Hs.101414:AB011129
 F-NT2RM2001671//ESTs//1.8e-08:63:98//Hs.158069:AI365356
 F-NT2RM2001675
 F-NT2RM2001681//ESTs//0.16:197:63//Hs.20585:R10305
 F-NT2RM2001688//ESTs//1.8e-24:130:100//Hs.162504:AA668211
 F-NT2RM2001695//EST//5.6e-51:189:89//Hs.162197:AA535216
 F-NT2RM2001696//ESTs, Highly similar to gene ERCC5 protein [H.sapiens] //5.8e-16:144:84//Hs.14671:T79937
 F-NT2RM2001698//ESTs//0.14:184:63//Hs.148080:AI277415
 F-NT2RM2001699//ESTs//6.5e-14:136:79//Hs.127790:AI003817
 F-NT2RM2001700//Homo sapiens putative seven pass transmembrane protein (TM7SF1) mRNA, complete cds//0.95:270:61//Hs.15791:AF027826
 F-NT2RM2001706//ESTs//2.8e-47:304:86//Hs.146811:AA410788
 F-NT2RM2001716//Semenogelin I//0.98:153:64//Hs.1968:M81650
 F-NT2RM2001718
 F-NT2RM2001723//Homo sapiens clone 23770 mRNA sequence//4.4e-28:163:95//

Hs.12457:AF052123

F-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds//2.0e-112:530:98//Hs.129937:AB007931

F-NT2RM2001730//Homo sapiens mRNA for KIAA0560 protein, complete cds//0.95:269:58//Hs.129952:AB011132

F-NT2RM2001743

F-NT2RM2001753//Human AF-6 mRNA, complete cds//0.095:350:59//Hs.100469:AB011399

F-NT2RM2001760//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:AI016073

F-NT2RM2001768//ESTs//0.61:189:62//Hs.144847:AI222742

F-NT2RM2001771//Zinc finger protein 10 (K0X 1)//1.1e-66:669:71//Hs.2479:X78933

F-NT2RM2001782//YY1 transcription factor//0.094:149:65//Hs.97496:M77698

F-NT2RM2001784//ESTs//8.2e-31:190:92//Hs.144587:AI193595

F-NT2RM2001785//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//1.6e-48:476:74//Hs.132898:AC004770

F-NT2RM2001797//Human mRNA for KIAA0065 gene, partial cds//6.1e-66:481:72//Hs.70617:D31763

F-NT2RM2001800//Human mRNA for transcriptional activator hSNF2b, complete cds//0.49:142:66//Hs.78202:U29175

F-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//2.7e-179:827:99//Hs.31323:AF044195

F-NT2RM2001805//EST//1.0:45:80//Hs.159007:AI381341

F-NT2RM2001813//EST//0.41:268:58//Hs.150031:AI292068

F-NT2RM2001823//H.sapiens mRNA for 218kD Mi-2 protein//9.7e-21:554:60//Hs.74441:X86691

F-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds//1.2e-132:738:90//Hs.7753:AF013759

F-NT2RM2001840//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.8e-58:32
9:86//Hs.113283:AF018080

F-NT2RM2001855//ADP-ribosylation factor 5//1.0:301:60//Hs.77541:M57567

F-NT2RM2001867//ESTs, Weakly similar to ZK792.1 [C.elegans] //3.0e-28:421
:66//Hs.8763:W30741

F-NT2RM2001879//ESTs//6.3e-43:234:94//Hs.122546:AA186723

F-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds//6.
1e-189:866:97//Hs.4198:AB014610

F-NT2RM2001896//Homo sapiens mRNA for JM23 protein, complete coding sequ
ence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin)
)//3.0e-13:606:57//Hs.23170:AJ005892

F-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds//9.4
e-178:859:97//Hs.129937:AB007931

F-NT2RM2001930//Homo sapiens semaphorin F homolog mRNA, complete cds//4.
2e-08:481:59//Hs.27621:U52840

F-NT2RM2001935//ESTs, Highly similar to MULTIDRUG RESISTANCE PROTEIN HO
MOLOG 50 [Drosophila melanogaster] //0.37:424:60//Hs.118634:U66688

F-NT2RM2001936//Homo sapiens clone 614 unknown mRNA, complete sequence//
2.2e-139:653:98//Hs.21811:AF091080

F-NT2RM2001950//ESTs//0.12:91:76//Hs.107295:W80392

F-NT2RM2001982

F-NT2RM2001983//Homo sapiens Tax interaction protein 2 mRNA, partial cds
//1.2e-21:123:98//Hs.6454:AF089816

F-NT2RM2001989//Homo sapiens mRNA for DRIM protein//0.71:319:59//Hs.1041
35:AJ006778

F-NT2RM2001997//ESTs//1.7e-25:135:100//Hs.126894:AA932538

F-NT2RM2001998//ESTs, Weakly similar to Mi-2 protein [H.sapiens] //0.99:2
71:60//Hs.63888:AA203398

F-NT2RM2002004//Homo sapiens mRNA for KIAA0731 protein, partial cds//3.5

e-37:509:65//Hs.6214:AB018274
F-NT2RM2002014//Homo sapiens mRNA for CRM1 protein, complete cds//0.79:4
29:58//Hs.79090:D89729
F-NT2RM2002030//Glutamine-fructose-6-phosphate transaminase//9.0e-89:822
:73//Hs.1674:M90516
F-NT2RM2002049//ESTs//0.99:109:71//Hs.19303:AA928427
F-NT2RM2002055//ESTs//1.1e-91:453:98//Hs.158370:AI382154
F-NT2RM2002088//ESTs//6.1e-75:302:96//Hs.153471:AI198377
F-NT2RM2002091//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.69:293:58//Hs.896
31:U48508
F-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partia
l//2.5e-165:776:98//Hs.99423:AJ010840
F-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (G
AC1) mRNA, complete cds//7.6e-145:684:98//Hs.26312:AF030435
F-NT2RM2002128
F-NT2RM2002142//ESTs//0.0031:183:66//Hs.144505:AA757274
F-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP mRNA, c
omplete cds//1.4e-144:800:92//Hs.20815:AF084928
F-NT2RM2002178//Homo sapiens mRNA for KIAA0467 protein, partial cds//1.7
e-165:787:97//Hs.11147:AB007936
F-NT2RM2002580//Keratin 10 (epidermolytic hyperkeratosis; keratosis palm
aris et plantaris)//0.064:291:61//Hs.99936:X14487
F-NT2RM4000024//RNA polymerase II polypeptide B (140 kD)//8.0e-10:610:59
//Hs.148027:X63563
F-NT2RM4000027//ESTs//1.6e-64:352:94//Hs.21331:H93074
F-NT2RM4000030//ESTs//1.0:115:63//Hs.131055:AI391464
F-NT2RM4000046//ESTs//2.6e-09:207:65//Hs.143533:AI094674
F-NT2RM4000061//ESTs//0.89:207:60//Hs.98445:AI038511
F-NT2RM4000085//ESTs, Weakly similar to The KIAA0134 gene product is rel

ated to human RNA helicase A. [H.sapiens]//1.6e-30:369:70//Hs.114623:AI2
04280
F-NT2RM4000086
F-NT2RM4000104//Homo sapiens chromosome 16 zinc finger protein ZNF210 (Z
NF210) mRNA, complete cds//1.3e-24:345:69//Hs.13128:AF060865
F-NT2RM4000139
F-NT2RM4000155
F-NT2RM4000156//ESTs//5.9e-73:345:100//Hs.155958:AA573632
F-NT2RM4000167//Homo sapiens kinesin family member protein KIF3A mRNA, c
omplete cds//9.8e-30:676:61//Hs.159228:AF041853
F-NT2RM4000169//ESTs//2.0e-103:483:99//Hs.43729:AA497044
F-NT2RM4000191//TRICHOHYALIN//0.011:324:60//Hs.82276:L09190
F-NT2RM4000197//ESTs//1.5e-48:311:88//Hs.136144:W27744
F-NT2RM4000199//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
RY !!!! [H.sapiens]//0.13:322:61//Hs.145088:AI221147
F-NT2RM4000200
F-NT2RM4000202//Homo sapiens mRNA for KIAA0288 gene, complete cds//0.002
7:424:60//Hs.91400:AB006626
F-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds//4.
4e-184:856:98//Hs.111138:AB018255
F-NT2RM4000215//SET translocation (myeloid leukemia-associated)//0.0013
:358:60//Hs.75055:M93651
F-NT2RM4000229//Homo sapiens mRNA for KIAA0722 protein, complete cds//0.
65:572:60//Hs.47061:AF045458
F-NT2RM4000233//ESTs//2.0e-37:269:85//Hs.148873:T33582
F-NT2RM4000244//EST//0.83:319:57//Hs.162412:AA573439
F-NT2RM4000251//ESTs, Weakly similar to CUT1 PROTEIN [Schizosaccharomyce
s pombe]//1.1e-16:112:92//Hs.93841:AA442297
F-NT2RM4000265//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, comp

lete cds//1.8e-48:229:83//Hs.46328:D87942
 F-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds//2.5e-154:609:93//Hs.31305:M99438
 F-NT2RM4000324//Homo sapiens hCPE-R mRNA for CPE-receptor, complete cds//0.070:460:59//Hs.5372:AB000712
 F-NT2RM4000327//ESTs//0.019:269:60//Hs.153697:AI240707
 F-NT2RM4000344//ESTs, Highly similar to YME1 PROTEIN [Saccharomyces cerevisiae]//2.7e-83:432:95//Hs.12796:W27884
 F-NT2RM4000349//Human mRNA for KIAA0005 gene, complete cds//5.2e-53:666:68//Hs.155291:D13630
 F-NT2RM4000354//ESTs, Weakly similar to lethal(2)denticleless [D.melanogaster]//0.0078:55:92//Hs.59075:AI023761
 F-NT2RM4000356//ESTs//1.0:225:60//Hs.161175:AI418425
 F-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds//5.3e-135:628:99//Hs.8152:AB014542
 F-NT2RM4000368//ESTs//4.9e-13:323:63//Hs.143695:AA662745
 F-NT2RM4000386//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//2.0e-72:843:68//Hs.23796:AL022718
 F-NT2RM4000395//Nitric oxide synthase 2A (inducible, hepatocytes)//0.63:166:65//Hs.946:X73029
 F-NT2RM4000414//Homo sapiens XYLB mRNA for xylulokinase, complete cds//4.9e-17:114:94//Hs.137580:AB015046
 F-NT2RM4000421
 F-NT2RM4000425//Homo sapiens mRNA for KIAA0594 protein, partial cds//1.1e-42:432:74//Hs.154872:AB011166
 F-NT2RM4000433//Colony stimulating factor 3 receptor (granulocyte)//0.02

3:543:58//Hs.2175:M59820

F-NT2RM4000457

F-NT2RM4000471//Human transcriptional corepressor hKAP1/TIF1B mRNA, complete cds//0.060:178:63//Hs.66369:U95040

F-NT2RM4000486//ESTs//9.2e-48:237:99//Hs.160685:AI280004

F-NT2RM4000496//ESTs//0.069:252:61//Hs.155958:AA573632

F-NT2RM4000511//EST//0.92:191:58//Hs.61517:AA028915

F-NT2RM4000514

F-NT2RM4000515//ESTs//7.3e-93:450:98//Hs.120975:AA034409

F-NT2RM4000520//ESTs//0.13:183:65//Hs.144828:AI221305

F-NT2RM4000531//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//1.8e-153:756:96//Hs.125870:AI364967

F-NT2RM4000532//ESTs//7.7e-43:388:78//Hs.105665:H78987

F-NT2RM4000534

F-NT2RM4000585

F-NT2RM4000590//Homo sapiens mRNA for KIAA0469 protein, complete cds//1.2e-19:593:62//Hs.7764:AB007938

F-NT2RM4000595//ESTs, Highly similar to HYPOTHETICAL 54.9 KD PROTEIN CO 2F5.7 IN CHROMOSOME III [Caenorhabditis elegans]//3.1e-104:532:96//Hs.6092:T75227

F-NT2RM4000603//Human mRNA for KIAA0392 gene, partial cds//1.7e-15:305:68//Hs.40100:AB002390

F-NT2RM4000611//EST//0.76:268:58//Hs.150031:AI292068

F-NT2RM4000616

F-NT2RM4000674

F-NT2RM4000689

F-NT2RM4000698//Apolipoprotein E//1.0:290:59//Hs.76260:M12529

F-NT2RM4000700

F-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA,

partial cds//3.5e-91:744:77//Hs.42400:AF022789
 F-NT2RM4000717//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PR
 ECURSOR [Mus musculus]//2.6e-163:771:97//Hs.6823:W18181
 F-NT2RM4000733//PUTATIVE TACHYKININ RECEPTOR//0.70:257:60//Hs.957:M84605
 F-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds//1.2
 e-159:743:98//Hs.137168:AB018303
 F-NT2RM4000741
 F-NT2RM4000751//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus
 musculus]//1.1e-75:388:96//Hs.112361:R99396
 F-NT2RM4000764//ESTs//3.8e-104:539:95//Hs.24739:H67815
 F-NT2RM4000778//ESTs//1.5e-85:419:97//Hs.99838:AA204731
 F-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds//1.
 8e-173:810:98//Hs.18586:AB007920
 F-NT2RM4000787//EST//0.011:182:65//Hs.159928:AA969186
 F-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216//4.5e-156:736:
 98//Hs.25817:AC005306
 F-NT2RM4000795//ESTs, Highly similar to LIVER CARBOXYLESTERASE PRECURSO
 R [Homo sapiens]//6.7e-19:160:80//Hs.124902:AI337820
 F-NT2RM4000796//Human K⁺ channel subunit gene, complete cds//0.96:292:62
 //Hs.124212:M64676
 F-NT2RM4000798//ESTs//1.9e-34:271:82//Hs.128203:AA972301
 F-NT2RM4000813//Homo sapiens snRNA activating protein complex 190kD subu
 nit (SNAP190) mRNA, complete cds//0.052:238:64//Hs.113265:AF032387
 F-NT2RM4000820//ESTs//0.053:274:61//Hs.23748:H16568
 F-NT2RM4000833
 F-NT2RM4000848//Human mRNA for KIAA0324 gene, partial cds//0.97:374:61//
 Hs.7841:AB002322
 F-NT2RM4000852//EST//1.0:222:60//Hs.120354:AA718934
 F-NT2RM4000855//ESTs, Highly similar to RAS-RELATED C3 BOTULINUM TOXIN

SUBSTRATE 2 [Homo sapiens] //4.4e-29:164:95//Hs.115095:AI392943
 F-NT2RM4000887
 F-NT2RM4000895//Homo sapiens HuUAP1 mRNA for UDP-N-acetylglucosamine pyrophosphorylase, complete cds//6.8e-22:407:64//Hs.21293:AB011004
 F-NT2RM4000950
 F-NT2RM4000971//ESTs//3.6e-27:142:100//Hs.130912:AI014546
 F-NT2RM4000979//Homo sapiens KIAA0415 mRNA, complete cds//3.7e-63:571:77
 //Hs.7289:AB007875
 F-NT2RM4000996//Zinc finger protein 3 (A8-51)//8.7e-34:381:67//Hs.2481:X
 78926
 F-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds//1.6
 e-171:803:98//Hs.19542:AB018272
 F-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds//1.1
 e-126:584:99//Hs.15711:AB014539
 F-NT2RM4001032//Homo sapiens mRNA for KIAA0711 protein, complete cds//4.
 8e-05:469:58//Hs.5333:AB018254
 F-NT2RM4001047//ESTs, Moderately similar to M025 PROTEIN [M.musculus]//7
 .0e-56:340:92//Hs.87310:AI247543
 F-NT2RM4001054//HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR I "A FORM
 " PRECURSOR//0.79:142:69//Hs.77424:M63835
 F-NT2RM4001084
 F-NT2RM4001092//Human mRNA for KIAA0050 gene, complete cds//0.045:235:62
 //Hs.108947:D30758
 F-NT2RM4001116
 F-NT2RM4001140//Human engrailed protein (EN2) gene, 5' end//0.00029:225:
 61//Hs.134989:L12701
 F-NT2RM4001151//ESTs//1.1e-07:190:65//Hs.151691:AA443730
 F-NT2RM4001155//ESTs//2.2e-12:181:74//Hs.128826:AI004145
 F-NT2RM4001160//EST//0.83:166:61//Hs.117051:AA677351

F-NT2RM4001187

F-NT2RM4001191//ESTs//1.3e-42:248:93//Hs.13475:R18220

F-NT2RM4001200//Zinc finger protein 10 (KOX 1)//4.0e-68:799:69//Hs.2479:
X78933

F-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete c
ds//1.4e-153:707:99//Hs.14934:AF004828

F-NT2RM4001204//ESTs, Moderately similar to HYPOTHETICAL 59.1 KD PROTEI
N ZK637.1 IN CHROMOSOME III [Caenorhabditis elegans]//0.19:291:62//Hs.31
582:AA877205

F-NT2RM4001217//Homo sapiens nuclear matrix protein NRP/B (NRPB) mRNA, c
omplete cds//7.0e-63:715:70//Hs.104925:AF059611

F-NT2RM4001256//ESTs, Weakly similar to probable CBP3 protein homolog [C
.elegans]//1.1e-67:208:96//Hs.26676:AA033997

F-NT2RM4001258//Homo sapiens mRNA for KIAA0481 protein, complete cds//0.
0019:435:59//Hs.6360:AB007950

F-NT2RM4001309//Human Chromosome 16 BAC clone CIT987SK-254P9//0.019:356:
59//Hs.26971:AC003003

F-NT2RM4001313//H.sapiens mRNA for phosphatidylinositol 3-kinase//8.0e-7
9:474:89//Hs.32971:Z46973

F-NT2RM4001316//ESTs//1.2e-14:126:84//Hs.154344:AA258335

F-NT2RM4001320//Human mRNA for Neuroblastoma, complete cds//3.6e-43:642:
66//Hs.87435:D89016

F-NT2RM4001340//EST//0.40:135:70//Hs.161198:AI418988

F-NT2RM4001344//ESTs, Highly similar to HYPOTHETICAL GTP-BINDING PROTEI
N IN PMI40-PAC2 INTERGENIC REGION [Saccharomyces cerevisiae]//0.0096:284
:58//Hs.120997:R56714

F-NT2RM4001347//ESTs, Weakly similar to weakly similar to ANK repeat reg
ion of Fowlpox virus BamHI-orf7 protein [C.elegans]//3.7e-52:252:100//Hs
.15301:AA167818

F-NT2RM4001371//EST//0.52:262:59//Hs.145991:AI277656
 F-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds//7.2e-
 169:790:98//Hs.5151:AF098799
 F-NT2RM4001384
 F-NT2RM4001410//ESTs//1.1e-47:290:91//Hs.72447:AA160575
 F-NT2RM4001411//Homo sapiens mRNA for APS, complete cds//2.5e-23:475:64/
 /Hs.105052:AB000520
 F-NT2RM4001412
 F-NT2RM4001414//ESTs, Moderately similar to F18547_1 [H.sapiens]//5.2e-1
 8:133:87//Hs.28209:AI073817
 F-NT2RM4001437//Human mRNA for KIAA0118 gene, partial cds//2.5e-42:611:7
 0//Hs.154326:D42087
 F-NT2RM4001444
 F-NT2RM4001454//ESTs//3.9e-31:169:96//Hs.117982:AA644658
 F-NT2RM4001455//ESTs//0.0054:48:100//Hs.14920:AA910914
 F-NT2RM4001483//ESTs, Weakly similar to ZINC FINGER PROTEIN ZFP-36 [H.sa
 piens]//1.1e-71:313:99//Hs.163754:AA587784
 F-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds//3.
 9e-157:724:99//Hs.153121:AB014585
 F-NT2RM4001519//ESTs//0.66:264:59//Hs.139891:AA553619
 F-NT2RM4001522//ESTs, Weakly similar to D9481.12 gene product [S.cerevis
 iae]//1.3e-114:536:99//Hs.88820:AA456247
 F-NT2RM4001557
 F-NT2RM4001565//ESTs//1.7e-107:509:99//Hs.146139:AA731487
 F-NT2RM4001566//Human phosphatidylinositol 3-kinase catalytic subunit p1
 10delta mRNA, complete cds//1.0:255:60//Hs.14207:U86453
 F-NT2RM4001569//ESTs//1.4e-86:417:98//Hs.153044:AI198859
 F-NT2RM4001582
 F-NT2RM4001592//EST//0.61:142:64//Hs.162900:AA664566

F-NT2RM4001594//Homo sapiens mRNA for KIAA0522 protein, partial cds//0.0
072:484:60//Hs.129892:AB011094

F-NT2RM4001597//ESTs, Moderately similar to red-1 [M.musculus]//2.3e-72:
387:95//Hs.114722:AA448077

F-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds//1.
1e-163:750:99//Hs.23255:AB018334

F-NT2RM4001611//ESTs, Weakly similar to F25H9.6 [C.elegans]//8.6e-05:91:
79//Hs.24647:W19739

F-NT2RM4001629//ESTs, Moderately similar to 55 KD ERYTHROCYTE MEMBRANE
PROTEIN [Homo sapiens]//0.0042:153:68//Hs.114832:AI147946

F-NT2RM4001650//Human mRNA for KIAA0341 gene, partial cds//0.95:328:60//
Hs.101761:AB002339

F-NT2RM4001662//Human mRNA for KIAA0322 gene, partial cds//8.3e-83:449:9
3//Hs.153685:AB002320

F-NT2RM4001666//ESTs//2.1e-11:78:96//Hs.152446:AA555323

F-NT2RM4001682//EST//0.027:145:70//Hs.133253:AI052638

F-NT2RM4001710//ESTs//0.098:140:62//Hs.5796:AA767384

F-NT2RM4001714//Human mRNA for KIAA0202 gene, partial cds//2.2e-86:748:7
4//Hs.80712:D86957

F-NT2RM4001715//ESTs//1.3e-104:490:99//Hs.127336:AI332905

F-NT2RM4001731//Human involucrin mRNA//0.23:432:59//Hs.157091:M13903

F-NT2RM4001741//Human mRNA for KIAA0320 gene, partial cds//6.9e-80:737:7
3//Hs.150443:AB002318

F-NT2RM4001746//H.sapiens NF-H gene, exon 1 (and joined CDS)//2.1e-07:41
8:61//Hs.75735:X15306

F-NT2RM4001754//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTE
IN [Mus musculus]//2.0e-27:205:83//Hs.110601:AA206719

F-NT2RM4001758//H.sapiens mRNA for serine/threonine protein kinase EMK//
2.1e-86:729:75//Hs.157199:X97630

F-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds//7.4
e-175:803:99//Hs.39871:AB018270

F-NT2RM4001783//ESTs, Weakly similar to T12D8.i [C.elegans] //3.1e-71:376
:95//Hs.108396:AA160677

F-NT2RM4001810//Homo sapiens centrosomal Nek2-associated protein 1 (C-NA
P1) mRNA, complete cds//0.99:446:58//Hs.27910:AF049105

F-NT2RM4001813//Homo sapiens clone 24820 mRNA sequence//6.6e-14:249:70//
Hs.146312:AF070547

F-NT2RM4001819//Cell division cycle 2-like 1 (PITSLRE proteins)//1.4e-35
:195:95//Hs.963:M37712

F-NT2RM4001823//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapien
s] //2.3e-40:252:90//Hs.119294:AI379442

F-NT2RM4001828//Zinc finger protein 157 (HZF22)//1.8e-75:688:72//Hs.8989
7:U28687

F-NT2RM4001836//NUCLEOBINDIN PRECURSOR//0.0022:588:59//Hs.953:M96824

F-NT2RM4001841//ESTs//0.86:156:67//Hs.146276:AI214204

F-NT2RM4001842//ESTs//0.20:191:62//Hs.107657:AA126814

F-NT2RM4001856

F-NT2RM4001858//Human putative cerebral cortex transcriptional regulator
T-Brain-1 (Tbr-1) mRNA, complete cds//8.0e-10:244:66//Hs.22138:U49250

F-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC//2.
3e-150:704:98//Hs.61628:Y17711

F-NT2RM4001876//Human mRNA for KIAA0231 gene, partial cds//9.1e-44:621:6
6//Hs.7938:D86984

F-NT2RM4001880

F-NT2RM4001905//ESTs//7.5e-11:137:75//Hs.86950:AI204212

F-NT2RM4001922//ESTs//2.5e-51:291:93//Hs.26660:AI312633

F-NT2RM4001930//Homo sapiens mRNA for putative glucosyltransferase, part
ial cds//0.98:359:57//Hs.155356:AJ224875

F-NT2RM4001938

F-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//3.6e-172:808:98//Hs.118631:AF098162

F-NT2RM4001953//Human mRNA for KIAA0118 gene, partial cds//5.0e-54:362:83//Hs.154326:D42087

F-NT2RM4001965//ESTs, Weakly similar to KIAA0157 gene product is novel. [H. sapiens] //1.8e-65:337:96//Hs.130135:AA905493

F-NT2RM4001969//ESTs//0.00024:261:63//Hs.157579:AI312862

F-NT2RM4001979//Homo sapiens mRNA for KIAA0798 protein, complete cds//3.2e-63:527:76//Hs.159277:AB018341

F-NT2RM4001984//EST//7.1e-05:235:61//Hs.105444:AA508082

F-NT2RM4001987//Homo sapiens mRNA for KIAA0467 protein, partial cds//0.73:181:65//Hs.11147:AB007936

F-NT2RM4002013//ESTs//0.97:185:63//Hs.103345:AI302271

F-NT2RM4002018//ESTs//2.5e-76:398:94//Hs.119544:T95601

F-NT2RM4002034

F-NT2RM4002044//ESTs//9.6e-83:410:97//Hs.128162:AA815048

F-NT2RM4002054//EST//8.5e-12:176:71//Hs.137181:R56912

F-NT2RM4002055//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.3e-173:803:98//Hs.153026:AB014540

F-NT2RM4002062//ESTs, Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus] //7.0e-94:396:94//Hs.59346:AI126802

F-NT2RM4002063

F-NT2RM4002066//Homo sapiens OPA-containing protein mRNA, complete cds//1.1e-74:889:69//Hs.85313:AF071309

F-NT2RM4002067//ESTs//2.3e-34:455:69//Hs.118273:AA626040

F-NT2RM4002073//Insulin-like growth factor binding protein 2//3.2e-10:470:61//Hs.162:X16302

F-NT2RM4002075//Homo sapiens actin binding protein MAYVEN mRNA, complete

cds//2.9e-24:588:61//Hs.122967:AF059569
 F-NT2RM4002093//Polypyrimidine tract binding protein (hnRNP I) {alternative products} //9.2e-34:532:65//Hs.146459:X66975
 F-NT2RM4002109//Homo sapiens mitotic centromere-associated kinesin mRNA, complete cds//0.99:408:62//Hs.69360:U63743
 F-NT2RM4002128//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.93:202:63//Hs.8152:AB014542
 F-NT2RM4002140//Human p300 protein mRNA, complete cds//0.99:320:59//Hs.25272:U01877
 F-NT2RM4002145//CARBOXYPEPTIDASE N 83 KD CHAIN//2.7e-06:388:59//Hs.73858:J05158
 F-NT2RM4002146//ESTs, Highly similar to similar to mago nashi [H.sapiens] //1.6e-135:646:97//Hs.104650:AI037879
 F-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds//1.4e-150:763:95//Hs.22464:AF084535
 F-NT2RM4002174
 F-NT2RM4002189//Mucin 2, intestinal/tracheal//0.087:298:61//Hs.315:L21998
 F-NT2RM4002194//Human semaphorin III family homolog mRNA, complete cds//7.3e-11:454:60//Hs.32981:U38276
 F-NT2RM4002205//EST//2.6e-21:270:71//Hs.120013:AA707454
 F-NT2RM4002213//Homo sapiens mRNA for KIAA0610 protein, partial cds//0.52:313:61//Hs.118087:AB011182
 F-NT2RM4002226//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster] //8.4e-125:588:98//Hs.23900:U82984
 F-NT2RM4002251//ESTs//1.0:77:74//Hs.155135:AA910966
 F-NT2RM4002256//ESTs//7.5e-28:358:74//Hs.13356:AI205764
 F-NT2RM4002266//Human kinase Myt1 (Myt1) mRNA, complete cds//0.73:502:57//Hs.77783:AF014118

F-NT2RM4002278//EST//0.33:138:63//Hs.144096:AI032180
 F-NT2RM4002281
 F-NT2RM4002287//ESTs//0.00037:55:98//Hs.11134:T62979
 F-NT2RM4002294//Human mRNA for KIAA0281 gene, complete cds//6.7e-50:511:
 72//Hs.31463:D87457
 F-NT2RM4002301
 F-NT2RM4002323//ESTs//3.6e-09:105:87//Hs.131737:AI343331
 F-NT2RM4002339
 F-NT2RM4002344//EST//0.16:166:64//Hs.128600:AA906454
 F-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds//9.
 1e-151:708:98//Hs.26163:AB014549
 F-NT2RM4002374//Homo sapiens mRNA for KIAA0720 protein, partial cds//0.0
 040:303:63//Hs.23741:AB018263
 F-NT2RM4002383//ESTs//8.0e-16:153:78//Hs.155243:N70293
 F-NT2RM4002390
 F-NT2RM4002398
 F-NT2RM4002409
 F-NT2RM4002438//ESTs, Weakly similar to probable CBP3 protein homolog [C
 .elegans]//1.1e-55:282:96//Hs.26676:AA033997
 F-NT2RM4002446//Homo sapiens clone 24574 mRNA sequence//0.59:339:60//Hs.
 18686:AF052151
 F-NT2RM4002452
 F-NT2RM4002457//Homo sapiens mRNA for epiregulin, complete cds//3.2e-25:
 228:81//Hs.115263:D30783
 F-NT2RM4002460//EST//1.0:142:65//Hs.145370:AI252780
 F-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete
 cds//8.9e-165:777:98//Hs.8765:AF083255
 F-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds//7.
 3e-95:464:97//Hs.94781:AB014591

F-NT2RM4002493

F-NT2RM4002499//ESTs//1.3e-44:653:67//Hs.23790:N99347

F-NT2RM4002504//Small inducible cytokine A5 (RANTES)//4.3e-30:225:83//Hs.155464:AF088219

F-NT2RM4002527//Human pre-B cell enhancing factor (PBEF) mRNA, complete cds//0.99:290:60//Hs.154968:U02020

F-NT2RM4002532//Human mRNA for KIAA0238 gene, partial cds//1.0:232:61//Hs.82042:D87075

F-NT2RM4002534//Homo sapiens angiotensin/vasopressin receptor AII/AVP mRNA, complete cds//1.0:100:70//Hs.159483:AF054176

F-NT2RM4002558//Homo sapiens amphipysin II mRNA, complete cds//0.17:393:61//Hs.6619:U84004

F-NT2RM4002565//Homo sapiens mRNA for Asparaginyl tRNA Synthetase, complete cds//1.0:226:60//Hs.84043:D84273

F-NT2RM4002567//ESTs, Weakly similar to C17G10.1 [C.elegans]//3.3e-88:48:4:93//Hs.105837:AA536054

F-NT2RM4002571//ESTs, Weakly similar to UDP-GalNAc:polypeptide N-acetylglucosaminyltransferase [H.sapiens]//0.059:121:70//Hs.155413:AA429394

F-NT2RM4002593//ESTs//1.0e-15:103:95//Hs.108920:W28151

F-NT2RM4002594//Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds//1.0e-06:499:59//Hs.79357:D78275

F-NT2RM4002623//ESTs//1.2e-11:92:92//Hs.164046:T97402

F-NT2RP1000018//Homo sapiens mRNA for KIAA0687 protein, partial cds//2.0e-102:746:81//Hs.3628:AB014587

F-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//3.7e-155:747:96//Hs.159597:AJ012449

F-NT2RP1000040//ESTs//1.3e-58:338:92//Hs.17534:H16907

F-NT2RP1000063//ESTs//0.0013:72:83//Hs.108196:W81647

F-NT2RP1000086//Human mRNA for KIAA0360 gene, partial cds//5.4e-185:548:

91//Hs.79971:X98834

F-NT2RP1000101//Homo sapiens hook2 protein (HOOK2) mRNA, complete cds//0.33:247:61//Hs.30792:AF044924

F-NT2RP1000111

F-NT2RP1000112//TTK protein kinase//3.2e-40:324:81//Hs.2052:M86699

F-NT2RP1000124//ESTs//2.4e-42:268:89//Hs.146078:AI084025

F-NT2RP1000130//ESTs, Moderately similar to HEPATOMA-DERIVED GROWTH FACTOR [H.sapiens]//1.4e-71:382:94//Hs.127842:W38901

F-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds//2.1e-06:77:90//Hs.3760:AF011792

F-NT2RP1000170//EST//0.68:130:63//Hs.146994:AI184430

F-NT2RP1000174//Homo sapiens clone 24432 mRNA sequence//8.3e-140:679:97//Hs.78019:AF070535

F-NT2RP1000191//ESTs//1.3e-71:405:93//Hs.24054:N46499

F-NT2RP1000202//H.sapiens mRNA for cytokine inducible nuclear protein//2.0e-05:591:58//Hs.74019:X83703

F-NT2RP1000243

F-NT2RP1000259

F-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds//5.4e-109:528:97//Hs.4214:AF067730

F-NT2RP1000324//ESTs//3.4e-98:499:96//Hs.42530:N41661

F-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds//1.3e-148:693:98//Hs.31584:AF053551

F-NT2RP1000333//Homo sapiens monocyte/macrophage Ig-related receptor MIR-10 (MIR cl-10) mRNA, complete cds//0.28:328:60//Hs.22405:AF004231

F-NT2RP1000348//Human plectin (PLEC1) mRNA, complete cds//0.018:337:62//Hs.79706:U53204

F-NT2RP1000357

F-NT2RP1000358//DYNAMIN-1//0.96:273:59//Hs.126:L07807
 F-NT2RP1000363//Homo sapiens mRNA for KIAA0638 protein, partial cds//3.2
 e-126:497:86//Hs.77864:AB014538
 F-NT2RP1000376//Homo sapiens calcium-independent phospholipase A2 mRNA,
 complete cds//5.9e-178:877:96//Hs.120360:AF064594
 F-NT2RP1000409//ESTs//5.4e-59:415:83//Hs.140578:AA828031
 F-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds//3.
 0e-179:710:98//Hs.21862:AB011159
 F-NT2RP1000416//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PR
 ECURSOR [Mus musculus]//7.3e-177:857:97//Hs.6823:W18181
 F-NT2RP1000418//Homo sapiens calcium-activated potassium channel (KCNN3)
 mRNA, complete cds//0.46:222:60//Hs.89230:AF031815
 F-NT2RP1000439//EST//0.98:339:56//Hs.137377:AA101603
 F-NT2RP1000443//Human SLP-76 associated protein mRNA, complete cds//1.0:
 356:59//Hs.58435:AF001862
 F-NT2RP1000460
 F-NT2RP1000470//Human DNA from chromosome 19-specific cosmid R27090, gen
 omic sequence//3.7e-134:665:96//Hs.143187:AC002985
 F-NT2RP1000478//Human beta-tubulin class III isotype (beta-3) mRNA, comp
 lete cds//6.2e-57:440:80//Hs.159154:U47634
 F-NT2RP1000481//ESTs//4.8e-21:154:87//Hs.17392:AA535102
 F-NT2RP1000493
 F-NT2RP1000513//ESTs//2.2e-71:409:91//Hs.121029:AA480977
 F-NT2RP1000522//Homo sapiens clone DT1P1A11 mRNA, CAG repeat region//0.2
 1:255:62//Hs.98834:U92992
 F-NT2RP1000547//H.sapiens mRNA for transmembrane protein rnp24//1.9e-06:
 337:63//Hs.75914:X92098
 F-NT2RP1000574//Homo sapiens homeobox protein MEIS2 (MEIS2) mRNA, partia
 l cds//1.4e-82:295:92//Hs.104105:AF017418

F-NT2RP1000577//Human sialoprotein mRNA, complete cds//0.014:235:65//Hs.121552:J05213

F-NT2RP1000581//VON WILLEBRAND FACTOR PRECURSOR//1.6e-33:223:89//Hs.110802:X04385

F-NT2RP1000609//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//2.2e-49:506:73//Hs.132898:AC004770

F-NT2RP1000629//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//3.6e-19:556:62//Hs.152936:D63475

F-NT2RP1000630

F-NT2RP1000677//Human breast tumor autoantigen mRNA, complete sequence//2.4e-05:389:59//Hs.3844:U24576

F-NT2RP1000688//ESTs, Weakly similar to T06E6.d [C.elegans]//2.5e-43:232:95//Hs.3487:AA425553

F-NT2RP1000695//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//9.2e-53:312:90//Hs.7049:AI141736

F-NT2RP1000701//Myogenic factor 3//0.81:186:63//Hs.2834:AF027148

F-NT2RP1000721//Homo sapiens mRNA for repressor protein, partial cds//4.0e-33:278:78//Hs.58167:D30612

F-NT2RP1000730//ESTs, Weakly similar to putative p150 [H.sapiens]//6.2e-40:297:84//Hs.18122:AI338045

F-NT2RP1000733//G1 to S phase transition 1//1.4e-31:286:78//Hs.2707:X17644

F-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds//2.6e-123:604:96//Hs.21771:AF101434

F-NT2RP1000746

F-NT2RP1000767

F-NT2RP1000782//Human globin gene//3.6e-21:140:91//Hs.100090:M69023

F-NT2RP1000796//H.sapiens mRNA for ROX protein//0.17:404:57//Hs.25497:X96401

F-NT2RP1000825//Human DNA sequence from PAC 127B20 on chromosome 22q11.2
-qter, contains gene for GTPase-activating protein similar to rhoGAP pro
tein. ribosomal protein L6 pseudogene, ESTs and CA repeat//2.7e-23:147:9
1//Hs.102336:Z83838

F-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, com
plete cds//5.4e-143:424:96//Hs.18953:AF067223

F-NT2RP1000834//ESTs//0.18:280:60//Hs.157215:AI332903

F-NT2RP1000836//EST//0.60:103:66//Hs.145708:AI267990

F-NT2RP1000846//EST//1.2e-15:322:65//Hs.149925:AI288838

F-NT2RP1000851//ESTs//6.1e-96:459:98//Hs.121586:AA423875

F-NT2RP1000856//Human globin gene//6.7e-22:140:91//Hs.100090:M69023

F-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds//2.2e-107:551:95//
Hs.125156:AF064094

F-NT2RP1000902//EST//1.8e-28:218:85//Hs.145258:AI218683

F-NT2RP1000915//ESTs//8.8e-11:102:81//Hs.163740:AI248847

F-NT2RP1000916//ESTs, Weakly similar to coded for by C. elegans cDNA cm0
4e9 [C.elegans]//2.2e-27:159:94//Hs.122153:AA780270

F-NT2RP1000943//Human hSIAH2 mRNA, complete cds//0.45:130:68//Hs.20191:U
76248

F-NT2RP1000944//EST//0.99:116:63//Hs.116633:AA668400

F-NT2RP1000947//Human E2 ubiquitin conjugating enzyme UbCH5B (UBCH5B) mR
NA, complete cds//2.7e-26:185:87//Hs.108332:U39317

F-NT2RP1000954//Homo sapiens BACH1 mRNA, complete cds//0.81:329:56//Hs.1
54276:AB002803

F-NT2RP1000958//ESTs//1.3e-20:129:92//Hs.163740:AI248847

F-NT2RP1000959//Ribosomal protein, large, P0//0.36:76:73//Hs.73742:M1788
5

F-NT2RP1000966//NUCLEOLIN//1.2e-72:353:98//Hs.79110:M60858

F-NT2RP1000980//ESTs//1.6e-109:555:96//Hs.84429:N28866

F-NT2RP1000988//Human chromosome 3p21.1 gene sequence//2.6e-73:665:80//H
s.82837:L13435

F-NT2RP1001011

F-NT2RP1001013//ESTs//3.4e-40:393:74//Hs.120206:AI089163

F-NT2RP1001014

F-NT2RP1001033//Tubulin, gamma polypeptide//0.00041:313:59//Hs.150785:M6
1764

F-NT2RP1001073//Glucocorticoid receptor//1.0:204:61//Hs.75772:M10901

F-NT2RP1001079//ESTs//1.0:174:62//Hs.158209:AI360531

F-NT2RP1001080//Homo sapiens forkhead protein (FKHRL1) mRNA, complete cd
s//0.57:215:64//Hs.14845:AF032886

F-NT2RP1001113//ESTs, Weakly similar to coded for by C. elegans cDNA CEE
SB82F [C.elegans]//1.4e-65:293:95//Hs.32751:H38087

F-NT2RP1001173

F-NT2RP1001177//Homo sapiens histone macroH2A1.2 mRNA, complete cds//6.1
e-26:259:74//Hs.75258:AF054174

F-NT2RP1001185//EST//1.4e-27:266:77//Hs.122245:AA781524

F-NT2RP1001199//ESTs//0.97:75:73//Hs.131498:AI022150

F-NT2RP1001247//Human endometrial bleeding associated factor mRNA, compl
ete cds//1.6e-19:120:95//Hs.25195:U81523

F-NT2RP1001248//ESTs//3.0e-21:143:93//Hs.157243:AI337094

F-NT2RP1001253//PUTATIVE GLUCOSAMINE-6-PHOSPHATE ISOMERASE//1.2e-89:344:
93//Hs.3090:AJ002231

F-NT2RP1001286//H.sapiens mRNA for adenosine triphosphatase, calcium//0.
026:392:57//Hs.5541:Y15724

F-NT2RP1001294

F-NT2RP1001302

F-NT2RP1001310//Homo sapiens creatine transporter mRNA, complete cds//3.
6e-07:379:61//Hs.154503:U36341

F-NT2RP1001311//ESTs//9.5e-73:403:93//Hs.24739:H67815
 F-NT2RP1001313//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730)
 containing the hFEN1 gene//3.1e-87:437:97//Hs.132898:AC004770
 F-NT2RP1001361//ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE
 SUBUNIT B14.5B [Bos taurus]//6.8e-101:480:94//Hs.75017:AA166853
 F-NT2RP1001385//EST//0.86:127:65//Hs.156304:AI336859
 F-NT2RP1001395//Homo sapiens stannin mRNA, complete cds//0.75:355:58//Hs
 .76691:AF070673
 F-NT2RP1001410//Thromboxane A2 receptor//1.0:157:63//Hs.89887:D38081
 F-NT2RP1001424//ESTs//5.3e-20:118:95//Hs.159792:R60700
 F-NT2RP1001432//ESTs//5.3e-20:118:95//Hs.159792:R60700
 F-NT2RP1001449//Homo sapiens clone 24733 mRNA sequence//5.7e-86:422:97//
 Hs.21970:AF052149
 F-NT2RP1001457//H.sapiens DAP-kinase mRNA//0.40:231:61//Hs.153924:X76104
 F-NT2RP1001466
 F-NT2RP1001475//ESTs//1.2e-98:495:97//Hs.14347:AA287742
 F-NT2RP1001482
 F-NT2RP1001494
 F-NT2RP1001543//ESTs//1.2e-38:207:98//Hs.131063:AI016400
 F-NT2RP1001546//Homo sapiens mRNA for DAP-1 beta, complete cds//0.00077:
 254:64//Hs.75814:AB000277
 F-NT2RP1001569
 F-NT2RP1001616//Homo sapiens Tax interaction protein 1 mRNA, partial cds
 //2.5e-41:496:74//Hs.12956:U90913
 F-NT2RP1001665//ESTs//9.4e-58:311:96//Hs.127391:AA954420
 F-NT2RP2000001//Homo sapiens clone 617 unknown mRNA, complete sequence//
 4.7e-137:685:96//Hs.93677:AF091081
 F-NT2RP2000006//ESTs, Weakly similar to B0035.14 [C.elegans]//8.2e-47:30
 0:89//Hs.6473:AA853955

F-NT2RP2000007//Human mRNA for KIAA0392 gene, partial cds//1.1e-15:241:68//Hs.40100:AB002390

F-NT2RP2000008//Human mRNA for KIAA0065 gene, partial cds//1.5e-29:526:66//Hs.70617:D31763

F-NT2RP2000027//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HO MOLOG [Homo sapiens]//2.0e-26:214:82//Hs.140385:AA773359

F-NT2RP2000032//ESTs//0.91:368:57//Hs.131209:AI038867

F-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds//6.1e-78:383:97//Hs.8309:AB018290

F-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//7.8e-97:467:97//Hs.6216:AF061749

F-NT2RP2000054//HOMEBOX/POU DOMAIN PROTEIN RDC-1//1.0:110:70//Hs.74095:L20433

F-NT2RP2000056//Human HPTP epsilon mRNA for protein tyrosine phosphatase epsilon//1.2e-27:146:100//Hs.155991:X54134

F-NT2RP2000067//Human DNA sequence from clone 1052M9 on chromosome Xq25.

Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//8.1e-41:767:61//Hs.23796:AL022718

F-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence//6.5e-08:344:58//Hs.159402:AC005609

F-NT2RP2000076//H.sapiens mRNA for TFIIA//0.00023:356:62//Hs.121686:D14887

F-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds//6.8e-79:278:97//Hs.54877:AF050078

F-NT2RP2000079//ESTs//1.2e-36:202:94//Hs.17606:AI279879

F-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds//7.1e-160:752:98//Hs.22926:AB018338

F-NT2RP2000091
 F-NT2RP2000097
 F-NT2RP2000098//ESTs//0.086:92:69//Hs.159389:AI371963
 F-NT2RP2000108//Human mRNA for KIAA0392 gene, partial cds//1.4e-18:200:77//Hs.40100:AB002390
 F-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds//1.6e-15:551:97//Hs.17706:AB018356
 F-NT2RP2000120//ESTs, Weakly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [C.elegans]//0.019:72:81//Hs.5268:W22670
 F-NT2RP2000126//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//1.4e-120:607:96//Hs.159273:AF054177
 F-NT2RP2000133//Neuronal pentraxin II//0.00014:401:61//Hs.3281:U29195
 F-NT2RP2000147//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//2.2e-18:559:60//Hs.152936:D63475
 F-NT2RP2000153//Homo sapiens splicing factor (CC1.3) mRNA, complete cds//0.33:85:70//Hs.256:L10910
 F-NT2RP2000157//ESTs//0.53:75:81//Hs.24885:R49291
 F-NT2RP2000161//ESTs//2.6e-06:89:84//Hs.21738:AI188190
 F-NT2RP2000173
 F-NT2RP2000175
 F-NT2RP2000183//Homo sapiens mRNA for dihydropyrimidinase related protein 4, complete cds//0.0018:324:58//Hs.100058:AB006713
 F-NT2RP2000195//ESTs, Weakly similar to C37E2.2 [C.elegans]//3.6e-37:233:90//Hs.56750:AI148761
 F-NT2RP2000205//ESTs//5.6e-58:317:93//Hs.49559:AA401050
 F-NT2RP2000208
 F-NT2RP2000224//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds//0.0071:243:61//Hs.143641:AB009462
 F-NT2RP2000232//EST//0.0087:187:62//Hs.151024:Z39990

F-NT2RP2000233//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.17:34
2:59//Hs.8546:U97669

F-NT2RP2000239//Human mRNA for KIAA0380 gene, complete cds//1.0:227:60//
Hs.47822:AB002378

F-NT2RP2000248//EST//0.49:117:70//Hs.61016:AA019719

F-NT2RP2000257//Macrophage stimulating 1 (hepatocyte growth factor-like)
//0.51:227:60//Hs.30223:X90846

F-NT2RP2000258//ESTs//3.1e-48:261:94//Hs.128230:AA972691

F-NT2RP2000270//ESTs//2.9e-38:357:75//Hs.140329:AA714011

F-NT2RP2000274//ESTs//1.1e-106:508:98//Hs.47646:AA307599

F-NT2RP2000283//EST//1.0:139:63//Hs.128256:AA972910

F-NT2RP2000288

F-NT2RP2000289

F-NT2RP2000297//Human repressor transcriptional factor (ZNF85) mRNA, com
plete cds//4.2e-60:744:70//Hs.37138:U35376

F-NT2RP2000298//ESTs//6.1e-46:322:85//Hs.159490:AI123467

F-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA
, complete cds//4.3e-13:140:80//Hs.58218:U82381

F-NT2RP2000327//ESTs//4.3e-18:108:98//Hs.126212:AI417006

F-NT2RP2000328//ESTs//6.3e-88:437:96//Hs.127336:AI332905

F-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//6.6e-41:607:66
//Hs.101642:X60673

F-NT2RP2000337//Homo sapiens neurocan (CSPG3) mRNA, complete cds//0.96:1
26:69//Hs.153706:AF026547

F-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA,
complete cds//1.2e-130:627:97//Hs.76556:U83981

F-NT2RP2000369//Homo sapiens mRNA for KIAA0630 protein, partial cds//0.5
6:464:57//Hs.12259:AB014530

F-NT2RP2000412//ESTs//1.0:214:60//Hs.91226:AA649047

F-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds//1.6e-67
:375:93//Hs.808:L28010
F-NT2RP2000420//ESTs, Moderately similar to zinc finger protein [H.sapie
ns]//3.9e-75:413:92//Hs.36779:AA626790
F-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA,
complete cds//6.7e-128:609:96//Hs.5819:AF102265
F-NT2RP2000438//ESTs//1.3e-05:50:98//Hs.156532:AA913381
F-NT2RP2000448//EST//1.1e-24:136:98//Hs.160402:AI393918
F-NT2RP2000459//H.sapiens mRNA for imogen 38//1.9e-22:158:87//Hs.154655:
Z68747
F-NT2RP2000498//ESTs//1.0e-17:181:79//Hs.155243:N70293
F-NT2RP2000503//ESTs//4.5e-41:205:100//Hs.62751:AA765702
F-NT2RP2000510
F-NT2RP2000516
F-NT2RP2000523//ESTs, Highly similar to APOLIPOPROTEIN B MRNA EDITING P
ROTEIN [Rattus norvegicus]//3.2e-15:167:75//Hs.10984:AA806768
F-NT2RP2000603//Homo sapiens mRNA for KIAA0572 protein, partial cds//5.6
e-38:196:98//Hs.14409:AB011144
F-NT2RP2000617//Myosin, heavy polypeptide 6, cardiac muscle, alpha (card
iomyopathy, hypertrophic 1)//1.0:242:57//Hs.114001:Z20656
F-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds//4.2
e-151:732:97//Hs.7314:AB014514
F-NT2RP2000644//ESTs//0.035:276:60//Hs.43660:N33174
F-NT2RP2000656
F-NT2RP2000658//ESTs//0.032:281:59//Hs.124853:AA420602
F-NT2RP2000668
F-NT2RP2000678//ESTs//2.9e-16:310:65//Hs.126867:AI093453
F-NT2RP2000704//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTE
IN KINASE C41C4.4 IN CHROMOSOME II PRECURSOR [Caenorhabditis elegans]//2

.4e-31:233:78//Hs.114905:AA088442
 F-NT2RP2000710
 F-NT2RP2000715
 F-NT2RP2000731
 F-NT2RP2000758//EST//1.0e-14:199:71//Hs.162409:AA573242
 F-NT2RP2000764//ESTs, Weakly similar to NIFS-LIKE 54.5 KD PROTEIN [Sacch
 aromyces cerevisiae] //1.6e-74:445:89//Hs.21421:AA911739
 F-NT2RP2000809//ESTs//1.2e-36:235:89//Hs.154580:N34101
 F-NT2RP2000812//Homo sapiens pendrin (PDS) mRNA, complete cds//0.22:351:
 58//Hs.159275:AF030880
 F-NT2RP2000814
 F-NT2RP2000816//Homo sapiens mRNA for KIAA0610 protein, partial cds//1.0
 :311:61//Hs.118087:AB011182
 F-NT2RP2000819
 F-NT2RP2000841//Human mRNA for KIAA0294 gene, complete cds//3.4e-28:390:
 70//Hs.20695:AB002292
 F-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, compl
 ete cds//9.5e-29:167:94//Hs.75794:U80811
 F-NT2RP2000845//ESTs//1.0e-83:403:98//Hs.156828:AI336850
 F-NT2RP2000863//ESTs, Highly similar to HYPOTHETICAL 36.7 KD PROTEIN C2
 F7.02C IN CHROMOSOME I [Schizosaccharomyces pombe] //6.4e-34:207:92//Hs.1
 35235:AI081880
 F-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds//7.
 7e-142:732:94//Hs.3615:AB018284
 F-NT2RP2000892//ESTs, Weakly similar to mitogen-activated kinase kinase
 kinase 5 [H.sapiens] //0.50:189:65//Hs.46146:AA418097
 F-NT2RP2000931//MATRIN 3//1.1e-130:610:98//Hs.78825:AB018266
 F-NT2RP2000932//Homo sapiens BAC clone GS166A23 from 7p21//5.5e-66:326:9
 7//Hs.15144:AC005014

F-NT2RP2000938//ESTs//1.8e-28:296:75//Hs.22822:H06408
 F-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds//1.
 9e-113:533:98//Hs.19822:AB018298
 F-NT2RP2000965//ESTs//5.3e-59:328:94//Hs.35575:R96494
 F-NT2RP2000970
 F-NT2RP2000985//ESTs, Weakly similar to HYPOTHETICAL 96.8 KD PROTEIN IN
 SIS2-MTD1 INTERGENIC REGION [*Saccharomyces cerevisiae*]//7.3e-76:385:96//
 Hs.21875:AA243700
 F-NT2RP2000987//ESTs//5.6e-11:177:72//Hs.15776:T91944
 F-NT2RP2001036//ESTs//2.0e-55:352:88//Hs.122131:AA789292
 F-NT2RP2001044//EST//0.069:267:60//Hs.102808:N67117
 F-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
 0488//1.0e-145:696:97//Hs.67619:AB007957
 F-NT2RP2001065
 F-NT2RP2001070//Human mRNA for KIAA0315 gene, partial cds//1.0:310:60//H
 s.3989:AB002313
 F-NT2RP2001081
 F-NT2RP2001094//ESTs//0.0071:262:64//Hs.128115:AI356560
 F-NT2RP2001119//Small inducible cytokine A5 (RANTES)//2.2e-34:311:78//Hs
 .155464:AF088219
 F-NT2RP2001127//Human mRNA for KIAA0234 gene, complete cds//3.5e-33:519:
 63//Hs.80358:U52191
 F-NT2RP2001137//ESTs, Highly similar to RAB GDP DISSOCIATION INHIBITOR
 ALPHA [*Bos taurus*]//6.4e-34:201:91//Hs.118470:AI336362
 F-NT2RP2001149//EST//3.9e-27:244:78//Hs.162236:AA551582
 F-NT2RP2001168//ESTs//0.0023:216:62//Hs.134938:AI091361
 F-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds//7.
 4e-114:567:96//Hs.26247:AB007949
 F-NT2RP2001174//H.sapiens ZNF81 gene//0.21:256:59//Hs.104020:X68011

F-NT2RP2001196
 F-NT2RP2001218//ESTs//1.1e-65:337:96//Hs.115710:AA524598
 F-NT2RP2001226//Guanylate cyclase 1, soluble, alpha 2//0.030:395:59//Hs.
 2685:Z50053
 F-NT2RP2001233//Zinc finger protein 136 (clone pHZ-20)//4.4e-58:656:70//
 Hs.69740:U09367
 F-NT2RP2001245//EST//0.018:228:62//Hs.116798:AA633813
 F-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds//8.1
 e-108:514:97//Hs.7531:AB018353
 F-NT2RP2001277//EST//0.42:127:66//Hs.42834:N20277
 F-NT2RP2001290//Homo sapiens alpha SNAP mRNA, complete cds//1.8e-62:527:
 76//Hs.75848:U39412
 F-NT2RP2001295//ESTs//3.4e-29:90:100//Hs.123321:AA810287
 F-NT2RP2001312//ESTs//1.0:121:61//Hs.160261:AI146387
 F-NT2RP2001327//Human B12 protein mRNA, complete cds//1.9e-30:359:71//Hs
 .76090:M80783
 F-NT2RP2001328//ESTs//5.2e-103:532:94//Hs.69476:AA628522
 F-NT2RP2001347//ESTs//4.3e-28:217:82//Hs.31775:H41883
 F-NT2RP2001366//ESTs, Weakly similar to ZK1058.5 [C.elegans]//1.8e-72:41
 8:91//Hs.107039:W27244
 F-NT2RP2001378
 F-NT2RP2001381//ESTs//0.59:235:62//Hs.118569:AI377558
 F-NT2RP2001392//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155),
 complete sequence//0.28:225:62//Hs.159402:AC005609
 F-NT2RP2001394//ESTs//8.3e-22:133:78//Hs.109655:AI189767
 F-NT2RP2001397//ESTs//0.090:265:60//Hs.152775:AA633088
 F-NT2RP2001420
 F-NT2RP2001423//ESTs, Weakly similar to hypothetical protein [H.sapiens]
 //0.030:443:59//Hs.140506:AA308018

F-NT2RP2001427//EST//1.9e-19:174:79//Hs.132635:AI032875
 F-NT2RP2001436//EST//0.16:132:66//Hs.128265:AA972966
 F-NT2RP2001440//Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide//9.8e-56:603:72//Hs.75544:Z82248
 F-NT2RP2001445//ESTs//2.2e-26:193:86//Hs.128610:AA504218
 F-NT2RP2001449
 F-NT2RP2001450
 F-NT2RP2001467
 F-NT2RP2001506
 F-NT2RP2001511//ESTs, Weakly similar to F48F7.1 [C.elegans]//3.2e-83:409:98//Hs.156161:AI333779
 F-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARAL AR1//6.4e-138:657:97//Hs.4277:Y14494
 F-NT2RP2001526//EST//1.0:180:61//Hs.136311:AA437134
 F-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//5.2e-105:384:94//Hs.99742:AF035586
 F-NT2RP2001560
 F-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA 0488//1.4e-124:590:98//Hs.67619:AB007957
 F-NT2RP2001576//Erythrocyte membrane protein band 4.9 (dematin)//0.046:521:60//Hs.75936:U28389
 F-NT2RP2001581//EST//1.0:28:96//Hs.148002:AI264876
 F-NT2RP2001597//Casein kinase 2, alpha prime polypeptide//0.069:165:65//Hs.82201:M55268
 F-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.3e-138:647:98//Hs.27197:AB018340
 F-NT2RP2001613
 F-NT2RP2001628//ESTs//4.9e-45:238:96//Hs.135222:AI082229
 F-NT2RP2001634//Homo sapiens alpha-catenin related protein (ACRP) mRNA,

complete cds//4.9e-124:604:96//Hs.58488:U97067

F-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mRNA, complete cds//1.3e-145:687:97//Hs.159558:AF058718

F-NT2RP2001663//Enolase 1, (alpha)//4.2e-38:372:74//Hs.675:M14328

F-NT2RP2001675//X-LINKED HELICASE II//0.040:454:58//Hs.96264:U72936

F-NT2RP2001677//Homo sapiens mRNA for KIAA0771 protein, partial cds//0.028:285:63//Hs.6162:AB018314

F-NT2RP2001678//Homo sapiens semaphorin F homolog mRNA, complete cds//1.7e-34:328:76//Hs.27621:U52840

F-NT2RP2001699//EST//0.029:94:68//Hs.125936:AA889091

F-NT2RP2001720//ESTs, Highly similar to Rap2 interacting protein 8 [M.musculus]//1.0:173:62//Hs.107361:AI197870

F-NT2RP2001721

F-NT2RP2001740//Homo sapiens Rigui (RIGUI) mRNA, complete cds//0.58:403:57//Hs.8114:AF022991

F-NT2RP2001748//Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase)//1.2e-19:151:86//Hs.77393:D14697

F-NT2RP2001762//Homo sapiens exonuclease 1a (EXO1a) mRNA, complete cds//5.2e-34:191:96//Hs.47504:AF091754

F-NT2RP2001813//EST//0.46:183:57//Hs.144096:AI032180

F-NT2RP2001839//EST//2.5e-12:86:94//Hs.133226:AI052250

F-NT2RP2001861//Homo sapiens mRNA for paraplegin//0.068:146:71//Hs.78497:Y16610

F-NT2RP2001869//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//0.0013:174:62//Hs.9443:AF027219

F-NT2RP2001876//Allograft inflammatory factor 1//2.2e-08:162:67//Hs.76364:Y14768

F-NT2RP2001883
 F-NT2RP2001898//75 KD INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECURS
 OR//3.0e-113:633:90//Hs.142189:M74161
 F-NT2RP2001900//EST//1.9e-14:132:84//Hs.130049:AA902650
 F-NT2RP2001907//ESTs, Weakly similar to ankyrin 3, long form [H.sapiens]
 //0.37:263:62//Hs.106377:H29757
 F-NT2RP2001926//ESTs//1.1e-87:430:97//Hs.133487:AI393754
 F-NT2RP2001936
 F-NT2RP2001943
 F-NT2RP2001946//ESTs//1.0:110:69//Hs.7941:AA894797
 F-NT2RP2001947
 F-NT2RP2001969//ESTs//3.3e-93:433:93//Hs.9622:W44489
 F-NT2RP2001976//Homo sapiens KIAA0432 mRNA, complete cds//0.20:238:63//H
 s.155174:AB007892
 F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 protein, partial cds//7.4
 e-05:235:62//Hs.129943:AB011117
 F-NT2RP2001991//EST//0.0027:163:68//Hs.162458:AA579196
 F-NT2RP2002025//Homo sapiens mRNA for KIAA0756 protein, partial cds//3.2
 e-62:314:97//Hs.116604:AB018299
 F-NT2RP2002032
 F-NT2RP2002033//EST//1.2e-16:224:74//Hs.150409:AI003543
 F-NT2RP2002041//EST//0.022:139:69//Hs.127219:AA939336
 F-NT2RP2002046//ESTs//1.1e-35:218:92//Hs.130678:R51509
 F-NT2RP2002047//ESTs//0.43:131:64//Hs.153939:AI284198
 F-NT2RP2002058//Homo sapiens mRNA for KIAA0741 protein, complete cds//0.
 96:137:71//Hs.3615:AB018284
 F-NT2RP2002066//Homo sapiens transmembrane receptor UNC5C (UNC5C) mRNA,
 complete cds//3.1e-36:509:66//Hs.44553:AF055634
 F-NT2RP2002070//ESTs//0.00027:107:72//Hs.4852:R84241

F-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence//3.4e-129:643:96/
/Hs.11039:AF052183

F-NT2RP2002078//EST//1.0:83:65//Hs.115996:AA609014

F-NT2RP2002079//ESTs//6.2e-06:326:60//Hs.134202:AI313156

F-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein//3.2e
-112:533:97//Hs.155218:AJ007509

F-NT2RP2002105//Homo sapiens serine threonine kinase 11 (STK11) mRNA, co
mplete cds//6.1e-07:408:60//Hs.122755:AF032986

F-NT2RP2002124//ESTs//1.3e-90:459:96//Hs.142053:AA224286

F-NT2RP2002137//ATPase, Ca++ transporting, plasma membrane 4//0.0032:319
:59//Hs.995:M83363

F-NT2RP2002154//Homo sapiens mRNA for C17orf1 protein//1.0:149:65//Hs.10
0217:AJ008112

F-NT2RP2002172//EST//4.4e-14:276:67//Hs.148392:AI085314

F-NT2RP2002185//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]
//6.8e-61:354:91//Hs.109966:C06057

F-NT2RP2002192//Human 75-kD autoantigen (PM-Sc1) mRNA, complete cds//3.7
e-37:194:97//Hs.91728:M58460

F-NT2RP2002193//Homo sapiens protein inhibitor of activated STAT protein
PIASx-alpha mRNA, complete cds//6.8e-15:228:67//Hs.111323:AF077954

F-NT2RP2002208

F-NT2RP2002219//ESTs//0.0059:247:61//Hs.36495:AA151628

F-NT2RP2002231//ESTs//0.29:167:63//Hs.112013:AI394318

F-NT2RP2002235//H.sapiens mRNA for PHAPI2b protein//0.86:67:82//Hs.84264
:U70439

F-NT2RP2002252//Homo sapiens mRNA for KIAA0527 protein, partial cds//0.7
9:264:59//Hs.129748:AB011099

F-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cd
s//2.1e-51:315:89//Hs.150595:AF005418

F-NT2RP2002259//Human L-myc protein gene, complete cds//1.2e-26:343:71//
Hs.92137:M19720

F-NT2RP2002270//ESTs, Weakly similar to AF-9 PROTEIN [H.sapiens]//1.3e-3
1:206:88//Hs.4029:Z78373

F-NT2RP2002292//ESTs//1.3e-07:153:67//Hs.13533:H23079

F-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA,
partial cds//5.0e-95:467:96//Hs.24812:AF069532

F-NT2RP2002316//ESTs//0.95:194:63//Hs.157214:AA805445

F-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA
, complete cds//1.3e-124:640:95//Hs.31034:AB015594

F-NT2RP2002333//Protein-tyrosine kinase tyk2 (non-receptor)//1.0:257:60/
/Hs.75516:X54637

F-NT2RP2002373

F-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant m
RNA, complete cds//3.1e-139:673:97//Hs.109051:AF038958

F-NT2RP2002394//Human clone 23695 mRNA sequence//0.16:456:59//Hs.90798:U
79289

F-NT2RP2002408//HOMEBOX/POU DOMAIN PROTEIN RDC-1//0.00069:265:65//Hs.74
095:L20433

F-NT2RP2002426//EST//4.3e-33:271:79//Hs.145743:AI269098

F-NT2RP2002439//ESTs//0.0041:129:68//Hs.146064:AA714326

F-NT2RP2002442//ESTs, Weakly similar to similar to molybdoterin biosynth
esis MOEB proteins [C.elegans]//5.6e-26:169:89//Hs.25198:AA904265

F-NT2RP2002457//ESTs//0.00031:121:71//Hs.134860:AI091436

F-NT2RP2002464//Human mRNA for KIAA0086 gene, complete cds//0.0013:207:6
3//Hs.1560:D42045

F-NT2RP2002475//ESTs//1.0:85:75//Hs.155371:AI139929

F-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complet
e cds//7.6e-125:607:96//Hs.125856:AB005289

F-NT2RP2002498

F-NT2RP2002503//Human zinc finger protein (FDZF2) mRNA, complete cds//2.
2e-89:314:87//Hs.102681:U95044

F-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds//3.
8e-159:761:97//Hs.23255:AB018334

F-NT2RP2002520//RAB6, member RAS oncogene family//0.99:216:59//Hs.107563
:M28212

F-NT2RP2002537

F-NT2RP2002546//EST//0.81:161:65//Hs.120562:AA741096

F-NT2RP2002549//ESTs//0.76:228:61//Hs.146313:AA594979

F-NT2RP2002591//Homo sapiens mRNA for KIAA0798 protein, complete cds//2.
9e-33:285:78//Hs.159277:AB018341

F-NT2RP2002595//Adenylate cyclase 8 (brain)//0.39:377:59//Hs.2522:Z35309

F-NT2RP2002606//Human Line-1 repeat mRNA with 2 open reading frames//6.4
e-24:144:95//Hs.23094:M19503

F-NT2RP2002609//Human guanine nucleotide regulatory protein (tim1) mRNA,
complete cds//1.0:120:68//Hs.334:U02082

F-NT2RP2002618//H.sapiens mRNA for arginine methyltransferase, splice va
riant, 1262 bp//4.3e-28:460:63//Hs.20521:Y10805

F-NT2RP2002621

F-NT2RP2002643//Human p300/CBP-associated factor (P/CAF) mRNA, complete
cds//0.0022:210:64//Hs.155302:U57317

F-NT2RP2002672//ESTs//7.4e-30:226:84//Hs.94694:W52493

F-NT2RP2002701//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK
757.1 IN CHROMOSOME III [Caenorhabditis elegans]//8.3e-56:278:97//Hs.109
857:AA088385

F-NT2RP2002706//CEREBELLIN 1 PRECURSOR//0.00042:367:61//Hs.662:M58583

F-NT2RP2002710//Homo sapiens mRNA for KIAA0672 protein, complete cds//8.
0e-42:631:65//Hs.6336:AB014572

F-NT2RP2002727
 F-NT2RP2002736//ESTs//3.2e-67:336:97//Hs.86583:AA761217
 F-NT2RP2002740//EST//1.0e-70:352:97//Hs.145168:AI150297
 F-NT2RP2002741//Human mRNA for Neuroblastoma, complete cds//2.4e-30:628:
 62//Hs.87435:D89016
 F-NT2RP2002750//Human mRNA for KIAA0331 gene, complete cds//2.1e-29:285:
 75//Hs.146395:AB002329
 F-NT2RP2002752//EST//2.2e-06:126:74//Hs.159913:AA862709
 F-NT2RP2002753//ESTs//4.3e-14:137:81//Hs.133478:T79705
 F-NT2RP2002769//Human plectin (PLEC1) mRNA, complete cds//0.017:507:57//
 Hs.79706:U53204
 F-NT2RP2002778//EST//1.6e-57:319:93//Hs.147519:AI216407
 F-NT2RP2002800
 F-NT2RP2002839//ESTs//0.075:177:62//Hs.132445:AA921763
 F-NT2RP2002857//ESTs//0.99:88:69//Hs.132104:AI382142
 F-NT2RP2002862
 F-NT2RP2002880
 F-NT2RP2002891//Homo sapiens mRNA for KIAA0673 protein, partial cds//1.0
 :237:62//Hs.106487:AB014573
 F-NT2RP2002925//ESTs//1.6e-33:318:77//Hs.16808:W22606
 F-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, comp
 lete cds//3.9e-136:623:99//Hs.116674:AF038392
 F-NT2RP2002929//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.24:15
 8:65//Hs.108447:AJ000517
 F-NT2RP2002939
 F-NT2RP2002954
 F-NT2RP2002959//Human E2 ubiquitin conjugating enzyme Ubch5B (UBCH5B) mR
 NA, complete cds//6.4e-21:135:91//Hs.108332:U39317
 F-NT2RP2002979

F-NT2RP2002980

F-NT2RP2002986//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//7.8e-11:272:61//Hs.122967:AF059569

F-NT2RP2002987//ESTs//8.2e-20:99:82//Hs.138965:AI004740

F-NT2RP2002993

F-NT2RP2003000//Small inducible cytokine A5 (RANTES)//2.1e-46:353:81//Hs.155464:AF088219

F-NT2RP2003034//ESTs//1.6e-08:263:66//Hs.164048:AA811741

F-NT2RP2003073//Human clone 230971 defective mariner transposon Hsmar2 mRNA sequence//4.6e-43:381:78//Hs.159176:U92019

F-NT2RP2003099//TRICHOHYALIN//0.98:183:62//Hs.82276:L09190

F-NT2RP2003108//H.sapiens nek2 mRNA for protein kinase//0.025:185:67//Hs.153704:U11050

F-NT2RP2003117//ESTs//7.6e-30:219:88//Hs.153408:AA416633

F-NT2RP2003121//ESTs//1.9e-13:158:73//Hs.129998:AI291379

F-NT2RP2003125//Serum response factor (c-fos serum response element-binding transcription factor)//4.5e-06:556:57//Hs.155321:J03161

F-NT2RP2003129//ESTs//0.095:218:63//Hs.70836:AA121544

F-NT2RP2003137

F-NT2RP2003157//Homo sapiens mRNA for KIAA0620 protein, partial cds//0.40:227:61//Hs.105958:AB014520

F-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds//5.7e-113:581:93//Hs.9736:D67025

F-NT2RP2003161//ESTs//0.0095:120:65//Hs.163532:AI424170

F-NT2RP2003164//EST//0.11:179:63//Hs.163299:AA853944

F-NT2RP2003165//Human mRNA for KIAA0355 gene, complete cds//1.0e-39:342:79//Hs.153014:AB002353

F-NT2RP2003177//ESTs//3.6e-80:414:96//Hs.4767:N91123

F-NT2RP2003194//ESTs//5.4e-20:119:95//Hs.149531:AI393223

F-NT2RP2003206//EST//0.095:182:60//Hs.88461:AA278594
 F-NT2RP2003228//CDC21 HOMOLOG//9.3e-138:726:93//Hs.154443:X74794
 F-NT2RP2003230//ESTs//3.0e-10:239:62//Hs.163720:AA526947
 F-NT2RP2003237//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.3e-62:543:77//Hs.108966:U48696
 F-NT2RP2003243//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.52:200:62//Hs.102732:U88153
 F-NT2RP2003265
 F-NT2RP2003272//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster] //5.8e-57:313:93//Hs.109966:C06057
 F-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds//4.9e-147:714:96//Hs.154919:AB014525
 F-NT2RP2003280
 F-NT2RP2003286//Homo sapiens mRNA for KIAA0587 protein, complete cds//0.0097:243:65//Hs.21862:AB011159
 F-NT2RP2003293//ESTs//5.5e-28:418:70//Hs.146227:AI269334
 F-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds//2.0e-86:416:97//Hs.7943:AB006572
 F-NT2RP2003297//EST//0.99:240:60//Hs.133228:AI052312
 F-NT2RP2003307//ESTs//5.6e-15:137:81//Hs.90020:AA442752
 F-NT2RP2003308
 F-NT2RP2003329//ESTs, Highly similar to HYPOTHETICAL 54.9 KD PROTEIN CO 2F5.7 IN CHROMOSOME III [Caenorhabditis elegans] //1.8e-102:532:95//Hs.6092:T75227
 F-NT2RP2003339//ESTs//0.13:166:63//Hs.149649:AI346765
 F-NT2RP2003347//ESTs//0.96:185:59//Hs.125003:H85963
 F-NT2RP2003367//Human HsLIM15 mRNA for HsLim15, complete cds//0.99:243:60//Hs.37181:D64108

F-NT2RP2003391

F-NT2RP2003393

F-NT2RP2003394//Homo sapiens Ran-GTP binding protein mRNA, partial cds//
0.86:416:57//Hs.4976:AF039023

F-NT2RP2003401

F-NT2RP2003433//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61
ALPHA SUBUNIT [Canis familiaris]//3.7e-33:303:77//Hs.14038:R06800

F-NT2RP2003445//EST//1.7e-06:154:65//Hs.142843:R36893

F-NT2RP2003446//Prostaglandin receptor, ep1 subtype//0.81:273:61//Hs.159
360:L22647

F-NT2RP2003456//EST//0.17:95:65//Hs.147190:AI193320

F-NT2RP2003466//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730)
containing the hFEN1 gene//4.3e-53:339:78//Hs.132874:AC004770

F-NT2RP2003480//Calpain, small polypeptide//1.1e-06:154:66//Hs.74451:X04
106

F-NT2RP2003499//Homo sapiens delta-catenin mRNA, complete cds//3.1e-10:4
81:60//Hs.80220:U96136

F-NT2RP2003506

F-NT2RP2003511//Spectrin, beta, non-erythrocytic 1//0.76:189:62//Hs.1071
64:M96803

F-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds//8.3e-78:403:9
4//Hs.78482:Y16270

F-NT2RP2003517//Platelet-derived growth factor beta polypeptide (simian
sarcoma viral (v-sis) oncogene homolog)//1.3e-24:151:95//Hs.1976:M12783

F-NT2RP2003522//Zinc finger protein 148 (pHZ-52)//1.1e-17:512:60//Hs.112
180:AF039019

F-NT2RP2003533//ESTs//1.8e-76:373:98//Hs.140402:AI138765

F-NT2RP2003543//ESTs//9.3e-65:363:92//Hs.70643:AA030010

F-NT2RP2003559//ESTs//0.00037:93:77//Hs.157564:AI356513

F-NT2RP2003564//Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro)//2.9e-28:664:63//Hs.1042:M62800

F-NT2RP2003567//Homo sapiens mRNA for KIAA0462 protein, partial cds//1.3e-114:541:98//Hs.129937:AB007931

F-NT2RP2003581//EST//1.0:59:76//Hs.158575:A1368947

F-NT2RP2003596//ESTs, Weakly similar to No definition line found [C.elegans]//1.3e-63:224:95//Hs.34627:AA126463

F-NT2RP2003604//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.7e-124:585:98//Hs.58488:U97067

F-NT2RP2003629//ESTs//2.0e-103:535:95//Hs.105633:AA479166

F-NT2RP2003643//Kallmann syndrome 1 sequence//0.85:216:61//Hs.89591:M97252

F-NT2RP2003668//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//9.4e-47:371:80//Hs.125231:AF068006

F-NT2RP2003687//EST//2.9e-14:134:80//Hs.132635:A1032875

F-NT2RP2003691//ESTs//8.2e-47:296:83//Hs.138852:AA284247

F-NT2RP2003702//DNA POLYMERASE EPSILON, CATALYTIC SUBUNIT A//0.85:190:61//Hs.18366:L09561

F-NT2RP2003704//ESTs, Weakly similar to putative p150 [H.sapiens]//5.1e-44:269:91//Hs.139757:N95271

F-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds//8.3e-110:518:98//Hs.78494:AB011097

F-NT2RP2003713

F-NT2RP2003714//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds//2.7e-56:252:83//Hs.86371:AF054180

F-NT2RP2003727//EST//0.52:277:59//Hs.69507:AA111879

F-NT2RP2003737//Human E2 ubiquitin conjugating enzyme Ubch5C (UBCH5C) mRNA, complete cds//4.0e-55:584:71//Hs.118797:U39318

F-NT2RP2003751

F-NT2RP2003760

F-NT2RP2003764

F-NT2RP2003769

F-NT2RP2003770//RETINOBLASTOMA BINDING PROTEIN 3//0.58:247:59//Hs.96055:
U47677

F-NT2RP2003777

F-NT2RP2003781//ESTs, Weakly similar to C47D12.3 [C.elegans]//3.7e-63:35
6:92//Hs.16131:AA568689

F-NT2RP2003793//ESTs//4.8e-68:392:92//Hs.93949:AA782955

F-NT2RP2003825//ESTs//7.6e-79:232:98//Hs.14347:AA287742

F-NT2RP2003840//DNAJ PROTEIN HOMOLOG HSJ1//0.95:300:59//Hs.77768:X63368

F-NT2RP2003857//EST//1.0:112:62//Hs.139216:AA244425

F-NT2RP2003859

F-NT2RP2003871//ESTs//2.5e-44:222:99//Hs.146295:AA935780

F-NT2RP2003885

F-NT2RP2003912//ESTs, Weakly similar to G2-SPECIFIC PROTEIN KINASE NIMA
[Emericella nidulans]//2.2e-113:632:92//Hs.50072:AI378221

F-NT2RP2003952//ESTs, Moderately similar to 60S RIBOSOMAL PROTEIN L32 [H
.sapiens]//1.0:146:67//Hs.156920:AA489296

F-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease,
complete cds//6.8e-30:165:96//Hs.35086:AB014458

F-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds//7.
9e-116:610:94//Hs.7302:AB007916

F-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds//3.2
e-161:783:96//Hs.7316:AB018347

F-NT2RP2003984

F-NT2RP2003986//ESTs//1.3e-39:296:83//Hs.152482:AI050036

F-NT2RP2003988//Thiopurine S-methyltransferase//7.1e-44:532:70//Hs.51124
:AF019369

F-NT2RP2004013//ESTs, Highly similar to TRANSCRIPTION FACTOR BTF3 [Homo sapiens] //7.0e-104:556:93//Hs.111081:AI380378

F-NT2RP2004014

F-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127//6.0e-11:120:80//Hs.10116:AC004780

F-NT2RP2004042

F-NT2RP2004066//Homo sapiens zinc finger protein (ZnF20) mRNA, complete cds//0.80:292:61//Hs.1147:AF011573

F-NT2RP2004081//ESTs//5.7e-87:427:96//Hs.102296:AI217942

F-NT2RP2004098//Homo sapiens leucine-rich repeat protein SHOC-2 (SHOC-2) mRNA, complete cds//0.15:199:60//Hs.104315:AF054828

F-NT2RP2004124//Homo sapiens mRNA for ephrin-A2//0.98:233:59//Hs.158306:AJ007292

F-NT2RP2004142

F-NT2RP2004152//ESTs//5.7e-35:187:96//Hs.98977:AA625872

F-NT2RP2004165//Homo sapiens serine kinase SRPK2 mRNA, complete cds//0.69:176:63//Hs.78353:U88666

F-NT2RP2004170//ESTs//3.9e-05:380:61//Hs.143748:AI419966

F-NT2RP2004172//ESTs//5.8e-18:104:99//Hs.157031:AI343501

F-NT2RP2004187//ESTs, Moderately similar to zinc finger protein [H.sapiens] //1.7e-16:276:67//Hs.36779:AA626790

F-NT2RP2004194//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//1.0:124:69//Hs.155302:U57317

F-NT2RP2004196

F-NT2RP2004207//ESTs//3.8e-11:92:88//Hs.22678:AA604756

F-NT2RP2004226//ESTs, Weakly similar to teg292 protein [M.musculus] //1.8e-80:386:98//Hs.68791:AA527270

F-NT2RP2004232//Protein kinase C, mu//3.9e-36:448:67//Hs.2891:X75756

F-NT2RP2004239//ESTs//0.12:196:61//Hs.127209:AA976680

F-NT2RP2004240//EST//1.0:134:63//Hs.104466:AA282536
 F-NT2RP2004242//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.27:313:59//Hs.129725:AF047487
 F-NT2RP2004245//ESTs, Weakly similar to No definition line found [C.elegans] //8.2e-51:474:74//Hs.108990:N25951
 F-NT2RP2004270//MUELLERIAN INHIBITING FACTOR PRECURSOR//1.6e-06:490:60//Hs.112432:AC005263
 F-NT2RP2004300//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 3//0.35:157:67//Hs.37121:Z37544
 F-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds//1.5e-151:735:97//Hs.61152:AF000416
 F-NT2RP2004321//ESTs//2.6e-64:385:88//Hs.133128:W27735
 F-NT2RP2004339//ESTs//3.3e-46:338:83//Hs.145091:AA814510
 F-NT2RP2004347//ESTs//1.0:184:61//Hs.134469:AA731632
 F-NT2RP2004364//ESTs//2.9e-70:366:95//Hs.14928:AA256202
 F-NT2RP2004365
 F-NT2RP2004366//Homo sapiens mRNA for DFFRY protein, abundant transcript //0.60:295:57//Hs.39163:AF000986
 F-NT2RP2004373
 F-NT2RP2004389//ESTs, Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III [Caenorhabditis elegans] //3.3e-97:477:98//Hs.30490:AA146916
 F-NT2RP2004392//ESTs//2.6e-61:305:98//Hs.43100:AA186588
 F-NT2RP2004396//Homo sapiens BAC clone RG135C18 from 7q21//1.4e-174:875:95//Hs.152759:AC005164
 F-NT2RP2004399//ESTs, Weakly similar to K01H12.1 [C.elegans] //1.2e-92:519:91//Hs.13275:AI341468
 F-NT2RP2004400//EST//0.018:150:65//Hs.158739:AI375367
 F-NT2RP2004412

F-NT2RP2004425//EST//0.049:145:64//Hs.160759:R36944
 F-NT2RP2004463//ESTs//1.5e-40:207:98//Hs.98057:C15687
 F-NT2RP2004476//Homo sapiens TWIK-related acid-sensitive K⁺ channel (TAS
 K) mRNA, complete cds//0.45:208:61//Hs.24040:AF006823
 F-NT2RP2004490
 F-NT2RP2004512//ESTs//0.0012:330:61//Hs.70258:AI091203
 F-NT2RP2004523//Human high-affinity copper uptake protein (hCTR1) mRNA,
 complete cds//1.3e-29:270:79//Hs.73614:U83460
 F-NT2RP2004538//Homo sapiens mRNA for KIAA0591 protein, partial cds//4.6
 e-139:687:96//Hs.129908:AB011163
 F-NT2RP2004551//ESTs//0.0075:285:62//Hs.149442:AI346891
 F-NT2RP2004568//Homo sapiens antigen NY-CO-16 mRNA, complete cds//8.8e-0
 6:291:61//Hs.132206:AF039694
 F-NT2RP2004580//Small inducible cytokine A5 (RANTES)//1.2e-45:334:82//Hs
 .155464:AF088219
 F-NT2RP2004587//Homo sapiens mRNA for KIAA0766 protein, complete cds//0.
 98:136:64//Hs.28020:AB018309
 F-NT2RP2004594//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//1.
 0:104:68//Hs.125729:N99898
 F-NT2RP2004600//Homo sapiens mRNA for Hrs, complete cds//0.20:260:60//Hs
 .24756:U43895
 F-NT2RP2004602//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
 RY !!!! [H.sapiens]//3.0e-59:273:93//Hs.12845:N28835
 F-NT2RP2004614//EST//0.99:103:68//Hs.148738:AI224908
 F-NT2RP2004655//Homo sapiens mRNA for leucine rich protein//8.4e-104:496
 :98//Hs.5198:AJ006291
 F-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds//5.2
 e-155:728:98//Hs.29956:AB007929
 F-NT2RP2004675//EST//0.65:151:62//Hs.130504:AI003839

F-NT2RP2004681

F-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds//4.1e-61:327:94//Hs.154919:AB014525

F-NT2RP2004709//ESTs//2.2e-05:98:77//Hs.161898:AA286942

F-NT2RP2004710//ESTs//0.0035:76:82//Hs.108470:R93780

F-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds//2.1e-118:582:96//Hs.4236:AB007947

F-NT2RP2004743//EST//0.11:170:64//Hs.112670:AA609242

F-NT2RP2004767//EST//1.5e-09:303:65//Hs.148374:AA948183

F-NT2RP2004768//ESTs, Highly similar to SERINE/THREONINE-PROTEIN KINASE PAK [Rattus norvegicus]//3.7e-110:548:96//Hs.85768:W16504

F-NT2RP2004775//Homo sapiens transcriptional regulatory protein p54 mRNA, complete cds//0.025:547:57//Hs.107474:AF045451

F-NT2RP2004791//Human endosome-associated protein (EEA1) mRNA, complete cds//0.99:121:64//Hs.2864:L40157

F-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//4.9e-118:594:95//Hs.40820:AF058953

F-NT2RP2004802//ESTs//5.6e-16:116:91//Hs.153841:N36043

F-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds//6.8e-103:495:97//Hs.67052:AF054179

F-NT2RP2004841//Human transposon-like element mRNA//3.0e-70:519:83//Hs.84775:M23161

F-NT2RP2004861//ESTs//6.7e-89:427:98//Hs.132980:A1290258

F-NT2RP2004897//ESTs//6.4e-81:431:94//Hs.130961:N79111

F-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds//6.5e-84:418:95//Hs.25619:AB007144

F-NT2RP2004936

F-NT2RP2004959

F-NT2RP2004961//Human mRNA for KIAA0065 gene, partial cds//7.2e-26:456:6

6//Hs.70617:D31763

F-NT2RP2004962//EST//2.8e-15:242:69//Hs.146794:AI149478

F-NT2RP2004967//ESTs//0.0022:218:63//Hs.131987:AI239735

F-NT2RP2004978//Homo sapiens mRNA for KIAA0458 protein, complete cds//1.0:218:61//Hs.7414:AB007927

F-NT2RP2004982//Human kinesin-like spindle protein HKSP (HKSP) mRNA, complete cds//0.13:260:60//Hs.41723:U37426

F-NT2RP2004985//Human mRNA for KIAA0144 gene, complete cds//4.8e-22:431:65//Hs.8127:D63478

F-NT2RP2004999

F-NT2RP2005000//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//0.99:269:58//Hs.124161:AF065164

F-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds//1.9e-160:782:97//Hs.155972:AB014515

F-NT2RP2005003//H. sapiens Staf50 mRNA//9.9e-44:430:75//Hs.68054:X82200

F-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, complete cds//4.5e-100:501:96//Hs.31575:AF100141

F-NT2RP2005018//Arachidonate 5-lipoxygenase//1.0:232:58//Hs.89499:J03600

F-NT2RP2005020//ESTs//1.2e-06:61:100//Hs.106160:AA527433

F-NT2RP2005022//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.095:271:60//Hs.139745:U39067

F-NT2RP2005031//Homo sapiens mRNA for SCP-1, complete cds//0.99:338:61//Hs.112743:D67035

F-NT2RP2005037//Homo sapiens mRNA for repressor protein, partial cds//0.098:217:60//Hs.58167:D30612

F-NT2RP2005038//Homo sapiens protease-activated receptor 4 mRNA, complete cds//0.22:498:59//Hs.137574:AF055917

F-NT2RP2005108//ESTs//0.74:145:63//Hs.116557:AA657838

F-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds//6.4

e-105:495:98//Hs.22616:AB014564
 F-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//9.2e-29:157:98//Hs.100555:X98743
 F-NT2RP2005139//ESTs//2.6e-91:479:95//Hs.125037:W42803
 F-NT2RP2005140//ESTs//0.81:308:59//Hs.27308:AA534947
 F-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds//8.3e-91:447:96//Hs.132226:AF045583
 F-NT2RP2005147
 F-NT2RP2005159//ESTs//1.5e-44:242:94//Hs.109819:AI357582
 F-NT2RP2005162//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.97:80:73//Hs.107747:AI357868
 F-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein//4.4e-127:633:96//Hs.155218:AJ007509
 F-NT2RP2005204//H.sapiens 5T4 gene for 5T4 Oncofetal antigen//0.0034:187:66//Hs.82128:AJ012159
 F-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//1.3e-66:340:95//Hs.8173:AC005189
 F-NT2RP2005239//EST//1.3e-05:215:66//Hs.129528:AA994783
 F-NT2RP2005254//H.sapiens mRNA for PHAPI2b protein//1.0:101:71//Hs.84264:U70439
 F-NT2RP2005270//Homo sapiens creatine transporter mRNA, complete cds//0.56:114:68//Hs.154503:U36341
 F-NT2RP2005276//Homo sapiens acyl-CoA synthetase 4 (ACS4) mRNA, complete cds//1.2e-40:594:65//Hs.81452:AF030555
 F-NT2RP2005287//ESTs//8.2e-07:175:70//Hs.117134:AI383932
 F-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.3e-123:604:96//Hs.27007:AF060219
 F-NT2RP2005289//Homo sapiens mRNA for XPR2 protein//1.3e-141:670:98//Hs.44766:AJ007590

F-NT2RP2005293//EST//1.9e-50:254:98//Hs.162017:AA505833

F-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds//3.6e-97:483:96//Hs.115763:AB014576

F-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds//2.6e-23:166:90//Hs.1569:U11701

F-NT2RP2005336//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds//0.016:353:62//Hs.113265:AF032387

F-NT2RP2005344//Homo sapiens mRNA for KIAA0566 protein, partial cds//2.8e-30:456:66//Hs.44697:AB011138

F-NT2RP2005354//ESTs//0.71:192:60//Hs.39063:AA708958

F-NT2RP2005358//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//1.4e-100:489:96//Hs.107254:AC005943

F-NT2RP2005360//ESTs//8.2e-35:190:95//Hs.163038:AA700122

F-NT2RP2005393//Homo sapiens CTG26 alternate open reading frame mRNA, complete cds//0.87:244:59//Hs.113252:U80761

F-NT2RP2005407

F-NT2RP2005436//Homo sapiens mRNA for KIAA0561 protein, partial cds//0.28:338:57//Hs.6189:AB011133

F-NT2RP2005441//ESTs//3.3e-45:238:96//Hs.5209:AA780068

F-NT2RP2005453//ESTs//2.1e-20:115:99//Hs.133087:AI091164

F-NT2RP2005457//ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B [Bos taurus]//8.5e-48:295:90//Hs.75017:AA166853

F-NT2RP2005464//ESTs//2.0e-99:495:96//Hs.3530:AA808243

F-NT2RP2005465//V-crk avian sarcoma virus CT10 oncogene homolog//0.032:176:64//Hs.16:D10656

F-NT2RP2005472//ESTs//1.4e-34:180:98//Hs.158892:AI378412

F-NT2RP2005476//Homo sapiens mRNA for KIAA0772 protein, complete cds//9.9e-48:432:77//Hs.15519:AB018315

F-NT2RP2005490//ESTs//4.5e-19:165:84//Hs.134382:AA083573

F-NT2RP2005491

F-NT2RP2005495//ESTs//5.6e-96:452:99//Hs.145417:AI084164

F-NT2RP2005496//Human mRNA for KIAA0326 gene, partial cds//4.4e-48:621:68//Hs.6833:AB002324

F-NT2RP2005498//Human protein phosphatase 2A beta subunit mRNA, complete cds//1.6e-63:503:78//Hs.7688:M64930

F-NT2RP2005501//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.56:139:66//Hs.8546:U97669

F-NT2RP2005509//Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD)//1.0:291:59//Hs.89709:L35546

F-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//1.2e-82:444:92//Hs.119023:AF092563

F-NT2RP2005525//Homo sapiens mRNA for KIAA0764 protein, complete cds//2.2e-19:112:99//Hs.6232:AB018307

F-NT2RP2005531//ESTs, Weakly similar to erythrocyte membrane protein 4.1 [H.sapiens] //3.5e-50:366:83//Hs.61833:AA036735

F-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//9.4e-155:747:97//Hs.159597:AJ012449

F-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds//1.9e-131:618:98//Hs.62515:AB007963

F-NT2RP2005549//ESTs, Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN C16 C10.10 IN CHROMOSOME III [C.elegans] //2.5e-51:292:93//Hs.105684:H24407

F-NT2RP2005555//EST//0.046:308:57//Hs.145962:AI276822

F-NT2RP2005557//ESTs//4.6e-48:382:79//Hs.125014:AI422839

F-NT2RP2005581//ESTs//6.3e-28:166:93//Hs.87803:AA034436

F-NT2RP2005600//ESTs//1.6e-40:228:93//Hs.160085:AI218627

F-NT2RP2005605//ESTs//5.7e-13:115:86//Hs.37718:H60071

F-NT2RP2005620//Homo sapiens epsin 2b mRNA, complete cds//3.1e-92:447:97//Hs.22396:AF062085

F-NT2RP2005622//ESTs//0.16:242:63//Hs.136395:AA523702
 F-NT2RP2005635
 F-NT2RP2005637//ESTs//0.055:96:69//Hs.105998:R90905
 F-NT2RP2005640//ESTs//4.5e-16:107:92//Hs.150823:AI292145
 F-NT2RP2005645//ESTs//2.7e-29:181:90//Hs.121653:AI375440
 F-NT2RP2005651//Oxysterol binding protein//0.00011:122:69//Hs.143065:M86
 917
 F-NT2RP2005654//Homo sapiens mRNA for KIAA0288 gene, complete cds//1.5e-
 08:351:62//Hs.91400:AB006626
 F-NT2RP2005669//ESTs//0.016:185:64//Hs.97713:AA442239
 F-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, co-
 mplete cds//7.7e-96:462:98//Hs.25664:AF089814
 F-NT2RP2005683//ESTs//0.83:242:62//Hs.136395:AA523702
 F-NT2RP2005690//PYRROLINE-5-CARBOXYLATE REDUCTASE//2.5e-11:328:61//Hs.79
 217:M77836
 F-NT2RP2005694
 F-NT2RP2005701//Homo sapiens protein phosphatase 2A B56-epsilon (PP2A) m
 RNA, complete cds//0.15:496:55//Hs.79326:L76703
 F-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds//5.1
 e-126:599:97//Hs.61638:AB018342
 F-NT2RP2005719//ESTs//0.58:326:60//Hs.157209:N57527
 F-NT2RP2005722//Zinc finger protein 136 (clone pHZ-20)//8.2e-46:415:77//
 Hs.69740:U09367
 F-NT2RP2005723//ESTs//1.0e-15:141:81//Hs.163747:AA174017
 F-NT2RP2005726//EST//3.4e-15:96:95//Hs.156170:AI334191
 F-NT2RP2005732//ESTs//0.99:162:62//Hs.154914:AA721086
 F-NT2RP2005741//Homo sapiens chondroadherin gene, 5' flanking region and/
 /0.80:362:58//Hs.97220:U96769
 F-NT2RP2005748//H.sapiens ZNF33B gene//0.47:99:65//Hs.72991:X68688

F-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds//2.5e-23:134:96//Hs.159651:AF068868

F-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//4.0e-102:486:98//Hs.26285:AF082516

F-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A-LIKE NUK-34//2.3e-05:425:56//Hs.79768:D21853

F-NT2RP2005767//Homolog 2 of Drosophila large discs//0.085:262:61//Hs.23205:X82895

F-NT2RP2005773//PYRROLINE-5-CARBOXYLATE REDUCTASE//2.0e-16:153:82//Hs.79217:M77836

F-NT2RP2005775//Human thimet oligopeptidase (THOP1) mRNA, complete cds//1.7e-42:645:64//Hs.78769:Z50115

F-NT2RP2005781//ESTs//1.1e-19:132:90//Hs.13550:AI378556

F-NT2RP2005784//Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein//2.9e-06:201:67//Hs.34853:U28368

F-NT2RP2005804//ESTs//1.2e-07:62:93//Hs.125509:AA883820

F-NT2RP2005812

F-NT2RP2005815//ESTs//1.9e-32:173:97//Hs.144587:AI193595

F-NT2RP2005835

F-NT2RP2005841//Homo sapiens retinal rod Na-Ca+K exchanger (NCKX1) mRNA, complete cds//0.94:148:65//Hs.59829:AB014602

F-NT2RP2005853

F-NT2RP2005857//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//5.4e-176:829:98//Hs.50758:AF092564

F-NT2RP2005859//ESTs//2.1e-97:537:92//Hs.131915:W22567

F-NT2RP2005868

F-NT2RP2005886//Human putative M phase phosphoprotein 1 (MPP1) mRNA, partial cds//0.26:728:57//Hs.240:L16782

F-NT2RP2005890//ESTs//2.0e-97:453:100//Hs.88671:AA279943

F-NT2RP2005901//ESTs//0.99:188:64//Hs.28639:R78360
 F-NT2RP2005908//ESTs//2.5e-43:325:82//Hs.152340:AA521399
 F-NT2RP2005933//ESTs, Highly similar to nucleoporin p54 [R.norvegicus]//
 7.9e-90:326:98//Hs.156882:AA292186
 F-NT2RP2005942//H.sapiens PAP mRNA//5.1e-48:618:67//Hs.49007:X76770
 F-NT2RP2005980//ESTs//2.8e-22:358:68//Hs.125446:AA883339
 F-NT2RP2006023
 F-NT2RP2006038//ESTs//8.0e-37:351:74//Hs.128787:AA418382
 F-NT2RP2006043//Human novel homeobox mRNA for a DNA binding protein//0.5
 1:271:59//Hs.37035:U07664
 F-NT2RP2006052//ESTs//4.0e-05:233:63//Hs.124864:AA663093
 F-NT2RP2006069//Human mRNA for KIAA0279 gene, partial cds//0.0082:770:58
 //Hs.57652:D87469
 F-NT2RP2006071//ESTs//2.1e-24:396:65//Hs.104404:AI337416
 F-NT2RP2006098//ESTs//0.97:125:67//Hs.97996:AA405970
 F-NT2RP2006100
 F-NT2RP2006103//ESTs//5.2e-11:102:83//Hs.125656:AA883135
 F-NT2RP2006106//ESTs//1.6e-78:456:90//Hs.133496:AA315349
 F-NT2RP2006141//ESTs//1.7e-20:262:72//Hs.128677:AA649240
 F-NT2RP2006166
 F-NT2RP2006184//H.sapiens p63 mRNA for transmembrane protein//1.0:94:73/
 /Hs.74368:X69910
 F-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds//2.5
 e-114:567:96//Hs.109299:AB014554
 F-NT2RP2006196//Homo sapiens mRNA for KIAA0772 protein, complete cds//2.
 0e-23:187:85//Hs.15519:AB018315
 F-NT2RP2006200//ESTs//1.0:224:62//Hs.144100:AI205503
 F-NT2RP2006219//H.sapiens mRNA for DGCR6 protein//4.4e-118:618:93//Hs.15
 3910:X96484

F-NT2RP2006237
 F-NT2RP2006238
 F-NT2RP2006258//ESTs//0.0034:143:69//Hs.145798:AI269970
 F-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK//
 0.019:111:71//Hs.157199:X97630
 F-NT2RP2006275//Homo sapiens mRNA for serin protease with IGF-binding mo
 tif, complete cds//2.4e-05:388:60//Hs.75111:D87258
 F-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//2.1e-121:
 598:97//Hs.3404:AF035262
 F-NT2RP2006320//ESTs, Moderately similar to maternal transcript Maid [M.
 musculus] //1.9e-29:151:100//Hs.36794:AI038407
 F-NT2RP2006321//ESTs//7.0e-15:141:82//Hs.71241:H09371
 F-NT2RP2006323//Homo sapiens mRNA for NBPhox, complete cds//4.7e-06:170:
 70//Hs.87202:D82344
 F-NT2RP2006333//Homo sapiens TRRAP protein (TRRAP) mRNA, complete cds//0
 .11:43:100//Hs.6892:AF076974
 F-NT2RP2006334//Homo sapiens mRNA for KIAA0602 protein, partial cds//3.1
 e-05:233:65//Hs.37656:AB011174
 F-NT2RP2006365//ESTs//8.9e-46:268:93//Hs.58403:AA058501
 F-NT2RP2006393//ESTs//1.2e-20:159:86//Hs.146018:AA280341
 F-NT2RP2006436//Human homeodomain-containing protein (HANF) mRNA, comple
 te cds//0.59:133:64//Hs.95838:AF059734
 F-NT2RP2006441//ESTs//1.6e-82:400:98//Hs.143514:AI221934
 F-NT2RP2006454//EST//5.2e-07:172:68//Hs.157742:AI360509
 F-NT2RP2006456
 F-NT2RP2006464//Homo sapiens mRNA for AND-1 protein//1.1e-149:545:98//Hs
 .72160:AJ006266
 F-NT2RP2006467
 F-NT2RP2006472

F-NT2RP2006534//ESTs//5.6e-05:192:66//Hs.135750:AA160048
 F-NT2RP2006554//EST//0.60:116:65//Hs.160110:AA922134
 F-NT2RP2006565//Homo sapiens secretory carrier-associated membrane prote
 in (SCAMP) mRNA, complete cds//2.1e-115:669:90//Hs.31218:AF038966
 F-NT2RP2006571//Cytochrome P450, subfamily IIA (phenobarbital-inducible)
 , polypeptide 6//2.1e-24:476:64//Hs.73864:U22029
 F-NT2RP2006573
 F-NT2RP2006598//ESTs//1.3e-16:137:85//Hs.131350:AA805223
 F-NT2RP3000002//ESTs//3.6e-32:215:86//Hs.155446:AA188180
 F-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (J
 M21)//1.9e-137:637:98//Hs.6764:AJ011972
 F-NT2RP3000046//Homo sapiens TTF-I interacting peptide 20 mRNA, partial
 cds//9.1e-07:568:61//Hs.79531:AF000560
 F-NT2RP3000047
 F-NT2RP3000050//Human repressor transcriptional factor (ZNF85) mRNA, com
 plete cds//1.2e-58:633:69//Hs.37138:U35376
 F-NT2RP3000055//ESTs//1.2e-07:200:66//Hs.127362:AA954961
 F-NT2RP3000068
 F-NT2RP3000072//EST//0.99:199:63//Hs.8469:T40769
 F-NT2RP3000080//Landsteiner-Wiener blood group glycoprotein//4.8e-41:353
 :78//Hs.108287:L27670
 F-NT2RP3000085//Propionyl-coA carboxylase alpha chain//7.9e-30:665:60//H
 s.80741:X14608
 F-NT2RP3000092//EST//2.0e-15:94:97//Hs.145389:AI253140
 F-NT2RP3000109//ESTs//6.8e-11:77:96//Hs.153931:AI243595
 F-NT2RP3000134//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//5.0e-94:
 438:100//Hs.8173:AC005189
 F-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds//2.9
 e-182:849:98//Hs.13273:AB011164

F-NT2RP3000149//Human Line-1 repeat mRNA with 2 open reading frames//4.1
e-20:133:94//Hs.23094:M19503

F-NT2RP3000186//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0492//6.6e-08:152:71//Hs.127338:AB007961

F-NT2RP3000197//ESTs//1.1e-58:301:96//Hs.87461:AA292779

F-NT2RP3000207

F-NT2RP3000220

F-NT2RP3000233//Homo sapiens actin binding protein MAYVEN mRNA, complete
cds//6.6e-20:509:58//Hs.122967:AF059569

F-NT2RP3000235//ESTs//1.7e-06:220:62//Hs.42771:N26740

F-NT2RP3000247//Human mRNA for KIAA0218 gene, complete cds//6.7e-111:691
:86//Hs.75863:D86972

F-NT2RP3000251//ESTs//6.7e-48:245:97//Hs.28249:AA203733

F-NT2RP3000252

F-NT2RP3000255

F-NT2RP3000267//ESTs//0.14:53:92//Hs.151586:W45568

F-NT2RP3000299//Homo sapiens enhancer of filamentation (HEF1) mRNA, comp
lete cds//1.7e-13:214:67//Hs.80261:L43821

F-NT2RP3000312//ESTs//2.6e-50:255:97//Hs.146263:AA255863

F-NT2RP3000320//Homo sapiens proline and glutamic acid rich nuclear prot
ein isoform mRNA, partial cds//0.0088:236:63//Hs.102732:U88153

F-NT2RP3000324//ESTs//3.8e-10:102:83//Hs.55495:AI091242

F-NT2RP3000333//ESTs, Weakly similar to mitogen-activated kinase kinase
kinase 5 [H.sapiens]//0.57:189:65//Hs.46146:AA418097

F-NT2RP3000341//Human mRNA for KIAA0392 gene, partial cds//1.1e-49:442:7
8//Hs.40100:AB002390

F-NT2RP3000348

F-NT2RP3000350//H.sapiens mRNA for GTP-binding protein//0.93:164:59//Hs.
78582:X80754

F-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//1.8e-43:649:66
 //Hs.101642:X60673
 F-NT2RP3000361//ESTs//2.6e-112:531:98//Hs.17672:AA305921
 F-NT2RP3000366//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-18A [Ly
 mnaea stagnalis]//4.0e-116:596:95//Hs.21094:AI337016
 F-NT2RP3000393//ESTs//2.6e-18:137:89//Hs.115600:AA351639
 F-NT2RP3000397//ESTs//8.7e-44:355:73//Hs.121961:AA777873
 F-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cd
 s//1.6e-175:841:97//Hs.28307:AF071185
 F-NT2RP3000418//Human Line-1 repeat mRNA with 2 open reading frames//2.7
 e-33:610:65//Hs.23094:M19503
 F-NT2RP3000433//ESTs//1.5e-32:246:69//Hs.120892:AA724948
 F-NT2RP3000439//Adenosine A2b receptor//0.44:210:62//Hs.45743:X68487
 F-NT2RP3000441
 F-NT2RP3000449//ESTs//0.60:177:64//Hs.132605:AI051562
 F-NT2RP3000451//Receptor protein-tyrosine kinase EDDR1//0.95:315:58//Hs.
 75562:U48705
 F-NT2RP3000456//ESTs//7.5e-23:140:92//Hs.5209:AA780068
 F-NT2RP3000484//EST//2.5e-06:166:67//Hs.149950:AI289822
 F-NT2RP3000487//ESTs//1.2e-63:311:98//Hs.143304:AI084058
 F-NT2RP3000512//Homeo box B3//3.1e-18:109:97//Hs.49931:X16667
 F-NT2RP3000526//ESTs//3.7e-74:424:93//Hs.42991:N21379
 F-NT2RP3000527//Human mRNA for KIAA0211 gene, complete cds//8.0e-36:706:
 63//Hs.79347:D86966
 F-NT2RP3000531//ESTs//9.6e-75:392:95//Hs.144148:H08308
 F-NT2RP3000542//ESTs//3.2e-88:448:96//Hs.30622:AA486412
 F-NT2RP3000561//EST//0.88:92:64//Hs.148290:AA908404
 F-NT2RP3000562//ESTs//1.1e-112:522:99//Hs.125153:AA453723
 F-NT2RP3000578

F-NT2RP3000582//ESTs//2.1e-82:413:97//Hs.118544:R17277
 F-NT2RP3000584
 F-NT2RP3000590//ESTs//1.0:134:64//Hs.12969:N56904
 F-NT2RP3000592//Paired basic amino acid cleaving system 4//3.4e-05:502:5
 7//Hs.77234:AB001914
 F-NT2RP3000596//ESTs//6.8e-71:361:95//Hs.118741:AA179811
 F-NT2RP3000599//ESTs, Weakly similar to T19B10.6 [C.elegans]//9.3e-61:35
 5:92//Hs.114622:AA693492
 F-NT2RP3000603//Human mRNA for KIAA0227 gene, partial cds//6.3e-10:553:5
 9//Hs.79170:D86980
 F-NT2RP3000605//ESTs//5.8e-51:283:94//Hs.127152:A1421203
 F-NT2RP3000622//ESTs//1.7e-10:72:98//Hs.155360:AA984683
 F-NT2RP3000624//64 KD AUTOANTIGEN D1//0.99:194:61//Hs.79386:X54162
 F-NT2RP3000628//ESTs//0.96:221:61//Hs.131161:A1017333
 F-NT2RP3000632//ESTs//4.4e-53:244:77//Hs.143010:AA767904
 F-NT2RP3000644//Small inducible cytokine A5 (RANTES)//3.0e-49:343:84//Hs.
 .155464:AF088219
 F-NT2RP3000661
 F-NT2RP3000665//Homo sapiens putative transcription factor CA150 mRNA, c
 omplete cds//0.62:305:59//Hs.13063:AF017789
 F-NT2RP3000685
 F-NT2RP3000690//EST//1.0:149:64//Hs.140263:AA709001
 F-NT2RP3000736//ESTs//5.3e-26:146:97//Hs.98613:D83884
 F-NT2RP3000739//ESTs//0.0046:66:87//Hs.6880:W26854
 F-NT2RP3000742//ESTs//5.5e-08:311:61//Hs.152224:A1369426
 F-NT2RP3000753//ESTs//2.6e-63:318:97//Hs.153000:AA777765
 F-NT2RP3000759//Homo sapiens mRNA for follistatin-related protein (FRP),
 complete cds//1.6e-38:245:91//Hs.2427:D89937
 F-NT2RP3000815

F-NT2RP3000825//EST//1.0:220:61//Hs.135944:N45132
 F-NT2RP3000826//Homo sapiens deltex (Dx) mRNA, complete cds//0.00040:263
 :65//Hs.124024:AF053700
 F-NT2RP3000836//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN A
 P47 HOMOLOG 2 [H.sapiens]//1.1e-71:363:96//Hs.23803:AA126476
 F-NT2RP3000841//EST//0.36:224:60//Hs.162094:AA524012
 F-NT2RP3000845//H.sapiens mRNA for serine/threonine protein kinase EMK//
 6.5e-48:593:68//Hs.157199:X97630
 F-NT2RP3000847//ESTs//0.0028:56:92//Hs.116406:AA209520
 F-NT2RP3000850//Small inducible cytokine A5 (RANTES)//2.0e-49:323:86//Hs
 .155464:AF088219
 F-NT2RP3000852
 F-NT2RP3000859//ESTs//0.39:169:62//Hs.148948:AA699918
 F-NT2RP3000865//EST//0.15:236:62//Hs.123366:AA811476
 F-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain ho
 molog (Doc1) mRNA, complete cds//6.4e-31:766:60//Hs.15432:U53445
 F-NT2RP3000869//Human plectin (PLEC1) mRNA, complete cds//1.1e-13:701:60
 //Hs.79706:U53204
 F-NT2RP3000875
 F-NT2RP3000901//ESTs//8.2e-26:191:87//Hs.18793:R99101
 F-NT2RP3000904//EST//2.4e-49:240:100//Hs.160842:AI348374
 F-NT2RP3000917
 F-NT2RP3000919//MAP KINASE PHOSPHATASE-1//0.19:340:60//Hs.109895:X68277
 F-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A//7.7e-44:351:83//Hs.2953:X844
 07
 F-NT2RP3000980//ESTs//6.5e-10:102:81//Hs.86950:AI204212
 F-NT2RP3000994//ESTs//4.1e-120:571:98//Hs.127295:AA918411
 F-NT2RP3001004//ESTs//1.1e-76:438:88//Hs.144554:N92198
 F-NT2RP3001007

F-NT2RP3001055//ESTs, Weakly similar to weak similarity to procollagen α 1(V) chain [C.elegans]//2.9e-121:588:98//Hs.128781:AA160707

F-NT2RP3001057//ESTs, Highly similar to ZINC FINGER PROTEIN 45 [Homo sapiens]//9.8e-54:282:97//Hs.30303:AI244662

F-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.7e-51:534:74//Hs.27007:AF060219

F-NT2RP3001084//Homo sapiens mRNA for KIAA0782 protein, partial cds//3.7e-16:474:60//Hs.21264:AB018325

F-NT2RP3001096//Homo sapiens mRNA for cartilage-associated protein (CASP) //4.4e-16:428:60//Hs.155481:AJ006470

F-NT2RP3001107//Human mRNA for KIAA0215 gene, complete cds//2.8e-34:712:64//Hs.82292:D86969

F-NT2RP3001109//ESTs//1.2e-67:323:99//Hs.134734:AI337050

F-NT2RP3001111

F-NT2RP3001113//EST//1.1e-33:173:99//Hs.112640:AA609088

F-NT2RP3001115//EST//1.3e-22:122:100//Hs.162990:AA688023

F-NT2RP3001116//ESTs//1.1e-15:93:98//Hs.58412:W74779

F-NT2RP3001119//Homo sapiens BC-2 protein mRNA, complete cds//0.96:258:61//Hs.12107:AF042384

F-NT2RP3001120//Zinc finger protein 136 (clone pHZ-20)//2.4e-77:687:75//Hs.69740:U09367

F-NT2RP3001126//Homo sapiens mRNA for KIAA0775 protein, complete cds//0.00018:341:60//Hs.94790:AB018318

F-NT2RP3001133//Homeo box A4//0.00011:484:59//Hs.77637:M74297

F-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds//1.1e-180:851:98//Hs.5378:AB018305

F-NT2RP3001147

F-NT2RP3001150//PUTATIVE TACHYKININ RECEPTOR//0.97:257:59//Hs.957:M84605

F-NT2RP3001155//Homo sapiens mRNA for AND-1 protein//1.7e-191:891:98//Hs

.72160:AJ006266
 F-NT2RP3001176
 F-NT2RP3001214//EST//0.88:218:60//Hs.161147:AI417859
 F-NT2RP3001216//ESTs//1.5e-66:340:96//Hs.105994:W19981
 F-NT2RP3001221//ESTs, Weakly similar to M05D6.7 [C.elegans]//1.7e-97:512
 :95//Hs.103816:AA130866
 F-NT2RP3001232//EST//0.0016:116:71//Hs.136498:AA594010
 F-NT2RP3001236//ESTs//3.7e-97:455:99//Hs.157488:AI362756
 F-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B//1.7e-20:501:62//Hs.10
 3042:L06237
 F-NT2RP3001245//ESTs//7.1e-80:434:93//Hs.22587:AA743132
 F-NT2RP3001253//Human prepromultimerin mRNA, complete cds//0.99:293:60//
 Hs.32934:U27109
 F-NT2RP3001260//Homo sapiens mRNA for KIAA0726 protein, complete cds//1.
 2e-48:761:64//Hs.107809:AB018269
 F-NT2RP3001268//Zinc finger protein 45 (a Kruppel-associated box (KRAB)
 domain polypeptide)//1.2e-42:454:72//Hs.41728:L75847
 F-NT2RP3001272//ESTs//5.0e-21:162:87//Hs.69149:AA102566
 F-NT2RP3001274
 F-NT2RP3001281//ESTs//2.1e-39:186:73//Hs.161662:AA836811
 F-NT2RP3001297//Human mRNA for KIAA0281 gene, complete cds//2.4e-48:544:
 69//Hs.31463:D87457
 F-NT2RP3001307//Human homeodomain protein (Prox 1) mRNA, complete cds//0
 .72:151:68//Hs.159437:U44060
 F-NT2RP3001318//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glyco
 gen debranching enzyme, glycogen storage disease type III)//0.012:522:56
 //Hs.904:U84010
 F-NT2RP3001325//ESTs//2.9e-80:396:97//Hs.99838:AA204731
 F-NT2RP3001338//Human mRNA for KIAA0211 gene, complete cds//1.6e-30:345:

73//Hs.79347:D86966
 F-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds//6.
 3e-67:559:80//Hs.18586:AB007920
 F-NT2RP3001340//Homo sapiens hyperpolarization-activated channel 1 (IH1)
 mRNA, partial cds//0.00019:473:61//Hs.124161:AF065164
 F-NT2RP3001355//ESTs, Weakly similar to ADP,ATP CARRIER PROTEIN, LIVER I
 SOFORM T2 [H.sapiens]//1.1e-81:421:96//Hs.32508:H29831
 F-NT2RP3001356//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.15:313:6
 0//Hs.129725:AF047487
 F-NT2RP3001374//ESTs//0.98:269:59//Hs.125303:AA873022
 F-NT2RP3001383//Homo sapiens mRNA for Sck, partial cds//0.73:173:65//Hs.
 30965:AB001451
 F-NT2RP3001384//Homa sapiens mRNA for HRIHFB2018, partial cds//2.1e-158:
 743:98//Hs.146214:AB015332
 F-NT2RP3001392//ESTs//0.013:246:63//Hs.95111:AA514595
 F-NT2RP3001396//ESTs//5.6e-16:141:85//Hs.97664:H10783
 F-NT2RP3001398//Zinc finger protein 45 (a Kruppel-associated box (KRAB)
 domain polypeptide)//1.0e-05:189:66//Hs.41728:L75847
 F-NT2RP3001399//Homo sapiens mitochondrial citrate transport protein (CT
 P) mRNA; 3' end//0.77:132:66//Hs.111024:L77567
 F-NT2RP3001407//EST//0.015:167:65//Hs.42217:H96658
 F-NT2RP3001420//ESTs//1.0:214:60//Hs.91226:AA649047
 F-NT2RP3001426
 F-NT2RP3001427
 F-NT2RP3001428//Neurotrophic tyrosine kinase, receptor, type 1//1.8e-73:
 431:91//Hs.85844:X66397
 F-NT2RP3001432//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNIN
 G ENTRY !!!! [H.sapiens]//6.9e-05:195:65//Hs.115868:AA568393
 F-NT2RP3001447

F-NT2RP3001449//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.00033:187:68//Hs.
89631:U48508

F-NT2RP3001453//ESTs//0.020:260:60//Hs.97882:AA203212

F-NT2RP3001457//ESTs//9.4e-29:165:94//Hs.71749:AA988323

F-NT2RP3001459

F-NT2RP3001472//Homo sapiens Sox-like transcriptional factor mRNA, complete cds//4.2e-10:168:70//Hs.32317:AF072836

F-NT2RP3001490//ESTs//3.1e-35:198:94//Hs.163665:AA250877

F-NT2RP3001495//ESTs//2.5e-47:239:98//Hs.128045:AA970231

F-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds//2.8e-172:804:98//Hs.28285:AF064801

F-NT2RP3001527//Human lymphoid-specific SP100 homolog (LYSP100-B) mRNA, complete cds//9.4e-139:743:91//Hs.85283:U36500

F-NT2RP3001529//ESTs, Moderately similar to topoisomerase I C-terminal fragment [H.sapiens]//0.28:224:65//Hs.105912:AI431328

F-NT2RP3001538//ESTs//4.1e-05:139:71//Hs.148425:AI198074

F-NT2RP3001554//Microtubule-associated protein 1A//9.8e-16:327:64//Hs.147918:U38291

F-NT2RP3001580//Insulin-like growth factor binding protein 2//1.9e-06:426:59//Hs.162:X16302

F-NT2RP3001587//Guanine nucleotide binding protein (G protein), alpha 11 (Gq class)//0.049:185:65//Hs.1686:M69013

F-NT2RP3001589//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//9.6e-51:345:82//Hs.144563:AF057280

F-NT2RP3001607//ESTs//1.3e-07:299:63//Hs.43231:N22688

F-NT2RP3001608//ESTs//5.7e-14:85:98//Hs.161133:AI091349

F-NT2RP3001621//ESTs//1.6e-106:310:96//Hs.128505:AA306435

F-NT2RP3001629

F-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds//1.4e-62:2

76:97//Hs.9899:AF099149

F-NT2RP3001642//ESTs//1.0:148:63//Hs.159495:T70173

F-NT2RP3001646

F-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//1.1e-172:816:98//Hs.159597:AJ012449

F-NT2RP3001672//ESTs//5.0e-16:138:82//Hs.151864:T69027

F-NT2RP3001676//ESTs, Highly similar to GTP-BINDING PROTEIN LEPA [*Pseudomonas fluorescens*]//9.0e-53:375:85//Hs.41127:AA555184

F-NT2RP3001678//Human mRNA for KIAA0233 gene, complete cds//0.21:321:65//Hs.79077:D87071

F-NT2RP3001679//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK 757.1 IN CHROMOSOME III [*Caenorhabditis elegans*]//4.0e-111:518:99//Hs.20364:AI420022

F-NT2RP3001688//Homo sapiens mRNA expressed in thyroid gland//1.0:230:63//Hs.7486:D83198

F-NT2RP3001690//EST//0.15:291:59//Hs.162336:AA564329

F-NT2RP3001698//ESTs//0.24:134:69//Hs.129551:AA885219

F-NT2RP3001708//ESTs, Weakly similar to TWISTED GASTRULATION PROTEIN PRECURSOR [*D.melanogaster*]//1.4e-31:191:94//Hs.131279:AA486291

F-NT2RP3001712//Human SLP-76 associated protein mRNA, complete cds//0.41:259:59//Hs.58435:AF001862

F-NT2RP3001716//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [*Mus musculus*]//7.6e-159:747:98//Hs.6823:W18181

F-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//4.4e-161:565:97//Hs.159273:AF054177

F-NT2RP3001727//ESTs, Highly similar to HYPOTHETICAL 37.7 KD PROTEIN ZK 686.3 IN CHROMOSOME III [*Caenorhabditis elegans*]//3.5e-116:554:98//Hs.144332:AA046836

F-NT2RP3001730//Human mRNA for KIAA0128 gene, partial cds//1.3e-105:811:

78//Hs.90998:D50918

F-NT2RP3001739

F-NT2RP3001752//ELK1, member of ETS oncogene family//7.2e-35:299:80//Hs.

116549:AL009172

F-NT2RP3001753//Human putative cerebral cortex transcriptional regulator

T-Brain-1 (Tbr-1) mRNA, complete cds//0.10:528:56//Hs.22138:U49250

F-NT2RP3001764//Human protein-tyrosine phosphatase mRNA, complete cds//2

.4e-47:725:64//Hs.41688:U27193

F-NT2RP3001777//Human eukaryotic translation initiation factor (eIF3) mR

NA, complete cds//0.42:198:61//Hs.57783:U78525

F-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds//9.1

e-153:710:98//Hs.28169:AB007928

F-NT2RP3001792//Human M4 protein mRNA, complete cds//5.6e-27:358:69//Hs.

79024:L03532

F-NT2RP3001799//ESTs//0.0088:178:64//Hs.134938:AI091361

F-NT2RP3001819//Collagen, type IX, alpha 3//0.026:530:58//Hs.53563:L4116

2

F-NT2RP3001844//Homo sapiens mRNA for hair keratin acidic 3-II//0.90:379

:58//Hs.32950:X82634

F-NT2RP3001854//ESTs//1.5e-100:501:96//Hs.72217:AA166729

F-NT2RP3001855//Human homeobox-containing protein mRNA, complete cds//7.

8e-35:481:67//Hs.158225:U68727

F-NT2RP3001857//ESTs//2.7e-85:414:98//Hs.151001:AA564706

F-NT2RP3001896//ESTs, Weakly similar to F20D12.3 gene product [C.elegans

]//2.9e-94:452:98//Hs.54952:AA872675

F-NT2RP3001898//Homo sapiens mRNA for synaptogyrin 1a//0.65:245:61//Hs.6

139:AL022326

F-NT2RP3001915//ESTs//1.1e-83:397:99//Hs.157125:AA723896

F-NT2RP3001926//EST//0.53:362:57//Hs.127917:AA969185

F-NT2RP3001929//ESTs//7.4e-16:141:82//Hs.138852:AA284247
 F-NT2RP3001931
 F-NT2RP3001938//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//0.0022
 :268:61//Hs.106070:U22398
 F-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds//5.
 8e-167:815:96//Hs.15869:AB014575
 F-NT2RP3001944//ESTs//0.00052:60:91//Hs.131731:AI339335
 F-NT2RP3001969
 F-NT2RP3001989//EST//0.00016:263:63//Hs.144096:AI032180
 F-NT2RP3002002//Small inducible cytokine A5 (RANTES)//4.0e-61:293:83//Hs
 .155464:AF088219
 F-NT2RP3002004//H.sapiens mRNA for FAST kinase//5.2e-28:104:100//Hs.7508
 7:X86779
 F-NT2RP3002007//ESTs//0.025:88:69//Hs.163310:AA856946
 F-NT2RP3002014//ESTs//4.8e-70:291:98//Hs.123693:AA283821
 F-NT2RP3002033//Homo sapiens mRNA for HYA22, complete cds//0.021:175:67/
 /Hs.147189:D88153
 F-NT2RP3002045//ESTs, Highly similar to ALPHA-ADAPTIN [M.musculus]//3.8e
 -48:353:81//Hs.127507:AA993745
 F-NT2RP3002054//ESTs, Weakly similar to KIAA0319 [H.sapiens]//3.0e-25:21
 2:83//Hs.71622:AA195155
 F-NT2RP3002056//ESTs, Highly similar to RETINOBLASTOMA BINDING PROTEIN
 1 [Homo sapiens]//4.2e-82:407:97//Hs.131888:AI091806
 F-NT2RP3002057//Human Line-1 repeat mRNA with 2 open reading frames//3.7
 e-21:168:85//Hs.23094:M19503
 F-NT2RP3002062//EST//0.46:198:62//Hs.157711:AI359710
 F-NT2RP3002063//Membrane metallo-endopeptidase (neutral endopeptidase, e
 nkephalinase, CALLA, CD10)//0.91:194:65//Hs.1298:J03779
 F-NT2RP3002081

F-NT2RP3002097//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.073:297:61//Hs.102732:U88153

F-NT2RP3002102//EST//2.8e-16:237:67//Hs.136255:T70256

F-NT2RP3002108

F-NT2RP3002142//ESTs//4.3e-138:654:98//Hs.5729:AA306018

F-NT2RP3002146//H.sapiens mRNA for RanGTPase activating protein 1//0.27:276:62//Hs.5923:X82260

F-NT2RP3002147//Human DNA sequence from clone 431H6 on chromosome 16. Contains a novel gene with some homology to mouse HN1 (Hematological and Neurological expressed sequence 1) downstream of a putative CpG island. Contains ESTs and GSSs//6.0e-51:204:99//Hs.107256:AL031009

F-NT2RP3002151//G1 to S phase transition 1//2.6e-37:292:81//Hs.2707:X17644

F-NT2RP3002163//Human DNA fragmentation factor-45 mRNA, complete cds//0.46:224:60//Hs.155344:U91985

F-NT2RP3002165//ESTs, Highly similar to TRANSCRIPTIONAL REGULATOR PROTEIN IN HCNGP [Mus musculus]//3.0e-61:340:93//Hs.11379:AA594140

F-NT2RP3002166//EST//0.039:114:69//Hs.140335:AA737046

F-NT2RP3002173//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//4.0e-39:255:72//Hs.141429:AA631915

F-NT2RP3002181//ESTs//3.6e-111:518:99//Hs.128505:AA306435

F-NT2RP3002244//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1)//0.98:242:57//Hs.114001:Z20656

F-NT2RP3002248

F-NT2RP3002255//ESTs//8.4e-19:227:75//Hs.122817:AA772261

F-NT2RP3002273//Homo sapiens homeobox protein A10 (HOXA10) gene, complete cds//0.42:189:62//Hs.110637:AC004080

F-NT2RP3002276//ESTs//8.2e-97:463:98//Hs.45120:AA225139

F-NT2RP3002303//ESTs//7.1e-10:96:87//Hs.135700:AA989386
 F-NT2RP3002304//Protein phosphatase 1, catalytic subunit, beta isoform//
 1.3e-05:496:60//Hs.21537:X80910
 F-NT2RP3002330//ESTs//1.3e-81:482:90//Hs.121460:AA744871
 F-NT2RP3002343//Homo sapiens potassium channel mRNA, complete cds//0.30:
 462:56//Hs.143624:AF033383
 F-NT2RP3002351//NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE//1
 .6e-65:588:75//Hs.154672:X16396
 F-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A)
 gene//4.2e-166:770:98//Hs.6483:Y16355
 F-NT2RP3002377//Homo sapiens mRNA for KIAA0788 protein, partial cds//7.5
 e-161:911:89//Hs.2397:Z70200
 F-NT2RP3002399
 F-NT2RP3002402//ESTs, Weakly similar to F02E9.6 [C.elegans]//4.3e-41:233
 :94//Hs.22880:AA056274
 F-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds//3.9
 e-140:649:99//Hs.12707:AB014578
 F-NT2RP3002484//ESTs//0.95:166:63//Hs.149993:AI291310
 F-NT2RP3002501//ESTs//0.92:43:90//Hs.119314:AA432108
 F-NT2RP3002512//Homo sapiens mRNA for KIAA0466 protein, partial cds//1.0
 :173:61//Hs.81234:AB007935
 F-NT2RP3002529//Human vacuolar protein sorting homolog h-vps45 mRNA, com
 plete cds//4.4e-146:763:93//Hs.57738:U35246
 F-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds//5.9
 e-180:833:98//Hs.19542:AB018272
 F-NT2RP3002549//ESTs, Weakly similar to POLYPOSIS LOCUS PROTEIN 1 [H.sap
 iens]//1.3e-42:510:70//Hs.96759:AA469984
 F-NT2RP3002566//Carnitine acetyltransferase//0.032:226:62//Hs.12068:X787

F-NT2RP3002587//EST//4.8e-31:330:74//Hs.139415:AA426054
 F-NT2RP3002590//EST//1.3e-40:202:100//Hs.144716:AI187919
 F-NT2RP3002602//RYANODINE RECEPTOR, SKELETAL MUSCLE//1.3e-06:280:63//Hs.
 89631:U48508
 F-NT2RP3002603
 F-NT2RP3002628//Homo sapiens mRNA for MSJ-1, complete cds//1.5e-05:264:6
 1//Hs.3845:AB014888
 F-NT2RP3002631//Homo sapiens ADAM 21 mRNA, partial cds//0.97:320:58//Hs.
 121287:AF029900
 F-NT2RP3002650//Homo sapiens mRNA for cartilage-associated protein (CASP
)//2.6e-13:441:63//Hs.155481:AJ006470
 F-NT2RP3002659//Human TAR RNA loop binding protein (TRP-185) mRNA, compl
 ete cds//1.7e-05:615:58//Hs.151518:U38847
 F-NT2RP3002660//ESTs//2.9e-32:164:100//Hs.152982:AA584308
 F-NT2RP3002663//ESTs, Highly similar to OXYSTEROL-BINDING PROTEIN [Homo
 sapiens]//4.1e-38:493:70//Hs.41086:AI337400
 F-NT2RP3002671//ESTs//3.7e-05:288:59//Hs.161359:AI421991
 F-NT2RP3002682//ESTs, Weakly similar to F17C11.8 [C.elegans]//1.6e-61:29
 4:100//Hs.128750:AI367584
 F-NT2RP3002687
 F-NT2RP3002688//EST//1.0:312:58//Hs.156800:AI352200
 F-NT2RP3002701//EST//0.00083:55:87//Hs.159750:AI393657
 F-NT2RP3002713//ESTs//0.93:229:61//Hs.150459:AI279514
 F-NT2RP3002763//ESTs//1.7e-97:419:96//Hs.121593:W86291
 F-NT2RP3002770//Homo sapiens G protein-coupled receptor kinase 6 (GRK6)
 gene, partial cds//0.91:161:62//Hs.129736:AF040753
 F-NT2RP3002785
 F-NT2RP3002799//EST//1.7e-17:199:73//Hs.118694:AA148713
 F-NT2RP3002810//ESTs, Weakly similar to KIAA0062 [H.sapiens]//1.4e-76:42

3:93//Hs.41068:AA844350
 F-NT2RP3002818//Homo sapiens jerky gene product homolog mRNA, complete cds//2.2e-55:615:70//Hs.105940:AF004715
 F-NT2RP3002861//ESTs//1.1e-88:468:94//Hs.159821:AA524070
 F-NT2RP3002869//ESTs//3.4e-23:132:97//Hs.148873:T33582
 F-NT2RP3002876//Homo sapiens mRNA for B120, complete cds//2.7e-90:557:88//Hs.123090:AB001895
 F-NT2RP3002877//ESTs//1.1e-19:160:84//Hs.118273:AA626040
 F-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds//1.8e-181:853:98//Hs.6162:AB018314
 F-NT2RP3002911//ESTs//2.8e-07:160:70//Hs.140402:AI138765
 F-NT2RP3002948//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//1.4e-133:645:97//Hs.3826:U69560
 F-NT2RP3002953//Homo sapiens mRNA for KIAA0588 protein, complete cds//5.2e-13:594:57//Hs.74599:AB011160
 F-NT2RP3002955//Homo sapiens mRNA for KIAA0719 protein, complete cds//0.76:412:57//Hs.21198:AB018262
 F-NT2RP3002969//EST//3.7e-50:272:94//Hs.162331:AA563870
 F-NT2RP3002972//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter//5.1e-35:361:75//Hs.8003:AC004997
 F-NT2RP3002978//ESTs//2.8e-46:253:95//Hs.151924:AI287703
 F-NT2RP3002985//Human TFIIIB related factor hBRF (HBRF) mRNA, complete cds//0.071:550:58//Hs.32935:U28838
 F-NT2RP3002988//EST//0.0016:180:63//Hs.147632:AI218308
 F-NT2RP3003008//Human DNA-binding protein (HRC1) mRNA, complete cds//0.59:201:63//Hs.72925:M91083
 F-NT2RP3003032//ESTs//9.1e-40:241:92//Hs.113363:C06446
 F-NT2RP3003059//ESTs//0.0015:399:58//Hs.136895:AA897749
 F-NT2RP3003061//Ankyrin 1, erythrocytic//4.5e-14:633:59//Hs.1242:X16609

F-NT2RP3003068//EST//0.00014:80:83//Hs.121993:AA777928
F-NT2RP3003071//ESTs//1.1e-62:315:98//Hs.16141:W56079
F-NT2RP3003078
F-NT2RP3003101
F-NT2RP3003121//EST, Moderately similar to !!!! ALU SUBFAMILY SC WARNING
ENTRY !!!! [H.sapiens]//0.98:88:68//Hs.99715:AA292700
F-NT2RP3003133//EST//8.0e-17:218:68//Hs.134815:AI090740
F-NT2RP3003138//Homo sapiens vasopressin-activated calcium mobilizing pu
tative receptor protein (VACM-1) mRNA, complete cds//0.013:438:57//Hs.10
1299:AF017061
F-NT2RP3003139//ESTs//0.020:260:61//Hs.59142:W88975
F-NT2RP3003145//Homo sapiens aortic carboxypeptidase-like protein ACLP m
RNA, complete cds//2.2e-20:430:63//Hs.118397:AF053944
F-NT2RP3003150
F-NT2RP3003157//Human repressor transcriptional factor (ZNF85) mRNA, com
plete cds//2.0e-72:894:68//Hs.37138:U35376
F-NT2RP3003185//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.0
45:410:59//Hs.6150:AB011093
F-NT2RP3003193//Zinc finger protein 10 (KOX 1)//2.4e-74:737:71//Hs.2479:
X78933
F-NT2RP3003197//ESTs//1.8e-24:130:100//Hs.162504:AA668211
F-NT2RP3003203//ESTs//3.5e-30:232:82//Hs.6880:W26854
F-NT2RP3003204//ESTs//3.1e-109:524:98//Hs.152982:AA584308
F-NT2RP3003210//ESTs//3.6e-16:113:91//Hs.121030:AA625325
F-NT2RP3003212//EST//1.0e-52:500:74//Hs.161635:W22525
F-NT2RP3003230//Human mRNA for actin binding protein p57, complete cds//
6.0e-55:587:70//Hs.109606:D44497
F-NT2RP3003242//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds/
/1.2e-129:617:98//Hs.155223:AF055460

F-NT2RP3003251//H.sapiens Staf50 mRNA//1.1e-68:651:76//Hs.68054:X82200
 F-NT2RP3003264//Human bullous 230 kDa pemphigoid antigen (BPAG1) mRNA, complete cds//0.069:382:59//Hs.620:M69225
 F-NT2RP3003278//Homo sapiens hook2 protein (HOOK2) mRNA, complete cds//0.98:261:59//Hs.30792:AF044924
 F-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//4.2e-133:694:93//Hs.11702:L36983
 F-NT2RP3003290//Human mRNA for RTP, complete cds//6.3e-66:662:71//Hs.75789:D87953
 F-NT2RP3003301//EST//1.0:58:74//Hs.158575:AI368947
 F-NT2RP3003302//Human Line-1 repeat mRNA with 2 open reading frames//3.1e-91:681:80//Hs.23094:M19503
 F-NT2RP3003311//ESTs//0.95:308:59//Hs.27308:AA534947
 F-NT2RP3003313//ESTs//0.0016:345:61//Hs.143304:AI084058
 F-NT2RP3003327//H.sapiens Staf50 mRNA//8.0e-31:253:67//Hs.68054:X82200
 F-NT2RP3003330
 F-NT2RP3003344
 F-NT2RP3003346//H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase//1.2e-42:644:66//Hs.2638:Z28339
 F-NT2RP3003353//Breast cancer 1, early onset//0.30:145:67//Hs.66746:L78833
 F-NT2RP3003377//Human mRNA for cadherin-15, complete cds//0.019:416:60//Hs.148090:D83542
 F-NT2RP3003384//ESTs//1.1e-65:346:96//Hs.35012:R92791
 F-NT2RP3003385//ESTs, Highly similar to SKD3 [M.musculus]//7.0e-74:384:96//Hs.21263:H16363
 F-NT2RP3003403//ESTs//4.9e-12:335:63//Hs.87258:AA463850
 F-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds//3.2e-22:430:63//Hs.113272:U90653

F-NT2RP3003411//Human metallothionein-Ie gene (hMT-Ie)//0.99:116:62//Hs.
74170:M10942

F-NT2RP3003427//ESTs//0.24:447:61//Hs.160907:AI422830

F-NT2RP3003433//Protein tyrosine phosphatase, non-receptor type 12//1.0:
243:61//Hs.62:M93425

F-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete c
ds//1.7e-182:853:98//Hs.14934:AF004828

F-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds//5.2
e-175:826:98//Hs.26450:AB018268

F-NT2RP3003491//Ryanodine receptor 2 (cardiac)//1.0:148:66//Hs.90821:X98
330

F-NT2RP3003500//ESTs//0.86:211:62//Hs.136037:AA013302

F-NT2RP3003543//Homo sapiens clone 23790 unknown protein mRNA, complete
cds//0.64:626:58//Hs.150828:AF038169

F-NT2RP3003552

F-NT2RP3003555//ESTs//1.4e-12:81:98//Hs.144487:AI418322

F-NT2RP3003564//EST//4.5e-08:186:69//Hs.116769:AA630365

F-NT2RP3003572//EST//0.27:105:69//Hs.162134:AA526311

F-NT2RP3003576//ESTs//1.2e-57:277:84//Hs.138852:AA284247

F-NT2RP3003589//RAS-RELATED PROTEIN RAB-8//6.3e-38:373:73//Hs.123109:X56
741

F-NT2RP3003621//HEPATOCYTE GROWTH FACTOR ACTIVATOR PRECURSOR//8.0e-09:56
4:61//Hs.104:D14012

F-NT2RP3003625

F-NT2RP3003656

F-NT2RP3003659

F-NT2RP3003665//ESTs//0.015:221:62//Hs.153705:AA527586

F-NT2RP3003672//ESTs//0.70:351:57//Hs.27633:N76184

F-NT2RP3003680//Human Bcl2, p53 binding protein Bbp/53BP2 (BBP/53BP2) mR

NA, complete cds//0.013:190:63//Hs.44585:U58334

F-NT2RP3003686//Homo sapiens clone 24519 unknown mRNA, partial cds//0.69
:246:62//Hs.118463:AF055000

F-NT2RP3003701//EST//0.93:79:69//Hs.145285:AI249848

F-NT2RP3003716//Homo sapiens KIAA0405 mRNA, complete cds//8.3e-24:478:61
//Hs.48998:AB007865

F-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds//7.
4e-150:700:98//Hs.48513:AB018300

F-NT2RP3003746

F-NT2RP3003795//ESTs//7.1e-20:228:74//Hs.159571:AA454230

F-NT2RP3003799

F-NT2RP3003800//Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene ho
molog//4.7e-41:432:73//Hs.1422:M19722

F-NT2RP3003805//Myosin, heavy polypeptide 6, cardiac muscle, alpha (card
iomyopathy, hypertrophic 1)//0.98:242:57//Hs.114001:Z20656

F-NT2RP3003809//Human transcription factor, forkhead related activator 4
(FREAC-4) mRNA, complete cds//5.1e-07:624:59//Hs.96028:AF042832

F-NT2RP3003819//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' f
lanking sequence//0.84:171:63//Hs.102877:U41315

F-NT2RP3003825

F-NT2RP3003828//ESTs//2.1e-12:434:61//Hs.156864:AI346481

F-NT2RP3003831

F-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//2.6e-
48:242:98//Hs.25300:AF070611

F-NT2RP3003842//Integrin, beta 8//1.0:345:60//Hs.832:M73780

F-NT2RP3003846//Homo sapiens mRNA for KIAA0725 protein, partial cds//1.3
e-37:335:68//Hs.26450:AB018268

F-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds//1.
3e-175:805:99//Hs.118738:AB018343

F-NT2RP3003876//ESTs, Highly similar to Rabin3 [R.norvegicus] //6.8e-39:2
43:90//Hs.124832:AA846576

F-NT2RP3003914//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSY
LTRANSFERASE PRECURSOR [D.melanogaster] //1.1e-107:499:99//Hs.105794:AA70
1659

F-NT2RP3003918//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33)
mRNA, complete cds//8.3e-49:404:77//Hs.9006:AF057358

F-NT2RP3003932//ESTs//0.94:278:58//Hs.15661:W02396

F-NT2RP3003989//ESTs//1.0:174:64//Hs.8095:AI359006

F-NT2RP3003992//Cyclic nucleotide gated channel (photoreceptor), cGMP ga
ted 2 (beta)//0.00070:433:58//Hs.93909:AF042498

F-NT2RP3004013//ESTs, Moderately similar to M-phase phosphoprotein 4 [H.
sapiens] //2.8e-127:617:97//Hs.142151:AA984061

F-NT2RP3004016//Human p300/CBP-associated factor (P/CAF) mRNA, complete
cds//0.0086:283:62//Hs.155302:U57317

F-NT2RP3004041//EST//0.98:264:58//Hs.127552:AA953234

F-NT2RP3004051//Human mRNA for KIAA0319 gene, complete cds//7.0e-63:774:
67//Hs.26441:AB002317

F-NT2RP3004070//EST//6.8e-22:163:85//Hs.132635:AI032875

F-NT2RP3004078//Regulatory factor (trans-acting) 2 (influences HLA class
II expression)//5.3e-90:520:90//Hs.100007:X76091

F-NT2RP3004093

F-NT2RP3004095//Human clone 23732 mRNA, partial cds//3.3e-27:372:69//Hs.
81281:U79258

F-NT2RP3004110//Human mRNA for KIAA0392 gene, partial cds//1.2e-20:211:7
7//Hs.40100:AB002390

F-NT2RP3004125//ESTs, Highly similar to OOCYTE ZINC FINGER PROTEIN XLCO
F7.1 [Xenopus laevis] //1.0e-126:590:99//Hs.129888:AI096509

F-NT2RP3004145

F-NT2RP3004148

F-NT2RP3004155//Homo sapiens timing protein CLK-1 mRNA, complete cds//2.1e-121:578:98//Hs.157113:AF032900

F-NT2RP3004189//ESTs//1.3e-80:409:97//Hs.151001:AA564706

F-NT2RP3004206//Human mRNA for stac, complete cds//1.0:245:60//Hs.56045:D86640

F-NT2RP3004207//Transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)//0.095:281:62//Hs.101047:M31523

F-NT2RP3004209//ESTs//5.8e-87:458:94//Hs.155303:AI221835

F-NT2RP3004215//ESTs//0.074:56:80//Hs.163590:H43361

F-NT2RP3004242

F-NT2RP3004246//EST//0.20:219:63//Hs.161920:AA483240

F-NT2RP3004253//ESTs//1.2e-36:204:96//Hs.143588:AI149140

F-NT2RP3004258//Human gene for neurofilament subunit M (NF-M)//7.2e-07:369:59//Hs.71346:Y00067

F-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds//1.0e-154:733:98//Hs.158471:AF088982

F-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds//4.2e-26:597:61//Hs.19261:AF007871

F-NT2RP3004332

F-NT2RP3004334//ESTs//8.8e-27:142:99//Hs.28068:H06285

F-NT2RP3004341//EST//0.0068:213:64//Hs.153208:X98426

F-NT2RP3004348//ESTs//1.2e-18:126:93//Hs.58595:AA830999

F-NT2RP3004349//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//3.9e-45:337:83//Hs.141429:AA631915

F-NT2RP3004378//ESTs, Weakly similar to weak similarity to procollagen alpha chain 1(V) chain [C.elegans]//4.3e-125:608:98//Hs.128781:AA160707

F-NT2RP3004399//H.sapiens mRNA for leucine-rich primary response protein

1//2.3e-141:804:90//Hs.123122:X97249
 F-NT2RP3004424//ESTs, Weakly similar to JTV-1 [H.sapiens]//3.2e-122:609:
 96//Hs.20132:AA203113
 F-NT2RP3004428//Homo sapiens ALR mRNA, complete cds//0.00044:458:60//Hs.
 153638:AF010403
 F-NT2RP3004451//Bone morphogenetic protein 8 (osteogenic protein 2)//0.0
 0023:357:59//Hs.99948:M97016
 F-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds//2.
 0e-124:583:99//Hs.27349:AB007917
 F-NT2RP3004466//Homo sapiens mRNA for KIAA0664 protein, partial cds//0.4
 8:399:58//Hs.22616:AB014564
 F-NT2RP3004470//EST//1.3e-56:331:91//Hs.136830:AA769219
 F-NT2RP3004472
 F-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds//9.8
 e-152:715:98//Hs.5003:AB007925
 F-NT2RP3004480//ESTs, Highly similar to VACUOLAR SORTING PROTEIN 35 [Sa
 ccharomyces cerevisiae]//4.6e-118:547:99//Hs.124768:AA307735
 F-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds//2.3e-156:75
 2:97//Hs.158311:AB012851
 F-NT2RP3004498//ESTs, Moderately similar to ROSA26AS [M.musculus]//3.5e-
 89:425:99//Hs.126082:AI077718
 F-NT2RP3004503//EST//5.3e-49:399:81//Hs.162335:AA564256
 F-NT2RP3004504//Homo sapiens mRNA for KIAA0479 protein, partial cds//1.0
 :370:59//Hs.158244:AB007948
 F-NT2RP3004507//Human zinc finger protein (MAZ) mRNA//0.86:129:66//Hs.76
 47:M94046
 F-NT2RP3004527//EST//0.053:260:62//Hs.123314:AA810110
 F-NT2RP3004534//ESTs//3.5e-78:370:99//Hs.132808:AI031571
 F-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds//2.7

e-146:679:98//Hs.75970:AB014532
 F-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds//9.1
 e-171:793:98//Hs.74750:AB011126
 F-NT2RP3004566//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus
 musculus] //2.2e-66:362:94//Hs.125870:AI364967
 F-NT2RP3004569
 F-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF150) mRN
 A, complete cds//3.3e-181:860:97//Hs.122752:AF026445
 F-NT2RP3004578//Homo sapiens mRNA for KIAA0454 protein, partial cds//4.0
 e-85:422:97//Hs.129928:AB007923
 F-NT2RP3004594//Homo sapiens mRNA for AND-1 protein//3.7e-160:796:95//Hs
 .72160:AJ006266
 F-NT2RP3004617//ESTs, Weakly similar to estrogen-responsive finger prote
 in, efp [H.sapiens] //6.4e-13:356:64//Hs.124138:AI266336
 F-NT2RP3004618//ESTs//1.5e-42:481:70//Hs.130768:AA909232
 F-NT2RP3004669//Human plectin (PLEC1) mRNA, complete cds//0.0099:538:56/
 /Hs.79706:U53204
 F-NT2RP3004670//Homo sapiens sox1 gene//0.11:311:58//Hs.144029:Y13436
 F-NT2RP4000008//ESTs, Highly similar to CHLORINE CHANNEL PROTEIN P64 [B
 os taurus] //8.0e-177:827:98//Hs.118991:AA675919
 F-NT2RP4000023//ESTs//1.4e-33:182:96//Hs.122722:AA455668
 F-NT2RP4000035//ESTs//1.1e-23:283:72//Hs.142147:AA706495
 F-NT2RP4000049//Homo sapiens decoy receptor 2 mRNA, complete cds//6.8e-8
 3:556:85//Hs.129844:AF029761
 F-NT2RP4000051//Homo sapiens mRNA for cartilage-associated protein (CASP
)//4.9e-13:441:62//Hs.155481:AJ006470
 F-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//8.0e
 -151:720:97//Hs.159597:AJ012449
 F-NT2RP4000102//ESTs//8.8e-33:184:82//Hs.93054:H47743

F-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds//1.4e-167:774:9
9//Hs.57929:AB011538
F-NT2RP4000111
F-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds//1.1
e-115:548:98//Hs.64691:AB007952
F-NT2RP4000147//Human mRNA for KIAA0041 gene, partial cds//0.00045:212:6
3//Hs.75520:D26069
F-NT2RP4000150
F-NT2RP4000151//Homo sapiens chromosome 7q22 sequence//0.98:431:59//Hs.3
386:AF053356
F-NT2RP4000159
F-NT2RP4000167
F-NT2RP4000185//ESTs//1.1e-51:240:68//Hs.33020:N31946
F-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds//1.6
e-175:825:98//Hs.13999:AB014600
F-NT2RP4000212//ESTs//1.6e-10:74:95//Hs.111885:AA422006
F-NT2RP4000214//ESTs//3.9e-11:225:68//Hs.59793:AA451731
F-NT2RP4000218//Human G protein-coupled receptor (STRL22) mRNA, complete
cds//6.2e-34:425:71//Hs.46468:U45984
F-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP
)//8.6e-158:771:97//Hs.155481:AJ006470
F-NT2RP4000246//ESTs, Highly similar to NPC DERIVED PROLINE RICH PROTEIN
1 [M.musculus]//1.9e-62:384:89//Hs.115498:AA436298
F-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence//
9.4e-130:604:99//Hs.43728:AF091092
F-NT2RP4000263
F-NT2RP4000290//EST//1.0:149:63//Hs.136928:AA812580
F-NT2RP4000312//Human mRNA for KIAA0147 gene, partial cds//1.5e-42:685:6
3//Hs.158132:D63481

F-NT2RP4000321//Homo sapiens gene for insulin receptor substrate-2, complete cds//8.6e-05:547:57//Hs.143648:AB000732

F-NT2RP4000323//Human HCF1 gene related mRNA sequence//0.48:589:58//Hs.83634:U52112

F-NT2RP4000355

F-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds//6.4e-142:654:99//Hs.107479:AB018281

F-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//8.5e-137:649:97//Hs.31323:AF044195

F-NT2RP4000370//ESTs, Weakly similar to MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR [S.cerevisiae]//1.2e-09:157:76//Hs.97950:AI382073

F-NT2RP4000376//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//0.098:291:59//Hs.994:M95678

F-NT2RP4000381//Myosin, heavy polypeptide 7, cardiac muscle, beta//0.00025:509:59//Hs.929:M57965

F-NT2RP4000398//Zinc finger protein 140 (clone pHZ-39)//4.9e-60:469:68//Hs.154205:U09368

F-NT2RP4000415//ESTs//0.85:89:67//Hs.152312:AA485688

F-NT2RP4000417//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//0.014:178:66//Hs.125315:AF027156

F-NT2RP4000424//Human G protein-coupled receptor (STRL22) mRNA, complete cds//2.0e-34:431:73//Hs.46468:U45984

F-NT2RP4000448//Human mRNA for KIAA0118 gene, partial cds//1.9e-37:360:75//Hs.154326:D42087

F-NT2RP4000449//EST//0.84:113:65//Hs.145274:AI249468

F-NT2RP4000455//ALPHA-2C-1 ADRENERGIC RECEPTOR//0.063:221:61//Hs.123022:J03853

F-NT2RP4000457//H.sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HAUSP)//1.1e-05:532:57//Hs.78683:Z72499

F-NT2RP4000480//Homo sapiens mRNA, complete cds//0.056:655:60//Hs.133151
:AB001535

F-NT2RP4000481//Human mRNA for KIAA0268 gene, partial cds//0.46:272:58//
Hs.78862:D87742

F-NT2RP4000498//Human DNA binding protein FKHL15 (FKHL15) mRNA, complete
cds//0.94:133:69//Hs.159234:U89995

F-NT2RP4000500//V-myb avian myeloblastosis viral oncogene homolog-like 2
//0.60:335:61//Hs.74605:X13293

F-NT2RP4000515//ESTs//2.9e-45:253:95//Hs.104898:AA429594

F-NT2RP4000517//EST//0.043:131:64//Hs.99030:AA443904

F-NT2RP4000518//Homo sapiens mRNA for ATP-dependent RNA helicase, partia
l//2.0e-34:203:93//Hs.99423:AJ010840

F-NT2RP4000519//Human mRNA for KIAA0374 gene, complete cds//0.33:154:66/
/Hs.100837:AB002372

F-NT2RP4000524

F-NT2RP4000528

F-NT2RP4000541//ESTs//2.1e-51:251:99//Hs.157240:AI348154

F-NT2RP4000556//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L11 [R.nor
vegicus] //1.1e-27:162:93//Hs.25597:H93026

F-NT2RP4000560//ESTs//2.5e-09:181:66//Hs.122609:AA778351

F-NT2RP4000588//ESTs//1.4e-46:533:70//Hs.8836:AA181053

F-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complet
e cds//1.0e-139:666:98//Hs.4214:AF067730

F-NT2RP4000638//Fibroblast growth factor 2 (basic)//1.0:226:61//Hs.56066
:J04513

F-NT2RP4000648//ESTs//2.5e-11:116:80//Hs.115449:AA418396

F-NT2RP4000657//Homo sapiens bone morphogenetic protein 11 (BMP11) mRNA,
complete cds//0.00056:367:60//Hs.144626:AF100907

F-NT2RP4000704//Homo sapiens mRNA expressed in 19week fetal lung, clone

IMAGE:300856//8.0e-167:676:98//Hs.50748:AB004848
 F-NT2RP4000713//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//6.9e-07:494:61//Hs.113286:U77783
 F-NT2RP4000724//ESTs, Weakly similar to pol/env ORF [H.sapiens]//2.8e-46:411:78//Hs.111817:T80622
 F-NT2RP4000728//Homo sapiens mRNA for KIAA0606 protein, partial cds//9.9e-43:350:71//Hs.38176:AB011178
 F-NT2RP4000737//Human mRNA for KIAA0252 gene, partial cds//0.97:409:60//Hs.83419:D87440
 F-NT2RP4000739//DESMOPLAKIN I AND II//0.99:192:63//Hs.74316:AL031058
 F-NT2RP4000781//Homo sapiens mRNA for APC 2 protein, complete cds//0.023:351:60//Hs.20912:AB012162
 F-NT2RP4000787//Human mRNA for ESP1/CRP2, complete cds//0.0051:276:58//Hs.70327:D42123
 F-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds//4.8e-176:816:98//Hs.25132:AB007939
 F-NT2RP4000833//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//1.3e-93:438:99//Hs.8173:AC005189
 F-NT2RP4000837//Homo sapiens SALL1 gene, partial//5.9e-05:470:59//Hs.123094:X98833
 F-NT2RP4000839//ESTs//5.7e-11:133:82//Hs.103852:W27603
 F-NT2RP4000855//Homo sapiens DNA-binding protein (CROC-1B) mRNA, complete cds//1.4e-37:680:63//Hs.75875:U49278
 F-NT2RP4000865//Zinc finger protein 136 (clone pHZ-20)//2.0e-96:415:78//Hs.69740:U09367
 F-NT2RP4000878//ESTs//2.7e-16:390:63//Hs.163451:A1206803
 F-NT2RP4000879//ESTs//0.89:184:64//Hs.122333:AA782843
 F-NT2RP4000907//Homo sapiens BAC clone RG118D07 from 7q31//4.5e-52:933:61//Hs.3781:AC004142

F-NT2RP4000915//Homo sapiens mRNA for ZNF198 protein//3.0e-80:584:78//Hs.109526:AJ224901

F-NT2RP4000918

F-NT2RP4000925//Homo sapiens KIAA0405 mRNA, complete cds//1.9e-47:861:61//Hs.48998:AB007865

F-NT2RP4000927//ESTs//0.37:159:63//Hs.147949:AI341503

F-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//1.1e-164:781:97//Hs.24812:AF069532

F-NT2RP4000929//ESTs//0.88:284:60//Hs.141317:AI281371

F-NT2RP4000955//Human mRNA for cadherin-15, complete cds//0.0019:495:58//Hs.148090:D83542

F-NT2RP4000973//Homo sapiens mRNA for MSJ-1, complete cds//1.2e-05:318:60//Hs.3845:AB014888

F-NT2RP4000975//ESTs//0.0051:345:61//Hs.143304:AI084058

F-NT2RP4000979

F-NT2RP4000984

F-NT2RP4000989//Homo sapiens Tax interaction protein 1 mRNA, partial cds//0.85:257:63//Hs.12956:U90913

F-NT2RP4000996//ESTs//4.3e-10:329:62//Hs.33085:AA258068

F-NT2RP4000997//Human plectin (PLEC1) mRNA, complete cds//1.0:218:58//Hs.79706:U53204

F-NT2RP4001004

F-NT2RP4001006//ESTs, Moderately similar to ROSA26AS [M.musculus]//7.4e-90:425:99//Hs.126082:AI077718

F-NT2RP4001010//Homo sapiens PSD-95/SAP90-associated protein-2 mRNA, partial cds//2.8e-19:689:61//Hs.113287:AF009204

F-NT2RP4001029//Human transcription factor LSF mRNA, complete cds//9.6e-84:778:74//Hs.154970:U03494

F-NT2RP4001041//Human endosome-associated protein (EEA1) mRNA, complete

cds//0.95:170:64//Hs.2864:L40157
 F-NT2RP4001057//EST//9.6e-05:122:72//Hs.132518:AA928157
 F-NT2RP4001064//Homo sapiens mRNA for cartilage-associated protein (CASP
)//7.2e-13:441:63//Hs.155481:AJ006470
 F-NT2RP4001078//ESTs//1.3e-29:165:95//Hs.113817:AA702497
 F-NT2RP4001079//Homo sapiens mRNA for putative Ca²⁺-transporting ATPase,
 partial//1.4e-131:634:98//Hs.106778:AJ010953
 F-NT2RP4001080//Polypyrimidine tract binding protein (hnRNP I) {alternat
 ive products} //0.025:166:66//Hs.146459:X66975
 F-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds//1.5
 e-85:604:86//Hs.13273:AB011164
 F-NT2RP4001095
 F-NT2RP4001100//ESTs, Weakly similar to C17G10.1 [C.elegans] //1.4e-93:44
 8:98//Hs.105837:AA536054
 F-NT2RP4001117//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61
 ALPHA SUBUNIT [Canis familiaris] //2.2e-26:171:92//Hs.14038:R06800
 F-NT2RP4001122//Human mRNA for histone H1x, complete cds//0.99:185:66//H
 s.109804:D64142
 F-NT2RP4001126//ESTs, Moderately similar to The KIAA0138 gene product is
 novel. [H.sapiens] //5.8e-37:185:100//Hs.126925:AA931237
 F-NT2RP4001138//ESTs//3.4e-09:125:77//Hs.143382:AA476266
 F-NT2RP4001143//ESTs//1.0:282:57//Hs.157423:AI358261
 F-NT2RP4001148//ESTs//0.82:206:62//Hs.129259:AA992207
 F-NT2RP4001149//EST//1.3e-17:140:88//Hs.101727:H16171
 F-NT2RP4001150//AXONIN-1 PRECURSOR//7.7e-07:562:59//Hs.2998:X67734
 F-NT2RP4001159//EST//0.26:125:66//Hs.152092:AA377324
 F-NT2RP4001174//ESTs//2.9e-103:502:98//Hs.125886:AA884264
 F-NT2RP4001206//EST//0.33:125:66//Hs.152092:AA377324
 F-NT2RP4001207

F-NT2RP4001210//ESTs//3.1e-95:460:97//Hs.46913:AI017636

F-NT2RP4001213//KRAB zinc finger protein {alternative products} //1.1e-45
:187:74//Hs.22556:U37251

F-NT2RP4001219//ESTs//1.4e-69:352:96//Hs.116392:AA936262

F-NT2RP4001228//Homo sapiens actin binding protein MAYVEN mRNA, complete
cds//7.2e-28:855:60//Hs.122967:AF059569

F-NT2RP4001235//Homo sapiens Jagged 2 mRNA, complete cds//1.0:257:59//Hs
.106387:AF029778

F-NT2RP4001256//Human mRNA for KIAA0273 gene, complete cds//0.96:247:62/
/Hs.75899:D87463

F-NT2RP4001260//Syntrophin, alpha (dystrophin-associated protein A1, 59k
D, acidic component)//0.015:246:62//Hs.31121:U40571

F-NT2RP4001274//Homo sapiens clone 24674 mRNA sequence//1.2e-06:259:64//
Hs.71168:AF070578

F-NT2RP4001276//Homo sapiens CAGF9 mRNA, partial cds//7.6e-06:266:62//Hs
.110826:U80736

F-NT2RP4001313//Homo sapiens mitochondrial outer membrane protein (TOM40
) mRNA, nuclear gene encoding mitochondrial protein, complete cds//2.3e-
31:535:65//Hs.30928:AF043250

F-NT2RP4001315//EST//9.5e-20:146:88//Hs.158755:AI375917

F-NT2RP4001336//ESTs//1.0:128:67//Hs.99598:AA603110

F-NT2RP4001339

F-NT2RP4001343

F-NT2RP4001345//Lecithin-cholesterol acyltransferase//8.0e-39:686:64//Hs
.112125:M12625

F-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain ho
molog (Doc1) mRNA, complete cds//2.0e-31:784:62//Hs.15432:U53445

F-NT2RP4001353//Homo sapiens chromosome 7q22 sequence//0.0034:497:57//Hs
.125742:AF053356

F-NT2RP4001372

F-NT2RP4001373//Homo sapiens clone Dt1P1b11 mRNA, CAG repeat region//0.4
3:290:58//Hs.82101:Z50194

F-NT2RP4001375

F-NT2RP4001379//TRICHOHYALIN//8.2e-05:591:58//Hs.82276:L09190

F-NT2RP4001389//EST//5.3e-27:212:84//Hs.160402:AI393918

F-NT2RP4001407//Homo sapiens mRNA for RGS5, complete cds//0.93:218:58//H
s.24950:AB008109

F-NT2RP4001414//Human mRNA for KIAA0202 gene, partial cds//6.3e-78:818:7
1//Hs.80712:D86957

F-NT2RP4001433//Zinc finger protein 10 (KOX 1)//1.1e-88:839:73//Hs.2479:
X78933

F-NT2RP4001442

F-NT2RP4001447//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.
0075:218:63//Hs.41153:AB018326

F-NT2RP4001474//ESTs, Weakly similar to probable CBP3 protein homolog [C
.elegans]//2.1e-90:460:96//Hs.26676:AA033997

F-NT2RP4001483//Oxoglutarate dehydrogenase (lipoamide)//8.1e-61:480:75//
Hs.75533:D10523

F-NT2RP4001498//ESTs, Weakly similar to GA BINDING PROTEIN BETA-2 CHAIN
[H.sapiens]//0.25:216:60//Hs.63220:AA522707

F-NT2RP4001502//ESTs//2.6e-41:206:99//Hs.159257:N40395

F-NT2RP4001507//H.sapiens mRNA for RanGTPase activating protein 1//0.51:
281:61//Hs.5923:X82260

F-NT2RP4001524//ESTs, Weakly similar to F13B12.1 [C.elegans]//9.4e-30:17
3:94//Hs.5570:AI377863

F-NT2RP4001529//Human transcription factor LSF mRNA, complete cds//1.3e-
35:329:76//Hs.154970:U03494

F-NT2RP4001547//Homo sapiens forkhead protein FREAC-2 mRNA, complete cds

//0.0015:221:65//Hs.44481:U13220
 F-NT2RP4001551//Human BRCA2 region, mRNA sequence CG003//0.56:428:59//Hs
 .30649:U50534
 F-NT2RP4001555//EST//0.99:225:64//Hs.96863:AA347174
 F-NT2RP4001567
 F-NT2RP4001568//ESTs, Weakly similar to HYPOTHETICAL 32.6 KD PROTEIN IN
 MET30-CBR5 INTERGENIC REGION [Saccharomyces cerevisiae]//1.1e-54:252:83/
 /Hs.158208:AA167836
 F-NT2RP4001571//ESTs//3.0e-94:475:96//Hs.65322:AA019410
 F-NT2RP4001574
 F-NT2RP4001575//Homo sapiens mRNA for ARE1-like protein//1.8e-169:796:98
 //Hs.108826:AL031228
 F-NT2RP4001592
 F-NT2RP4001610//Human involucrin mRNA//0.94:462:59//Hs.157091:M13903
 F-NT2RP4001614//ESTs//0.71:331:58//Hs.116533:AI343952
 F-NT2RP4001634
 F-NT2RP4001638//ESTs, Weakly similar to HYPOTHETICAL 117.9 KD PROTEIN IN
 FKH1-STH1 INTERGENIC REGION [S.cerevisiae]//8.6e-57:287:97//Hs.117439:C
 18436
 F-NT2RP4001644//Human mRNA for MNK1, complete cds//1.7e-53:415:80//Hs.55
 91:AB000409
 F-NT2RP4001656//ESTs, Highly similar to PHENYLALANYL-TRNA SYNTHETASE MI
 TOCHONDRIAL PRECURSOR [Saccharomyces cerevisiae]//1.0:311:59//Hs.57969:A
 A203629
 F-NT2RP4001677//Homo sapiens short form transcription factor C-MAF (c-ma
 f) mRNA, complete cds//0.19:162:67//Hs.30250:AF055376
 F-NT2RP4001679//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.2e-50:33
 2:86//Hs.113283:AF018080
 F-NT2RP4001696

F-NT2RP4001725//Galactokinase 1//1.0:202:63//Hs.92357:L76927
 F-NT2RP4001730//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//0.0035:247:62//Hs.92614:M62302
 F-NT2RP4001739//Complement component 8, gamma polypeptide//0.74:654:56//Hs.1285:U08198
 F-NT2RP4001753//Zinc finger protein 84 (HPF2)//4.5e-29:476:67//Hs.9450:M27878
 F-NT2RP4001760//ESTs//1.0:411:60//Hs.108548:AA081656
 F-NT2RP4001790//Homo sapiens PAC clone DJ0604G05 from 7q22-q31.1//9.1e-34:400:68//Hs.154212:AC004522
 F-NT2RP4001803//Human high conductance inward rectifier potassium channel alpha subunit mRNA, complete cds//0.028:580:58//Hs.2363:L36069
 F-NT2RP4001822//ESTs//3.4e-50:307:90//Hs.113509:AA132131
 F-NT2RP4001823//Human faciogenital dysplasia (FGD1) mRNA, complete cds//3.1e-07:509:59//Hs.1572:U11690
 F-NT2RP4001828
 F-NT2RP4001838//Human mRNA for KIAA0071 gene, partial cds//6.9e-55:555:73//Hs.78398:D31888
 F-NT2RP4001841//ESTs//0.99:215:60//Hs.136895:AA897749
 F-NT2RP4001849//Homo sapiens mRNA for KIAA0672 protein, complete cds//5.6e-57:813:65//Hs.6336:AB014572
 F-NT2RP4001861//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.8e-12:84:94//Hs.140232:AA705170
 F-NT2RP4001889
 F-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21//4.4e-108:535:97//Hs.15144:AC005014
 F-NT2RP4001896
 F-NT2RP4001901//ESTs//1.4e-50:291:93//Hs.67991:AA147848
 F-NT2RP4001927

F-NT2RP4001938//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens] //2.8e-54:375:84//Hs.119294:AI379442

F-NT2RP4001946//EST//0.050:268:60//Hs.148341:AA921894

F-NT2RP4001950//EST//7.9e-14:336:63//Hs.112810:AA610063

F-NT2RP4001953//ESTs//0.018:206:65//Hs.130105:AA904868

F-NT2RP4001966//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//1.7e-54:788:65//Hs.23796:AL022718

F-NT2RP4001975//Homo sapiens homeobox protein Six3 (SIX3) gene, complete cds//0.0019:279:65//Hs.159439:AF092047

F-NT2RP4002018//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster] //0.58:463:55//Hs.3826:U69560

F-NT2RP4002047//EST//2.5e-13:102:90//Hs.148997:AI243139

F-NT2RP4002052

F-NT2RP4002058//ESTs//5.2e-41:347:72//Hs.121961:AA777873

F-NT2RP4002071//Homo sapiens TTAGGG repeat binding factor 2 (hTRF2) mRNA, complete cds//0.97:227:60//Hs.100030:AF002999

F-NT2RP4002075

F-NT2RP4002078//ESTs, Moderately similar to zinc finger protein [H.sapiens] //1.0e-38:243:90//Hs.139115:AA325104

F-NT2RP4002081//TATA box binding protein//0.0059:310:60//Hs.1100:M55654

F-NT2RP4002083//H.sapiens Pur (pur-alpha) mRNA, complete cds//0.0015:152:70//Hs.25180:M96684

F-NT2RP4002408//Human protein kinase C-L (PRKCL) mRNA, complete cds//8.0e-10:401:59//Hs.89616:M55284

F-NT2RP4002791//Ataxin 1//1.0:215:61//Hs.74520:X79204

F-NT2RP4002888

F-NT2RP4002905//ESTs//3.4e-50:280:94//Hs.131697:H14960
 F-NT2RP5003459//Glyceraldehyde-3-phosphate dehydrogenase//1.3e-35:193:96
 //Hs.74456:U34995
 F-NT2RP5003461//ESTs//3.6e-104:513:98//Hs.88088:AA521071
 F-NT2RP5003477//Eukaryotic translation initiation factor 3 (eIF-3) p36 s
 ubunit//0.18:271:60//Hs.139745:U39067
 F-NT2RP5003492
 F-NT2RP5003500//Homo sapiens mRNA for heparan-sulfate 6-sulfotransferase
 , complete cds//6.1e-56:750:69//Hs.132884:AB006179
 F-NT2RP5003506//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//5
 .1e-14:348:62//Hs.154050:AC004131
 F-NT2RP5003512//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.9
 4:202:63//Hs.8152:AB014542
 F-NT2RP5003522
 F-NT2RP5003524//ESTs//8.7e-08:340:62//Hs.152730:AI308943
 F-NT2RP5003534
 F-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds//4.0
 e-69:373:94//Hs.108258:AB007934
 F-OVARC1000004//ESTs//6.0e-38:216:93//Hs.163801:AI391729
 F-OVARC1000006//ESTs, Highly similar to HISTONE H2A [Cairina moschata]/
 /4.4e-75:355:99//Hs.36727:AI051983
 F-OVARC1000013//ESTs//0.65:331:58//Hs.146326:AA534304
 F-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds//1.8e-171:81
 5:98//Hs.81449:AF058922
 F-OVARC1000017//Homo sapiens mRNA for NTAK, complete cds//0.50:482:58//H
 s.113264:AB005060
 F-OVARC1000035//Homo sapiens GA17 protein mRNA, complete cds//2.2e-37:23
 8:89//Hs.69469:AF064603
 F-OVARC1000058//ESTs//1.1e-23:132:97//Hs.61809:AA503549

F-OVARC1000060//ESTs, Highly similar to ribonuclease 6 precursor [H.sapiens]//6.7e-60:305:97//Hs.31696:H50008

F-OVARC1000068//ESTs//3.8e-10:69:100//Hs.89048:AA282798

F-OVARC1000071//ESTs//1.9e-36:202:95//Hs.125013:AA400543

F-OVARC1000085

F-OVARC1000087//EST//1.0:199:58//Hs.122919:AA768442

F-OVARC1000091//Homo sapiens Jagged 2 mRNA, complete cds//0.00017:414:59//Hs.106387:AF029778

F-OVARC1000092//ESTs//4.6e-06:410:60//Hs.152250:AA203600

F-OVARC1000106//ESTs, Weakly similar to C25A1.1 [C.elegans]//2.9e-73:406:92//Hs.109463:AI205174

F-OVARC1000109

F-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//5.3e-135:663:96//Hs.3688:AF069250

F-OVARC1000114//Homo sapiens mRNA for KIAA0562 protein, complete cds//3.4e-43:532:72//Hs.118401:AB011134

F-OVARC1000133//ESTs//9.4e-50:249:98//Hs.159146:AI384010

F-OVARC1000139

F-OVARC1000145//ESTs//1.6e-09:87:90//Hs.25219:AA291293

F-OVARC1000148//ESTs//4.4e-28:146:100//Hs.133223:AA677414

F-OVARC1000151

F-OVARC1000168//ESTs//2.3e-48:264:95//Hs.14539:H67305

F-OVARC1000191//Thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth and development factor)//0.10:504:59//Hs.154083:U70136

F-OVARC1000198//ESTs//1.3e-103:505:97//Hs.149341:AI249131

F-OVARC1000209//EST//1.0:73:72//Hs.162600:AA594840

F-OVARC1000212//ESTs//1.7e-17:121:91//Hs.50473:W68834

F-OVARC1000240//ESTs, Highly similar to THREONYL-TRNA SYNTHETASE, CYTOP

LASMIC [Homo sapiens] //2.7e-31:264:79//Hs.151895:AA196379
 F-OVARC1000241//Homo sapiens clone 23698 mRNA sequence//3.4e-35:466:68//
 Hs.8136:U81984
 F-OVARC1000288//ESTs, Weakly similar to Y53C12A.3 [C.elegans] //0.00084:1
 70:65//Hs.107747:AI357868
 F-OVARC1000302//EST//4.1e-05:249:60//Hs.136432:AA555306
 F-OVARC1000304//ESTs//1.0:252:64//Hs.12126:AA203287
 F-OVARC1000309//ESTs, Highly similar to BRAIN ENRICHED HYALURONAN BINDI
 NG PROTEIN PRECURSOR [Felis catus] //0.51:193:66//Hs.6194:AI378579
 F-OVARC1000321
 F-OVARC1000326//Homo sapiens T-type calcium channel alpha-1 subunit mRNA
 , complete cds//0.0018:507:60//Hs.122359:AF051946
 F-OVARC1000335//ESTs//9.3e-39:202:98//Hs.132849:AA779444
 F-OVARC1000347
 F-OVARC1000384//Homo sapiens (clone PEBP2aA1) core-binding factor, runt
 domain, alpha subunit 1 (CBFA1) mRNA, 3' end of cds//3.4e-06:353:62//Hs.
 121895:AF001450
 F-OVARC1000408//Human mRNA for KIAA0140 gene, complete cds//0.94:231:64/
 /Hs.156016:D50930
 F-OVARC1000411//EST//0.43:234:59//Hs.124673:AA858162
 F-OVARC1000414//EST//5.2e-05:105:72//Hs.98827:AA435682
 F-OVARC1000420//Human mRNA for KIAA0140 gene, complete cds//0.86:231:58/
 /Hs.156016:D50930
 F-OVARC1000427//ESTs, Moderately similar to ORF1 [H.sapiens] //1.7e-25:19
 0:84//Hs.139513:AA259082
 F-OVARC1000431//ESTs//0.041:356:57//Hs.139907:AA621615
 F-OVARC1000437//Filamin 1 (actin-binding protein-280)//0.93:281:60//Hs.7
 6279:X53416
 F-OVARC1000440//Human PINCH protein mRNA, complete cds//8.8e-21:116:99//

Hs.83987:U09284
 F-OVARC1000442//ESTs//2.0e-19:207:78//Hs.134071:AI377423
 F-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds//3.
 2e-140:566:99//Hs.12334:AB014583
 F-OVARC1000461//ESTs//1.0e-39:215:95//Hs.131532:AI024524
 F-OVARC1000465//Homo sapiens clone 24781 mRNA sequence//1.0:252:58//Hs.1
 08112:AF070640
 F-OVARC1000466//ESTs//3.6e-14:189:71//Hs.164041:R51854
 F-OVARC1000473//ESTs//0.00012:77:85//Hs.29173:AA134926
 F-OVARC1000479
 F-OVARC1000486//ESTs//4.2e-07:409:60//Hs.99280:AA453036
 F-OVARC1000496//ESTs//6.0e-14:240:69//Hs.131900:AI023327
 F-OVARC1000520//Homo sapiens supervillin mRNA, complete cds//6.9e-115:53
 9:99//Hs.111285:AF051850
 F-OVARC1000526//ESTs//2.9e-08:368:61//Hs.42771:N26740
 F-OVARC1000533//EST//3.4e-14:137:82//Hs.123405:AA813492
 F-OVARC1000543//ESTs//0.13:278:61//Hs.54894:N98475
 F-OVARC1000556//ESTs//1.4e-31:217:90//Hs.106385:W26667
 F-OVARC1000557//ESTs//3.8e-20:208:76//Hs.138919:AA827410
 F-OVARC1000564//Human dsRNA adenosine deaminase DRADA2b (DRADA2b) mRNA,
 complete cds//0.87:135:66//Hs.85302:U76421
 F-OVARC1000573//ESTs//2.1e-22:268:76//Hs.121852:AA776358
 F-OVARC1000576//ESTs//9.4e-22:124:98//Hs.24220:W22200
 F-OVARC1000578//EST//4.7e-31:335:74//Hs.162881:AA652729
 F-OVARC1000588//Human BMK1 alpha kinase mRNA, complete cds//0.67:263:63/
 /Hs.3080:U29725
 F-OVARC1000605//EST//1.0:148:62//Hs.163346:AA883722
 F-OVARC1000622//EST//4.3e-50:313:88//Hs.149580:AI281881
 F-OVARC1000640//ESTs//2.6e-55:441:80//Hs.105319:AA470097

F-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, complete cds//1.6e-78:424:93//Hs.86859:D43772

F-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//1.6e-100:536:94//Hs.111862:AB011162

F-OVARC1000678//EST//1.3e-08:131:77//Hs.145970:AI277106

F-OVARC1000679//ESTs//0.66:223:61//Hs.134782:H74279

F-OVARC1000681//EST//0.017:315:61//Hs.147799:AI221639

F-OVARC1000682//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//4.8e-153:549:99//Hs.125315:AF027156

F-OVARC1000689//Homo sapiens clone 24640 mRNA sequence//0.030:479:57//Hs.4764:AB018306

F-OVARC1000700

F-OVARC1000703//ESTs//0.41:100:68//Hs.160699:AI284320

F-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds//1.2e-110:451:91//Hs.13476:AF038661

F-OVARC1000730//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//2.9e-53:318:91//Hs.7049:AI141736

F-OVARC1000746//ESTs//3.2e-123:570:99//Hs.127295:AA918411

F-OVARC1000769//ESTs//0.072:177:67//Hs.142573:AA601196

F-OVARC1000771//ESTs, Moderately similar to RAS-RELATED PROTEIN RAB-2 [H.sapiens]//1.2e-38:194:99//Hs.157059:W28130

F-OVARC1000781//ESTs//4.0e-14:113:89//Hs.41972:AA626793

F-OVARC1000787//EST//0.92:91:64//Hs.163258:AA828835

F-OVARC1000800//ESTs//1.6e-44:193:81//Hs.163971:N27584

F-OVARC1000802//ESTs//4.6e-43:395:80//Hs.115401:AA400032

F-OVARC1000834//ESTs//1.9e-91:431:99//Hs.154450:AA069390

F-OVARC1000846//Homo sapiens mRNA for KIAA0643 protein, partial cds//1.9e-151:432:100//Hs.155995:AB014543

F-OVARC1000850//Homo sapiens PB39 mRNA, complete cds//3.3e-137:632:99//H

s.18910:AF045584

F-OVARC1000862//ESTs, Highly similar to gene Fif protein [M.musculus]//6
.1e-31:183:93//Hs.108620:AA418155

F-OVARC1000876//Human DNA binding protein FKHL15 (FKHL15) mRNA, complete
cds//0.54:133:69//Hs.159234:U89995

F-OVARC1000883//ESTs//0.44:154:63//Hs.98183:AA417143

F-OVARC1000885//EST//0.91:152:63//Hs.160765:AI313323

F-OVARC1000886//ESTs//4.6e-08:375:61//Hs.131653:AI025777

F-OVARC1000890

F-OVARC1000891

F-OVARC1000897//ESTs//1.1e-07:145:69//Hs.119878:AA706818

F-OVARC1000912//EST//3.6e-08:376:61//Hs.158782:AI376601

F-OVARC1000915//Homo sapiens mRNA for KIAA0600 protein, partial cds//2.3
e-85:419:97//Hs.9028:AF039691

F-OVARC1000924//ESTs//3.6e-113:540:98//Hs.66058:AA424456

F-OVARC1000936//Human endogenous retrovirus envelope region mRNA (PL1)//
4.3e-64:623:72//Hs.114440:M11119

F-OVARC1000937//EST//2.4e-39:170:96//Hs.129138:AA988078

F-OVARC1000945//ESTs, Weakly similar to protein tyrosine phosphatase [H.
sapiens]//2.4e-29:157:97//Hs.136243:AA307843

F-OVARC1000948

F-OVARC1000959//EST//0.65:293:55//Hs.134725:AI088986

F-OVARC1000960//Ley I-L//1.4e-41:425:72//Hs.37062:AC005952

F-OVARC1000964//ESTs//1.4e-95:486:96//Hs.57079:D45288

F-OVARC1000971//ESTs//0.19:198:62//Hs.153429:AI283069

F-OVARC1000984//Breakpoint cluster region protein BCR//0.26:365:56//Hs.2
557:Y00661

F-OVARC1000996//Human p300/CBP-associated factor (P/CAF) mRNA, complete
cds//6.8e-10:312:65//Hs.155302:U57317

F-OVARC1000999//Homo sapiens mRNA for chemokine LEC precursor, complete cds//0.0056:209:62//Hs.10458:AF088219

F-OVARC1001000//EST//4.2e-24:242:77//Hs.128952:AA984114

F-OVARC1001004

F-OVARC1001010

F-OVARC1001011//ESTs, Moderately similar to Tera [M.musculus]//3.8e-47:234:99//Hs.110327:AA205866

F-OVARC1001032//HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDING PROTEIN 2//0.0076:624:57//Hs.75063:AL023584

F-OVARC1001034//ESTs, Highly similar to mitogen-induced [M.musculus]//3.9e-97:578:89//Hs.111974:AI050735

F-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds//8.6e-152:733:97//Hs.9899:AF099149

F-OVARC1001040//ESTs//2.2e-38:204:96//Hs.128927:AI168074

F-OVARC1001044//EST//0.036:304:61//Hs.137342:AA017385

F-OVARC1001051

F-OVARC1001055//Human pre-B cell enhancing factor (PBEF) mRNA, complete cds//1.1e-46:381:81//Hs.154968:U02020

F-OVARC1001062//ESTs//0.020:265:60//Hs.146226:AI312873

F-OVARC1001065//ESTs, Weakly similar to C50F4.12 [C.elegans]//1.4e-21:183:84//Hs.46680:AA809451

F-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds//6.6e-132:620:98//Hs.3426:AF082657

F-OVARC1001072//ESTs//1.1e-24:289:74//Hs.139614:AA709013

F-OVARC1001074//ESTs//0.059:198:63//Hs.59974:AA001937

F-OVARC1001085//H.sapiens mRNA for sortilin//0.99:142:67//Hs.104247:X982

48

F-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone I MAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berl

in))//1.3e-75:289:95//Hs.21753:AJ005897
 F-OVARC1001107//Homo sapiens SKB1Hs mRNA, complete cds//1.2e-73:351:86//
 Hs.12912:AF015913
 F-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds//2.
 1e-151:710:98//Hs.26584:AF051782
 F-OVARC1001117//ESTs//3.8e-73:347:99//Hs.116029:AA813102
 F-OVARC1001118
 F-OVARC1001129
 F-OVARC1001154//Granulin//2.4e-94:686:83//Hs.75451:AF055008
 F-OVARC1001161//ESTs//2.2e-40:208:97//Hs.113006:AA621725
 F-OVARC1001162
 F-OVARC1001167
 F-OVARC1001169//ESTs//0.81:158:63//Hs.48527:AI078279
 F-OVARC1001170//ESTs//9.0e-87:412:99//Hs.116550:AA813287
 F-OVARC1001171//ESTs//4.9e-26:167:79//Hs.139158:AA226159
 F-OVARC1001173//ESTs, Moderately similar to GLUTAMATE DEHYDROGENASE 1 P
 RECURSOR [Homo sapiens]//1.8e-11:192:69//Hs.130020:AA887581
 F-OVARC1001176//Homo sapiens chromosome 19, cosmid R26529//0.61:387:58//
 Hs.91103:AC005551
 F-OVARC1001180//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]
 //1.5e-13:199:71//Hs.109966:C06057
 F-OVARC1001188//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN
 VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]//1.4e-52:324:90//Hs.114673:
 W72675
 F-OVARC1001200//ESTs//3.9e-16:104:94//Hs.125520:AA883889
 F-OVARC1001232//Cyclin A//0.95:124:67//Hs.85137:X51688
 F-OVARC1001240//EST//0.017:351:60//Hs.120655:AA745676
 F-OVARC1001243//ESTs//0.78:291:59//Hs.132458:AI424825
 F-OVARC1001244//RING3 PROTEIN//2.8e-19:118:95//Hs.75243:D42040

F-OVARC1001261//EST//1.9e-42:225:96//Hs.158854:AI377837
 F-OVARC1001268//ESTs//0.66:239:61//Hs.132525:AA576821
 F-OVARC1001270//ESTs//0.99:204:60//Hs.144647:AA625224
 F-OVARC1001271//Homo sapiens mRNA for KIAA0643 protein, partial cds//6.8
 e-144:644:96//Hs.155995:AB014543
 F-OVARC1001282//ESTs, Weakly similar to Ydr438wp [S.cerevisiae]//0.11:35
 5:60//Hs.108812:AA044835
 F-OVARC1001296//ESTs//1.1e-46:237:98//Hs.33746:N78172
 F-OVARC1001306//Homo sapiens nuclear receptor co-repressor N-CoR mRNA, c
 omplete cds//0.20:188:64//Hs.152455:AF044209
 F-OVARC1001329//ESTs//1.4e-97:486:97//Hs.125886:AA884264
 F-OVARC1001330
 F-OVARC1001339//Solute carrier family 4, anion exchanger, member 2 (eryt
 hrocyte membrane protein band 3-like 1)//0.021:232:62//Hs.79410:U62531
 F-OVARC1001341//ESTs, Weakly similar to C17G10.1 [C.elegans]//2.5e-76:36
 3:99//Hs.105837:AA536054
 F-OVARC1001342//EST//0.98:97:65//Hs.148210:AA897493
 F-OVARC1001344//EST//5.3e-10:241:64//Hs.138777:N67251
 F-OVARC1001357//Homo sapiens jerky gene product homolog mRNA, complete c
 ds//0.64:198:61//Hs.105940:AF004715
 F-OVARC1001360//ESTs//4.9e-87:429:97//Hs.130145:AI264633
 F-OVARC1001369//ESTs//6.3e-07:371:62//Hs.131653:AI025777
 F-OVARC1001372//Homo sapiens mRNA for KIAA0654 protein, partial cds//1.4
 e-69:533:74//Hs.109299:AB014554
 F-OVARC1001376//Homo sapiens neuronal thread protein AD7c-NTP mRNA, comp
 lete cds//2.5e-49:365:73//Hs.129735:AF010144
 F-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involve
 d in B-CLL//4.1e-149:683:99//Hs.151428:AJ224819
 F-OVARC1001391//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA

, complete cds//0.097:235:65//Hs.25674:AF072242
 F-OVARC1001399//ESTs//1.1e-35:264:83//Hs.59379:W28225
 F-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds//1.3e-150:707:98//
 Hs.21586:AB006651
 F-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds//1.6e-49:586
 :69//Hs.74597:U52426
 F-OVARC1001425//ESTs//2.4e-11:258:67//Hs.119197:T83651
 F-OVARC1001436
 F-OVARC1001442
 F-OVARC1001453
 F-OVARC1001476//ESTs, Weakly similar to HYPOTHETICAL 38.6 KD PROTEIN IN
 TIF4631-KRE11 INTERGENIC REGION [S.cerevisiae]//1.9e-125:581:99//Hs.1109
 50:AI041823
 F-OVARC1001480//ESTs//0.95:125:72//Hs.152584:AA584568
 F-OVARC1001489//EST//4.9e-72:341:100//Hs.148191:AA897343
 F-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete
 cds//2.6e-86:479:92//Hs.6534:AF016507
 F-OVARC1001506//Polycystic kidney disease 1 (autosomal dominant)//1.1e-9
 7:538:92//Hs.75813:L33243
 F-OVARC1001525
 F-OVARC1001542//Envoplakin//0.34:258:60//Hs.25482:U53786
 F-OVARC1001547//EST//0.0046:237:62//Hs.54638:N90595
 F-OVARC1001555
 F-OVARC1001577//Homo sapiens SRp46 splicing factor retropseudogene mRNA/
 /6.8e-57:275:98//Hs.155160:AF031166
 F-OVARC1001600//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
 RY !!!! [H.sapiens]//0.0035:271:60//Hs.108465:AI144299
 F-OVARC1001610//ESTs, Weakly similar to F22E10.5 [C.elegans]//1.4e-43:21
 6:99//Hs.120002:AI038398

F-OVARC1001611
 F-OVARC1001615//EST//0.99:135:68//Hs.129410:AA993500
 F-OVARC1001668//Homo sapiens mRNA for KIAA0572 protein, partial cds//3.3
 e-37:217:94//Hs.14409:AB011144
 F-OVARC1001702//Homo sapiens mRNA for hSOX20 protein, complete cds//5.9e
 -49:393:81//Hs.95582:AB006867
 F-OVARC1001703//EST//1.7e-24:172:88//Hs.121198:AA757229
 F-OVARC1001711//Fms-related tyrosine kinase 3 ligand//0.049:353:61//Hs.4
 28:U03858
 F-OVARC1001713//ESTs//8.9e-37:263:86//Hs.110298:AA621807
 F-OVARC1001726//ESTs//2.0e-12:121:82//Hs.153332:AA236863
 F-OVARC1001731//Tropomyosin beta chain (skeletal muscle)//1.7e-83:617:80
 //Hs.155652:X06825
 F-OVARC1001745//EST//0.75:174:64//Hs.146778:AI148588
 F-OVARC1001762
 F-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eI
 F3, p35 subunit mRNA, complete cds//1.4e-150:706:98//Hs.155377:U97670
 F-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds//9.
 8e-117:580:96//Hs.15869:AB014575
 F-OVARC1001768//ESTs//0.035:179:64//Hs.87279:AI218697
 F-OVARC1001791
 F-OVARC1001795//ESTs//0.19:68:76//Hs.37699:AA062830
 F-OVARC1001802//EST//3.7e-45:254:92//Hs.130620:AI005102
 F-OVARC1001805//Homo sapiens mRNA for KIAA0744 protein, complete cds//0.
 77:362:58//Hs.116753:AB018287
 F-OVARC1001809//Human N-type calcium channel alpha-1 subunit mRNA, compl
 ete cds//2.2e-07:435:62//Hs.69949:M94172
 F-OVARC1001812//ESTs//3.0e-47:360:83//Hs.141756:AA700825
 F-OVARC1001813//EST//1.8e-57:277:100//Hs.162414:AA573453

F-OVARC1001820//ESTs//1.4e-64:310:99//Hs.137398:AA164567
F-OVARC1001828//EST//1.0e-09:184:66//Hs.130435:AA923537
F-OVARC1001846//ESTs//1.8e-80:410:97//Hs.114539:N54973
F-OVARC1001861
F-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence//3.9e-20:122:95//Hs.25300:AF070611
F-OVARC1001879//Homo sapiens putative tumor suppressor gene 26 protein alpha 2 delta calcium channel subunit mRNA, complete cds//0.042:199:67//Hs.127436:AF040709
F-OVARC1001880//Interferon regulatory factor 5//1.1e-06:489:60//Hs.54434:U51127
F-OVARC1001883//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//9.5e-33:509:68//Hs.158095:AB007953
F-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//2.6e-57:300:96//Hs.6216:AF061749
F-OVARC1001901//ESTs//2.3e-07:185:69//Hs.145630:AI263834
F-OVARC1001911//EST//0.88:101:66//Hs.162622:AA601261
F-OVARC1001916//H.sapiens mRNA for prepronociceptin//1.0:540:58//Hs.89040:U48263
F-OVARC1001928
F-OVARC1001942//Human plectin (PLEC1) mRNA, complete cds//0.038:290:62//Hs.79706:U53204
F-OVARC1001943//ESTs, Weakly similar to HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME III [C.elegans] //2.3e-119:565:98//Hs.5392:AA313794
F-OVARC1001949//KRAB zinc finger protein {alternative products} //1.8e-17:294:67//Hs.22556:U37251
F-OVARC1001950//ESTs//1.5e-15:300:65//Hs.138501:AI051228
F-OVARC1001987//ESTs//6.7e-34:202:92//Hs.115600:AA351639
F-OVARC1001989//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT

RY !!!! [H.sapiens] //1.2e-23:213:78//Hs.105292:AA504776
 F-OVARC1002044//EST//0.26:164:66//Hs.161094:N30417
 F-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//6.6
 e-160:739:98//Hs.108258:AB007934
 F-OVARC1002066//ESTs//1.8e-103:482:99//Hs.124923:AI375865
 F-OVARC1002082//EST//2.5e-09:213:67//Hs.112810:AA610063
 F-OVARC1002107
 F-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds//2.7
 e-101:498:96//Hs.75258:AF054174
 F-OVARC1002127//ESTs//1.6e-76:397:96//Hs.33432:R83913
 F-OVARC1002138//Homo sapiens p60 katanin mRNA, complete cds//3.5e-20:399
 :62//Hs.112725:AF056022
 F-OVARC1002143//EST//4.2e-09:240:65//Hs.140547:AA812795
 F-OVARC1002156//EST//0.35:112:66//Hs.136761:AA738097
 F-OVARC1002158//ESTs, Weakly similar to Y53C12A.3 [C.elegans] //7.4e-07:3
 29:58//Hs.107747:AI357868
 F-OVARC1002165//H.sapiens BDP1 mRNA for protein-tyrosine-phosphatase//0.
 00010:300:64//Hs.118929:X79568
 F-OVARC1002182//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.19:17
 8:64//Hs.108447:AJ000517
 F-PLACE1000004//ESTs//0.79:332:59//Hs.120221:AA731230
 F-PLACE1000005//ESTs//1.8e-10:89:87//Hs.158913:AI378928
 F-PLACE1000007//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA,
 partial cds//1.2e-52:550:72//Hs.42400:AF022789
 F-PLACE1000014
 F-PLACE1000031
 F-PLACE1000040//ESTs//3.1e-18:123:91//Hs.138387:AA873088
 F-PLACE1000048//ESTs//1.2e-43:387:78//Hs.61199:AA024494
 F-PLACE1000050//ESTs//1.8e-84:421:96//Hs.128632:AI076755

F-PLACE1000061//Ribosomal protein L37a//5.5e-29:177:93//Hs.1946:L06499
 F-PLACE1000066//ESTs, Weakly similar to coded for by C. elegans cDNA yk1
 Oc10.3 [C.elegans] //1.4e-47:266:93//Hs.30026:AI356771
 F-PLACE1000078//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING E
 NTRY !!!! [H.sapiens] //6.4e-15:203:70//Hs.157422:R85366
 F-PLACE1000081//Human transporter protein (g17) mRNA, complete cds//0.30
 :324:60//Hs.76460:U49082
 F-PLACE1000094
 F-PLACE1000133//ESTs, Highly similar to TRANSCRIPTION FACTOR BTF3 [Homo
 sapiens] //6.2e-82:476:92//Hs.111081:AI380378
 F-PLACE1000142//ESTs, Weakly similar to enoyl-CoA hydratase [H.sapiens] /
 /7.7e-27:205:85//Hs.9670:AA632135
 F-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, compl
 ete cds//2.5e-151:737:97//Hs.151017:AF058291
 F-PLACE1000185
 F-PLACE1000213
 F-PLACE1000214//ESTs//0.00059:335:59//Hs.143849:AI167255
 F-PLACE1000236//Fanconi anemia, complementation group A//0.44:306:61//Hs
 .86297:X99226
 F-PLACE1000246//ESTs//7.3e-80:457:89//Hs.57209:W22022
 F-PLACE1000292//ESTs//1.8e-05:323:60//Hs.59962:AI278202
 F-PLACE1000308//EST//0.0024:253:62//Hs.144238:W52294
 F-PLACE1000332//EST//5.6e-18:223:74//Hs.99532:AA461047
 F-PLACE1000347//ESTs//6.4e-33:169:99//Hs.122975:AA428675
 F-PLACE1000374//Human CCAAT-box-binding factor (CBF) mRNA, complete cds/
 /0.26:45:95//Hs.147991:M37197
 F-PLACE1000380//Homo sapiens proline and glutamic acid rich nuclear prot
 ein isoform mRNA, partial cds//1.0:262:58//Hs.102732:U88153
 F-PLACE1000383//Myotubular myopathy 1//1.1e-50:669:67//Hs.75302:U46024

F-PLACE1000401//Homo sapiens mRNA for KIAA0616 protein, partial cds//0.0
36:471:58//Hs.6051:AB014516

F-PLACE1000406//ESTs, Highly similar to PTB-ASSOCIATED SPLICING FACTOR
[Homo sapiens]//8.7e-63:346:93//Hs.19501:AA742260

F-PLACE1000420//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.0
023:216:65//Hs.37656:AB011174

F-PLACE1000421//Human lipid-activated protein kinase PRK1 mRNA, complete
cds//0.55:212:63//Hs.2499:U33053

F-PLACE1000424

F-PLACE1000435//Homo sapiens mRNA for XPR2 protein//0.58:674:55//Hs.4476
6:AJ007590

F-PLACE1000444//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltrans
ferase, Bombay phenotype included)//2.7e-52:421:80//Hs.69747:M35531

F-PLACE1000453//Human mRNA for MTG8a protein, complete cds//0.026:240:60
//Hs.31551:D43638

F-PLACE1000481//Oxytocin receptor//1.6e-25:347:71//Hs.2820:X64878

F-PLACE1000492//Human mRNA for KIAA0355 gene, complete cds//0.58:302:60/
/Hs.153014:AB002353

F-PLACE1000540//EST//0.32:229:59//Hs.163011:AA700573

F-PLACE1000547//Human heparan sulfate proteoglycan (HSPG2) mRNA, complet
e cds//0.0046:223:65//Hs.75578:M85289

F-PLACE1000562

F-PLACE1000564//ESTs//8.0e-35:247:89//Hs.12999:AA278538

F-PLACE1000583//Homo sapiens clone 23939 mRNA sequence//6.6e-47:525:72//
Hs.21838:AF038179

F-PLACE1000588//Guanylate binding protein 1, interferon-inducible, 67kD/
/2.3e-85:503:88//Hs.62661:M55542

F-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//1.2e
-165:798:97//Hs.159597:AJ012449

F-PLACE1000599//ESTs//0.65:201:58//Hs.98216:AA758751
 F-PLACE1000610//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.9
 8:215:60//Hs.8152:AB014542
 F-PLACE1000611//ESTs//7.2e-20:406:64//Hs.128966:AA620986
 F-PLACE1000636
 F-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA,
 complete cds//5.0e-154:747:96//Hs.5819:AF102265
 F-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone I
 MAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin))//7.5e-158:775:97//Hs.2959
 5:AJ005896
 F-PLACE1000706//Homo sapiens transcription intermediary factor 1 (TIF1)
 mRNA, complete cds//1.0e-57:675:69//Hs.128763:AF009353
 F-PLACE1000712//EST//0.56:171:61//Hs.112790:AA609949
 F-PLACE1000716//Human mRNA for KIAA0258 gene, complete cds//6.1e-38:426:
 70//Hs.47313:D87447
 F-PLACE1000748//ESTs//2.6e-43:233:95//Hs.110754:AA112288
 F-PLACE1000749//Human MAGE-9 antigen (MAGE9) gene, complete cds//0.72:33
 1:57//Hs.37110:U10694
 F-PLACE1000755//NUCLEOLIN//0.0038:186:66//Hs.79110:M60858
 F-PLACE1000769
 F-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds//1.1
 e-139:663:98//Hs.31921:AB014548
 F-PLACE1000786//Myosin, heavy polypeptide 9, non-muscle//8.5e-06:362:59/
 /Hs.44782:Z82215
 F-PLACE1000793//ESTs//2.7e-62:315:97//Hs.16141:W56079
 F-PLACE1000798//ESTs//1.4e-55:316:93//Hs.139119:N32189
 F-PLACE1000841//EST//0.47:143:61//Hs.144096:AI032180
 F-PLACE1000849//Homo sapiens CAGF9 mRNA, partial cds//1.6e-06:266:63//Hs
 .110826:U80736

F-PLACE1000856//ESTs//2.6e-60:319:96//Hs.25994:AA470000
 F-PLACE1000863//EST//9.4e-29:249:78//Hs.121919:AA777428
 F-PLACE1000909//ESTs//0.97:214:60//Hs.128601:AA906455
 F-PLACE1000931//ESTs//2.1e-46:592:70//Hs.154244:AA195201
 F-PLACE1000948
 F-PLACE1000972//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds//7.9e-10:294:66//Hs.80261:L43821
 F-PLACE1000977//ESTs, Weakly similar to coded for by C. elegans cDNA yk2
 8h2.5 [C.elegans]//9.3e-45:309:88//Hs.13531:R61789
 F-PLACE1000979//Zinc finger protein 91 (HPF7, HTF10)//0.0034:229:62//Hs.
 8597:L11672
 F-PLACE1000987//Homo sapiens mRNA for KIAA0724 protein, complete cds//2.
 6e-141:694:96//Hs.158497:AB018267
 F-PLACE1001000//ESTs//0.0035:116:73//Hs.144532:H39913
 F-PLACE1001007//Guanylate cyclase 2D, membrane (retina-specific)//0.050:
 338:61//Hs.1974:M92432
 F-PLACE1001010//H.sapiens mRNA for retrotransposon//1.6e-45:371:80//Hs.6
 940:Z48633
 F-PLACE1001015//ESTs//8.6e-27:211:71//Hs.88040:AA256876
 F-PLACE1001024
 F-PLACE1001036//EST//1.0:133:65//Hs.161424:AI424741
 F-PLACE1001054//Human plectin (PLEC1) mRNA, complete cds//0.98:284:59//H
 s.79706:U53204
 F-PLACE1001062
 F-PLACE1001076//EST//0.84:223:59//Hs.161147:AI417859
 F-PLACE1001088
 F-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds//1.0e-96
 :489:96//Hs.95448:AF065485
 F-PLACE1001104//ESTs//0.19:249:64//Hs.152627:AA595817

F-PLACE1001118//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds//8.2e-66:676:71//Hs.150406:AF022158

F-PLACE1001136//Amphiregulin (schwannoma-derived growth factor)//1.5e-16:122:91//Hs.1257:M30704

F-PLACE1001168

F-PLACE1001171//ESTs//4.3e-12:214:72//Hs.141392:R95135

F-PLACE1001185//ESTs, Weakly similar to ZK792.1 [C.elegans]//1.6e-28:421:66//Hs.8763:W30741

F-PLACE1001238

F-PLACE1001241//ESTs//1.1e-22:225:79//Hs.159786:R49494

F-PLACE1001257//ESTs//1.9e-23:165:89//Hs.126518:AA913929

F-PLACE1001272//COATOMER BETA' SUBUNIT//0.012:50:96//Hs.75724:X70476

F-PLACE1001279//ESTs//0.97:377:59//Hs.152628:N51283

F-PLACE1001280//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.2e-08:586:58//Hs.124161:AF065164

F-PLACE1001294//Homo sapiens mRNA for myosin phosphatase target subunit 1 (MYPT1)//0.91:221:61//Hs.16533:D87930

F-PLACE1001304//Human zinc finger protein mRNA, complete cds//8.6e-08:370:60//Hs.42672:AF016052

F-PLACE1001311//ESTs//1.7e-44:480:73//Hs.155384:Z78385

F-PLACE1001323//ESTs//1.1e-25:151:95//Hs.134120:AA699591

F-PLACE1001351

F-PLACE1001366//Homo sapiens mRNA for KIAA0799 protein, partial cds//2.8e-26:155:95//Hs.61638:AB018342

F-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds//3.4e-44:393:79//Hs.152005:AF009615

F-PLACE1001383//ESTs//1.0:159:65//Hs.128501:AA973748

F-PLACE1001384//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//2.6e-09:117:84//Hs.21301:AF093419

F-PLACE1001387//ESTs, Weakly similar to EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 [H.sapiens]//0.00083:187:64//Hs.5399:N30646

F-PLACE1001395//Homo sapiens mRNA for putative DNA methyltransferase, complete CDS//0.0038:496:57//Hs.97681:AJ223333

F-PLACE1001399//Human melanoma antigen recognized by T-cells (MART-1) mRNA//7.0e-45:456:75//Hs.154069:U06452

F-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence//6.5e-71:365:96//Hs.110404:AF091087

F-PLACE1001414//EST//1.2e-75:364:98//Hs.136622:AA633232

F-PLACE1001440//ESTs//2.8e-05:163:66//Hs.141082:H18987

F-PLACE1001456//EST//0.95:132:61//Hs.20373:R09510

F-PLACE1001468//ESTs//0.00019:184:66//Hs.126536:AI379455

F-PLACE1001484//EST//8.6e-18:190:76//Hs.160992:H52716

F-PLACE1001502//Apolipoprotein E//2.5e-05:306:60//Hs.76260:M12529

F-PLACE1001503

F-PLACE1001517//ESTs//1.9e-12:138:78//Hs.120352:AA718914

F-PLACE1001534//EST//0.015:121:65//Hs.144156:R85753

F-PLACE1001545

F-PLACE1001551

F-PLACE1001570//EST//0.58:286:59//Hs.120202:AA728835

F-PLACE1001602//Human POU domain protein (Brn-3b) mRNA, complete cds//0.013:159:66//Hs.266:U06233

F-PLACE1001603//Homo sapiens nitrilase 1 (NIT1) mRNA, complete cds//1.1e-10:133:77//Hs.146406:AF069987

F-PLACE1001608//ESTs//0.022:187:60//Hs.145915:AI342230

F-PLACE1001610//ESTs//1.4e-77:377:97//Hs.115700:AA808005

F-PLACE1001611//Human faciogenital dysplasia (FGD1) mRNA, complete cds//0.96:141:66//Hs.1572:U11690

F-PLACE1001632//Homo sapiens mRNA for KIAA0798 protein, complete cds//3.

4e-76:702:75//Hs.159277:AB018341

F-PLACE1001634//ESTs//1.2e-43:260:92//Hs.134064:AI276198

F-PLACE1001640

F-PLACE1001672//EST//2.8e-21:201:82//Hs.123341:AA810927

F-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48

-18) mRNA, complete cds//2.8e-148:726:96//Hs.3688:AF069250

F-PLACE1001692//ESTs, Highly similar to S-ACYL FATTY ACID SYNTHASE THIO
ESTERASE, MEDIUM CHAIN [Rattus norvegicus]//1.1e-95:481:92//Hs.24309:AI1
25696

F-PLACE1001705//Human RNA polymerase III subunit (RPC39) mRNA, complete
cds//6.0e-30:347:76//Hs.101555:U93869

F-PLACE1001716//Human mRNA for KIAA0191 gene, partial cds//2.1e-69:369:7
3//Hs.12413:D83776

F-PLACE1001720//ESTs//1.2e-27:146:99//Hs.106432:AI391686

F-PLACE1001729//Homo sapiens mRNA for KIAA0522 protein, partial cds//0.0
084:484:60//Hs.129892:AB011094

F-PLACE1001739//Histidine-rich calcium binding protein//0.14:240:64//Hs.
1480:M60052

F-PLACE1001740//ESTs//4.9e-32:343:74//Hs.139158:AA226159

F-PLACE1001745

F-PLACE1001746//ESTs//7.0e-15:168:80//Hs.46601:N78361

F-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds/
/2.8e-160:773:97//Hs.4812:AF061243

F-PLACE1001756//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.7e-3
5:269:83//Hs.5247:AF029750

F-PLACE1001761//ESTs//6.9e-27:159:93//Hs.78277:AA131283

F-PLACE1001771//Human putative calcium influx channel (htrp3) mRNA, comp
lete cds//3.4e-52:548:72//Hs.150981:U47050

F-PLACE1001781

F-PLACE1001799//EST//5.4e-07:145:70//Hs.121840:AA776115
 F-PLACE1001810//ESTs//0.024:134:67//Hs.43134:AA766138
 F-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta s
 ubunit (SCS) mRNA, partial cds//3.6e-110:546:96//Hs.40820:AF058953
 F-PLACE1001821
 F-PLACE1001844//ESTs//5.4e-45:387:79//Hs.61199:AA024494
 F-PLACE1001845//ESTs//2.5e-47:232:100//Hs.120809:AA150214
 F-PLACE1001869//EST//1.0:139:59//Hs.122285:AA781906
 F-PLACE1001897//ESTs//0.29:348:57//Hs.139993:AI343257
 F-PLACE1001912//ESTs//4.0e-10:95:89//Hs.13475:R18220
 F-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cd
 s//4.0e-153:685:95//Hs.17839:AF099936
 F-PLACE1001928//H.sapiens HUMM9 mRNA//0.063:196:66//Hs.2750:X74837
 F-PLACE1001983//Homo sapiens Jagged 2 mRNA, complete cds//9.8e-06:431:58
 //Hs.106387:AF029778
 F-PLACE1001989
 F-PLACE1002004
 F-PLACE1002046
 F-PLACE1002052//Human mRNA for phospholipase C, complete cds//0.0092:465
 :58//Hs.153322:D42108
 F-PLACE1002066//EST//0.49:307:61//Hs.150652:AA908555
 F-PLACE1002072//EST//1.0:103:65//Hs.116488:F13707
 F-PLACE1002073//Homo sapiens mRNA for KIAA0606 protein, partial cds//4.2
 e-39:635:64//Hs.38176:AB011178
 F-PLACE1002090//Homo sapiens signal recognition particle 72 (SRP72) mRNA
 , complete cds//4.3e-83:388:99//Hs.5171:AF069765
 F-PLACE1002115//EST//0.18:215:62//Hs.135747:AI002637
 F-PLACE1002119//Human transcription factor ETR101 mRNA, complete cds//6.
 2e-13:384:61//Hs.737:M62831

F-PLACE1002140//EST, Moderately similar to ALPHA-1-ANTITRYPSIN PRECURSOR
R [Homo sapiens]//0.89:60:75//Hs.144290:T61747
F-PLACE1002150//ESTs//0.56:245:64//Hs.24119:AA115631
F-PLACE1002157//Human mRNA for KIAA0392 gene, partial cds//2.8e-51:440:7
9//Hs.40100:AB002390
F-PLACE1002163//ESTs//0.76:212:61//Hs.112494:AI366891
F-PLACE1002170//ESTs//6.5e-09:108:76//Hs.41418:H90627
F-PLACE1002171//ESTs//3.5e-81:493:89//Hs.122553:H66674
F-PLACE1002205//Human clone 23695 mRNA sequence//0.00080:472:60//Hs.9079
8:U79289
F-PLACE1002213//ESTs//0.041:146:67//Hs.119162:AA399989
F-PLACE1002227//ESTs//9.4e-06:173:66//Hs.127882:AI024442
F-PLACE1002256//ESTs//1.8e-93:440:99//Hs.128700:AA970935
F-PLACE1002259//Human Line-1 repeat mRNA with 2 open reading frames//2.3
e-75:434:83//Hs.23094:M19503
F-PLACE1002319//ESTs//0.82:188:62//Hs.50918:AA036675
F-PLACE1002342//EST//0.61:148:66//Hs.144319:AA280279
F-PLACE1002395//ESTs//1.2e-18:168:83//Hs.3853:AA034291
F-PLACE1002399//EST//0.0011:166:65//Hs.137500:AA436710
F-PLACE1002433//ESTs//1.2e-14:151:80//Hs.161837:AA421067
F-PLACE1002437//Human ATP binding cassette transporter (ABCR) mRNA, complete
cds//2.6e-23:458:66//Hs.40993:AF000148
F-PLACE1002438//EST//0.81:48:77//Hs.158575:AI368947
F-PLACE1002450//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA,
complete cds//7.1e-07:270:66//Hs.150406:AF022158
F-PLACE1002465
F-PLACE1002474//Homo sapiens mRNA for matrilin-4, partial//1.3e-14:369:6
3//Hs.129361:AJ007581
F-PLACE1002477//ESTs//3.5e-13:125:71//Hs.145032:AA343523

F-PLACE1002493

F-PLACE1002499

F-PLACE1002500//Human putative zinc transporter ZnT-3 (ZnT-3) mRNA, complete cds//4.3e-19:708:59//Hs.111967:U76010

F-PLACE1002514//ESTs//3.1e-07:178:66//Hs.70932:AA126482

F-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds//2.9e-144:583:95//Hs.88756:AB018256

F-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1//3.1e-115:566:96//Hs.99348:AC004774

F-PLACE1002537//Thiopurine S-methyltransferase//1.9e-28:198:86//Hs.51124:AF019369

F-PLACE1002571//Homo sapiens mRNA for TP55, complete cds//0.99:274:59//Hs.138202:AF027866

F-PLACE1002578//ESTs//7.3e-10:185:73//Hs.41418:H90627

F-PLACE1002583//EST//0.0028:348:61//Hs.160396:AI393725

F-PLACE1002591//Human mRNA for actin binding protein p57, complete cds//2.8e-27:279:74//Hs.109606:D44497

F-PLACE1002598//EST//0.011:209:62//Hs.131470:AI024187

F-PLACE1002604//EST//0.47:220:61//Hs.145434:AI198915

F-PLACE1002625

F-PLACE1002655//GELSOLIN PRECURSOR, PLASMA//1.7e-36:693:62//Hs.80562:X04412

F-PLACE1002665//EST//0.15:156:65//Hs.161793:AA380706

F-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds//1.1e-187:804:97//Hs.124903:AF068180

F-PLACE1002714//Human involucrin mRNA//3.6e-08:509:60//Hs.157091:M13903

F-PLACE1002722//Human protease-activated receptor 3 (PAR3) mRNA, complete cds//0.34:230:58//Hs.159196:U92971

F-PLACE1002768//EST//0.37:126:69//Hs.125353:AA877080

F-PLACE1002772//ESTs//0.0017:147:69//Hs.132439:AA923728
 F-PLACE1002775//EST//5.5e-09:129:75//Hs.135336:AI049827
 F-PLACE1002782//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//0.0031:298:62//Hs.26285:AF082516
 F-PLACE1002794//ESTs//0.71:125:66//Hs.97441:AI368926
 F-PLACE1002811//Human mRNA for KIAA0172 gene, partial cds//5.8e-46:567:70//Hs.77546:D79994
 F-PLACE1002815
 F-PLACE1002816//Homo sapiens mRNA for KIAA0600 protein, partial cds//4.3e-70:687:73//Hs.9028:AF039691
 F-PLACE1002834//ESTs//2.6e-41:393:74//Hs.120206:AI089163
 F-PLACE1002839//ESTs//0.26:177:63//Hs.149013:AI334167
 F-PLACE1002851//EST//0.0034:102:72//Hs.129630:AI000405
 F-PLACE1002853//ESTs//1.1e-20:136:90//Hs.125895:AA889024
 F-PLACE1002881//Interleukin 10//1.1e-41:454:72//Hs.2180:M57627
 F-PLACE1002908//ESTs//3.8e-48:325:88//Hs.54702:AI040029
 F-PLACE1002941//ESTs//5.0e-18:128:88//Hs.17376:AA855056
 F-PLACE1002962
 F-PLACE1002968//ESTs, Highly similar to trg gene product [R.norvegicus]//0.031:372:59//Hs.8021:AI041815
 F-PLACE1002991
 F-PLACE1002993
 F-PLACE1002996//ESTs, Weakly similar to T20D3.3 [C.elegans]//1.3e-12:104:86//Hs.124808:T86959
 F-PLACE1003025//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0510//0.99:192:64//Hs.92660:AB007979
 F-PLACE1003027//Homo sapiens mRNA for KIAA0516 protein, partial cds//2.0e-131:632:97//Hs.129872:AB011088
 F-PLACE1003044//Homo sapiens mRNA for KIAA0667 protein, partial cds//2.7

e-14:555:58//Hs.154740:AB014567
F-PLACE1003045
F-PLACE1003092//ESTs//1.1e-108:506:99//Hs.22119:AA885491
F-PLACE1003100//Human Hep27 protein mRNA, complete cds//2.9e-66:650:73//
Hs.102137:U31875
F-PLACE1003108//EST//0.016:181:65//Hs.119762:AA703419
F-PLACE1003136
F-PLACE1003145
F-PLACE1003153//ESTs//3.1e-09:209:65//Hs.111583:AA463590
F-PLACE1003174//ESTs//0.073:97:69//Hs.12992:W01997
F-PLACE1003176//ESTs//3.3e-60:296:90//Hs.58239:AA215797
F-PLACE1003190//Homo sapiens C19steroid specific UDP-glucuronosyltransfe
rase mRNA, complete cds//0.98:221:60//Hs.139756:U59209
F-PLACE1003200//EST//0.0021:309:60//Hs.140561:AA765532
F-PLACE1003205//EST//1.2e-07:204:65//Hs.147372:AI208770
F-PLACE1003238//ESTs//7.4e-62:343:94//Hs.121302:AA758208
F-PLACE1003249//Insulin-like growth factor 1 (somatomedia C)//0.99:175:6
2//Hs.85112:X57025
F-PLACE1003256
F-PLACE1003258//H.sapiens mRNA for ZYG homologue//0.00020:217:64//Hs.292
85:X99802
F-PLACE1003296//ESTs//2.6e-14:80:86//Hs.155441:AA533106
F-PLACE1003302//Human repressor transcriptional factor (ZNF85) mRNA, com
plete cds//4.3e-51:700:67//Hs.37138:U35376
F-PLACE1003334
F-PLACE1003342//ESTs//0.94:310:57//Hs.131502:AI023308
F-PLACE1003343//EST//1.2e-09:114:77//Hs.103418:AA035568
F-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 pro
tein (BCAR3) mRNA, complete cds//2.6e-144:773:92//Hs.6564:U92715

F-PLACE1003361//ESTs, Weakly similar to ATP SYNTHASE A CHAIN [Trypanosoma
a brucei brucei] //8.9e-35:332:78//Hs.163820:H71277

F-PLACE1003366//Homo sapiens dysferlin mRNA, complete cds//7.9e-06:502:5
7//Hs.143897:AF075575

F-PLACE1003369//NUCLEOLIN//0.00037:282:60//Hs.79110:M60858

F-PLACE1003373//EST//1.1e-11:420:63//Hs.156592:AI343009

F-PLACE1003375//EST//0.75:119:68//Hs.160270:AI149069

F-PLACE1003383

F-PLACE1003394//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-14 [Rat
tus norvegicus] //8.9e-113:590:94//Hs.125175:AI142546

F-PLACE1003401//ESTs//0.55:176:66//Hs.154292:AA886178

F-PLACE1003420//Macrophage stimulating 1 (hepatocyte growth factor-like)
//0.40:206:62//Hs.30223:X90846

F-PLACE1003454//ESTs//0.98:74:72//Hs.127131:AA150912

F-PLACE1003478//EST//5.0e-06:183:69//Hs.127524:AA952874

F-PLACE1003493//Protein-tyrosine kinase 7//0.98:232:63//Hs.90572:U33635

F-PLACE1003516//Human kpni repeat mRNA (cdna clone pcd-kpni-8), 3' end//
3.4e-85:357:86//Hs.103948:K00627

F-PLACE1003519//ESTs//1.6e-33:288:72//Hs.159510:AA297145

F-PLACE1003521//H.sapiens mRNA for retrotransposon//1.4e-45:269:76//Hs.6
940:Z48633

F-PLACE1003528//ESTs//0.65:120:68//Hs.162376:AA570248

F-PLACE1003537//ESTs, Weakly similar to ZK858.6 [C.elegans] //3.6e-110:54
3:97//Hs.120416:AA057428

F-PLACE1003553

F-PLACE1003566//ESTs//0.0015:508:59//Hs.5724:AA156780

F-PLACE1003575//Homo sapiens cdc14 homolog mRNA, complete cds//4.4e-05:4
99:58//Hs.65993:AF000367

F-PLACE1003583//ESTs//5.5e-19:448:63//Hs.161701:AA225932

F-PLACE1003584//EST//1.6e-46:263:94//Hs.147412:AI209194
 F-PLACE1003592//ESTs, Moderately similar to !!!! ALU CLASS B WARNING ENT
 RY !!!! [H.sapiens]//1.4e-50:287:93//Hs.154799:AA130620
 F-PLACE1003593//ESTs//0.0025:318:61//Hs.106771:AA806965
 F-PLACE1003596//Integral transmembrane protein 1//1.9e-54:685:68//Hs.896
 50:L38961
 F-PLACE1003602//Homo sapiens mRNA expressed in placenta//3.4e-140:679:97
 //Hs.56851:D83200
 F-PLACE1003605//Homo sapiens Cdc14B2 phosphatase mRNA, partial cds//0.00
 065:236:64//Hs.22116:AF064104
 F-PLACE1003611//EST//0.00015:318:59//Hs.28788:R66896
 F-PLACE1003618//Human Line-1 repeat mRNA with 2 open reading frames//1.3
 e-122:737:87//Hs.23094:M19503
 F-PLACE1003625//ESTs//1.6e-16:103:96//Hs.111223:N51105
 F-PLACE1003638//ESTs//0.60:305:57//Hs.19104:W07762
 F-PLACE1003669//ESTs, Weakly similar to 3-7 gene product [H.sapiens]//0.
 021:445:58//Hs.158275:AI365413
 F-PLACE1003704//Human mRNA for KIAA0301 gene, partial cds//0.014:622:56/
 /Hs.76730:AB002299
 F-PLACE1003709//Homo sapiens protein kinase (BUB1) mRNA, complete cds//1
 .4e-133:669:95//Hs.98658:AF053305
 F-PLACE1003711//ESTs//2.2e-14:178:77//Hs.114831:T57101
 F-PLACE1003723//Homo sapiens mRNA for T lymphocyte specific adaptor pro
 tein//8.5e-09:393:60//Hs.103527:AJ000553
 F-PLACE1003738//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapien
 s]//1.8e-53:260:99//Hs.102928:AI346344
 F-PLACE1003760//ESTs//5.1e-08:334:63//Hs.43675:AA805648
 F-PLACE1003762//ESTs//1.0:59:83//Hs.29863:W28983
 F-PLACE1003768//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//

2.7e-40:608:68//Hs.139107:K00629
F-PLACE1003771//ESTs//6.6e-10:226:65//Hs.15776:T91944
F-PLACE1003783
F-PLACE1003784//Homo sapiens mRNA for KIAA0765 protein, partial cds//1.0
:457:57//Hs.62318:AB018308
F-PLACE1003795//Human homologue of yeast sec7 mRNA, complete cds//0.85:3
14:60//Hs.1050:M85169
F-PLACE1003833//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.00059:201
:68//Hs.40806:AA018786
F-PLACE1003850//ESTs//0.0088:220:61//Hs.145504:AI254165
F-PLACE1003858//EST//0.77:137:61//Hs.146935:AI168124
F-PLACE1003864//ESTs//0.11:225:59//Hs.160910:AI370359
F-PLACE1003870//EST//7.2e-18:283:69//Hs.135497:AI091257
F-PLACE1003885//H.sapiens PAP mRNA//2.4e-75:759:72//Hs.49007:X76770
F-PLACE1003886
F-PLACE1003888//Human mRNA for phospholipase C, complete cds//8.4e-55:70
2:67//Hs.153322:D42108
F-PLACE1003892//ESTs//2.4e-13:258:67//Hs.28039:H24050
F-PLACE1003900//ESTs//3.5e-14:271:66//Hs.28589:AI004944
F-PLACE1003903//CTP synthetase//1.6e-49:528:71//Hs.84112:X52142
F-PLACE1003915//ESTs, Highly similar to ARGINYL-TRNA SYNTHETASE, MITOCH
ONDRIAL PRECURSOR [Saccharomyces cerevisiae]//1.2e-49:251:98//Hs.65831:F
03069
F-PLACE1003923//Interferon, alpha 16//0.48:278:60//Hs.56303:M28585
F-PLACE1003932//EST//0.00060:221:63//Hs.163044:AA707537
F-PLACE1003936//ESTs//0.86:211:62//Hs.150751:AI123536
F-PLACE1003968//Human 5'-AMP-activated protein kinase, gamma-1 subunit m
RNA, complete cds//2.0e-47:522:71//Hs.3136:U42412
F-PLACE1004103//ESTs//8.6e-35:226:89//Hs.78973:AI026812

F-PLACE1004104//ESTs//1.0:179:61//Hs.163935:AA506940
 F-PLACE1004114//ESTs//1.3e-52:323:89//Hs.35156:AA148516
 F-PLACE1004118//Spleen focus forming virus (SFFV) proviral integration o
 ncogene spil//0.85:164:64//Hs.153045:X52056
 F-PLACE1004128//Guanine nucleotide binding protein (G protein), beta pol
 ypeptide 1//3.1e-41:422:74//Hs.3620:X04526
 F-PLACE1004149//ESTs, Weakly similar to F48F7.1 [C.elegans]//8.2e-82:418
 :96//Hs.156161:AI333779
 F-PLACE1004156//ESTs//0.10:166:63//Hs.133279:AI053552
 F-PLACE1004161//Human mRNA for KIAA0200 gene, complete cds//0.85:269:64/
 /Hs.76986:D83785
 F-PLACE1004183//EST//1.3e-40:224:94//Hs.156603:AI343666
 F-PLACE1004197//ESTs//2.8e-91:441:98//Hs.97269:AA292201
 F-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precu
 sor, mRNA, complete cds//1.3e-145:695:98//Hs.24640:AF069493
 F-PLACE1004242//ESTs//0.99:213:60//Hs.117311:AA699722
 F-PLACE1004256//EST//0.019:364:58//Hs.122395:AA789273
 F-PLACE1004257//ESTs//0.77:154:64//Hs.112582:AA608689
 F-PLACE1004258//ESTs, Weakly similar to vanilloid receptor subtype 1 [R.
 norvegicus]//1.1e-98:479:97//Hs.31718:N29128
 F-PLACE1004270//Homo sapiens CAGF9 mRNA, partial cds//0.00010:369:63//Hs.
 .110826:U80736
 F-PLACE1004274//Homo sapiens mRNA for KIAA0445 protein, complete cds//0.
 085:573:56//Hs.154139:AB007914
 F-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, c
 omplete cds//2.0e-157:756:97//Hs.127007:AF084830
 F-PLACE1004284//ESTs//3.6e-71:344:99//Hs.145870:AI271884
 F-PLACE1004289//ESTs//2.6e-57:370:85//Hs.16740:AA586576
 F-PLACE1004302//FACTOR VIII INTRON 22 PROTEIN//0.032:513:59//Hs.83363:M3

4677

F-PLACE1004316//H.sapiens mRNA for apoptosis specific protein//9.3e-152:
797:94//Hs.11171:Y11588

F-PLACE1004336

F-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1
mRNA, complete cds//1.9e-140:688:97//Hs.16232:AF100153

F-PLACE1004376//ESTs, Weakly similar to F27D4.4 [C.elegans]//3.9e-109:52
1:98//Hs.14079:AA306552

F-PLACE1004384//Human HsLIM15 mRNA for HsLim15, complete cds//2.0e-49:46
6:76//Hs.37181:D64108

F-PLACE1004388

F-PLACE1004405//EST//0.010:191:64//Hs.147600:AI217871

F-PLACE1004425//ESTs//2.1e-20:124:80//Hs.94195:W03579

F-PLACE1004428//H.sapiens mRNA for Branched chain Acyl-CoA Oxidase//1.0:
552:58//Hs.9795:X95190

F-PLACE1004437//Human NAD⁺-specific isocitrate dehydrogenase beta subuni
t precursor, mRNA, nuclear gene encoding mitochondrial protein, complete
cds//9.9e-131:536:99//Hs.155410:U49283

F-PLACE1004451//ESTs//5.9e-18:203:73//Hs.156097:AI348867

F-PLACE1004460

F-PLACE1004467//ESTs//8.0e-17:345:66//Hs.112993:AA824363

F-PLACE1004471//EST//9.3e-69:463:84//Hs.116391:AA644085

F-PLACE1004473//ESTs//0.93:358:58//Hs.33263:AA724416

F-PLACE1004491//EST//2.5e-58:285:99//Hs.97603:AA398163

F-PLACE1004506//CD81 ANTIGEN//7.2e-06:228:63//Hs.54457:M33680

F-PLACE1004510//Homo sapiens cofactor of initiator function (CIF150) mRN
A, complete cds//2.5e-147:699:97//Hs.122752:AF026445

F-PLACE1004516//EST//1.0e-26:343:71//Hs.142595:N24150

F-PLACE1004518

F-PLACE1004548//EST//0.84:193:62//Hs.99583:AA461314
 F-PLACE1004550//ESTs, Weakly similar to No definition line found [C.elegans]//4.0e-120:627:94//Hs.107387:AA058854
 F-PLACE1004564//EST//1.0:240:62//Hs.16824:T91371
 F-PLACE1004629//Centromere protein B (80kD)//0.0015:242:64//Hs.85004:X05299
 F-PLACE1004645
 F-PLACE1004646//Retinal pigment epithelium-specific protein (65kD)//1.4e-12:386:63//Hs.2133:U18991
 F-PLACE1004658//ESTs//0.52:273:61//Hs.97252:AA291590
 F-PLACE1004664
 F-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene//1.5e-66:357:95//Hs.77705:U07563
 F-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds//1.4e-110:625:91//Hs.80019:AF035606
 F-PLACE1004681//EST//0.00092:303:61//Hs.149560:AI281589
 F-PLACE1004686//ESTs//3.0e-31:186:76//Hs.139130:AA704561
 F-PLACE1004691//Homo sapiens clone 23963 mRNA sequence//0.54:242:61//Hs.48483:AF007131
 F-PLACE1004693//ESTs, Weakly similar to pot. ORF III [H.sapiens]//0.56:96:71//Hs.125740:AA884845
 F-PLACE1004716//ESTs//2.0e-79:388:98//Hs.150999:AI306542
 F-PLACE1004722//ESTs//7.5e-06:105:72//Hs.128796:AA485891
 F-PLACE1004736//ESTs//1.7e-27:203:86//Hs.119593:AA700148
 F-PLACE1004740//ESTs//1.0e-25:174:89//Hs.29696:AA910680
 F-PLACE1004743
 F-PLACE1004751//ESTs, Highly similar to CMP-N-ACETYLNEURAMINATE-BETA-1, 4-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE [Rattus norvegicus]//2.0e-41:260:90//Hs.6863:W52470

F-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds//1.7e-1
72:828:97//Hs.104715:AF084367

F-PLACE1004777//Human myosin-IXb mRNA, complete cds//1.0e-29:556:63//Hs.
159629:U42391

F-PLACE1004793

F-PLACE1004804

F-PLACE1004813//EST//2.8e-42:296:83//Hs.155725:AI310340

F-PLACE1004814//ESTs, Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTE
IN 70 KD [*Xenopus laevis*]//2.4e-78:415:95//Hs.80965:AA493284

F-PLACE1004815//Human mRNA for KIAA0364 gene, complete cds//4.3e-14:294:
69//Hs.22111:AB002362

F-PLACE1004824//ESTs//0.0072:128:69//Hs.164062:AA934047

F-PLACE1004827//ESTs//0.78:38:100//Hs.18925:W30943

F-PLACE1004836//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.78:33
8:57//Hs.8546:U97669

F-PLACE1004838

F-PLACE1004840//Protein phosphatase 1, catalytic subunit, beta isoform//
0.89:200:66//Hs.21537:X80910

F-PLACE1004868

F-PLACE1004885//ESTs//0.41:181:61//Hs.116796:AA633772

F-PLACE1004900

F-PLACE1004902//ESTs//4.7e-72:367:96//Hs.54971:AI424382

F-PLACE1004913//ESTs//0.031:166:63//Hs.130110:AA904929

F-PLACE1004918//Human tumor susceptibility protein (TSG101) mRNA, complet
e cds//4.1e-24:402:64//Hs.118910:U82130

F-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cd
s//9.7e-86:519:88//Hs.17839:AF099936

F-PLACE1004934//ESTs//7.2e-43:231:78//Hs.133503:AA628592

F-PLACE1004937//ESTs//0.97:80:68//Hs.144264:C00851

F-PLACE1004969

F-PLACE1004972//Human retinoic acid- and interferon-inducible 58K protein RI58 mRNA, complete cds//0.031:235:60//Hs.27610:U34605

F-PLACE1004979//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.9e-43:331:83//Hs.153468:AB011147

F-PLACE1004982//ESTs//0.020:148:63//Hs.129377:AI218520

F-PLACE1004985//ESTs//7.9e-05:372:61//Hs.87606:AA242831

F-PLACE1005026//ESTs//4.6e-29:212:89//Hs.137451:AA351459

F-PLACE1005027//ESTs//6.5e-91:455:97//Hs.30890:H15159

F-PLACE1005046//ESTs//3.7e-56:250:96//Hs.152730:AI308943

F-PLACE1005052//EST//1.8e-36:370:73//Hs.123424:AA813594

F-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds//6.2e-161:761:98//Hs.14687:AB011148

F-PLACE1005066//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//3.0e-11:757:56//Hs.122967:AF059569

F-PLACE1005077//EST//0.79:283:59//Hs.89276:AA283899

F-PLACE1005085//ESTs//3.5e-18:231:72//Hs.142654:AA324740

F-PLACE1005086//Homo sapiens mRNA for KIAA0575 protein, complete cds//1.9e-49:401:80//Hs.153468:AB011147

F-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds//8.2e-20:194:80//Hs.75437:L40401

F-PLACE1005102//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds//8.9e-18:538:62//Hs.104640:AF000561

F-PLACE1005108//Treacher Collins syndrome susceptibility protein//0.73:405:57//Hs.73166:U76366

F-PLACE1005111//ESTs//0.66:191:63//Hs.106446:N93227

F-PLACE1005128//Breakpoint cluster region protein BCR//5.6e-08:291:63//Hs.2557:Y00661

F-PLACE1005146//ESTs, Weakly similar to hypothetical protein II [H.sapie

ns] //4.8e-12:360:63//Hs.142177:H11741
 F-PLACE1005162//Human mRNA for KIAA0118 gene, partial cds//3.9e-49:563:7
 2//Hs.154326:D42087
 F-PLACE1005176//Homo sapiens mRNA for KIAA0641 protein, complete cds//0.
 82:259:60//Hs.128316:AB014541
 F-PLACE1005181//ESTs, Weakly similar to No definition line found [C.eleg
 ans] //4.4e-126:583:99//Hs.25347:AI138605
 F-PLACE1005187//ESTs//6.2e-34:222:90//Hs.124265:N70417
 F-PLACE1005206//EST//0.089:167:62//Hs.140487:AA767009
 F-PLACE1005232//ESTs, Weakly similar to synapse-associated protein sap47
 -1 [D.melanogaster] //0.56:192:60//Hs.47334:W72370
 F-PLACE1005243
 F-PLACE1005261//ESTs//0.52:245:58//Hs.6682:T76941
 F-PLACE1005266//Kallmann syndrome 1 sequence//7.8e-06:484:60//Hs.89591:M
 97252
 F-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds//5.1
 e-150:706:98//Hs.118087:AB011182
 F-PLACE1005287//ESTs//8.1e-107:501:99//Hs.145703:AA447947
 F-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//4.4e-37:597:66
 //Hs.101642:X60673
 F-PLACE1005308//High-mobility group (nonhistone chromosomal) protein 2//
 0.83:239:62//Hs.80684:X62534
 F-PLACE1005313
 F-PLACE1005327//ESTs, Weakly similar to No definition line found [C.eleg
 ans] //6.0e-81:459:91//Hs.146177:R51650
 F-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569//3.7e-66:412:8
 8//Hs.134031:AC004794
 F-PLACE1005335//Homo sapiens mRNA for KIAA0754 protein, partial cds//0.9
 6:510:56//Hs.159183:AB018297

F-PLACE1005373
 F-PLACE1005374//ESTs//7.5e-77:437:91//Hs.143266:AI141348
 F-PLACE1005409//ESTs//2.4e-05:267:63//Hs.163307:AA856751
 F-PLACE1005453//ESTs//0.12:333:58//Hs.134672:AI087951
 F-PLACE1005467//HOMEBOX/POU DOMAIN PROTEIN RDC-1//0.0043:148:67//Hs.740
 95:L20433
 F-PLACE1005471//ESTs//3.4e-24:135:97//Hs.49275:N66925
 F-PLACE1005477//Human Line-1 repeat mRNA with 2 open reading frames//3.5
 e-126:744:87//Hs.23094:M19503
 F-PLACE1005480//ESTs//3.7e-26:184:70//Hs.113198:N39323
 F-PLACE1005481//EST//0.27:153:64//Hs.120066:AA707973
 F-PLACE1005494//ESTs//2.4e-50:257:98//Hs.159003:AA633029
 F-PLACE1005502//ESTs//0.15:408:57//Hs.45106:AA504105
 F-PLACE1005526//ESTs//3.2e-61:305:98//Hs.122574:AA776747
 F-PLACE1005528//ESTs//9.9e-32:249:78//Hs.142531:N91572
 F-PLACE1005530//ESTs//1.0e-94:491:95//Hs.131731:AI339335
 F-PLACE1005550//ESTs//0.084:290:58//Hs.157775:AI359385
 F-PLACE1005554//EST//0.38:213:58//Hs.102749:N64144
 F-PLACE1005557//ESTs, Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PRO
 TEIN L2 PRECURSOR [*Saccharomyces cerevisiae*]//4.5e-51:258:97//Hs.7736:W8
 1261
 F-PLACE1005574//ESTs//3.2e-09:236:66//Hs.146884:AI160278
 F-PLACE1005584//Fragile X mental retardation 2//1.2e-05:151:69//Hs.54472
 :U48436
 F-PLACE1005595//ESTs//2.1e-98:512:95//Hs.118552:W74594
 F-PLACE1005603//EST//1.0:90:66//Hs.111204:AA211851
 F-PLACE1005611//ESTs, Weakly similar to B0035.14 [*C.elegans*]//3.5e-32:19
 7:92//Hs.8241:AA283057
 F-PLACE1005623//ESTs//3.0e-30:191:92//Hs.77570:N48234.

F-PLACE1005630//ESTs//2.3e-32:175:97//Hs.122278:AA781867
 F-PLACE1005639//ESTs//0.88:218:58//Hs.117389:AA701991
 F-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete
 cds//2.1e-151:721:98//Hs.8765:AF083255
 F-PLACE1005656//Ribonucleotide reductase M2 polypeptide//3.9e-53:480:74/
 /Hs.75319:X59618
 F-PLACE1005666//Homo sapiens mRNA for KIAA0448 protein, complete cds//0.
 086:223:59//Hs.27349:AB007917
 F-PLACE1005698//Human membrane-associated lectin type-C mRNA//6.1e-65:37
 4:85//Hs.23759:M98457
 F-PLACE1005727//ESTs//8.7e-65:330:96//Hs.127027:AA935437
 F-PLACE1005730//ESTs//2.9e-14:270:67//Hs.28589:AI004944
 F-PLACE1005739//Homo sapiens mRNA for serin protease with IGF-binding mo
 tif, complete cds//0.75:289:59//Hs.75111:D87258
 F-PLACE1005755//Insulin-like growth factor binding protein 2//3.6e-05:37
 7:62//Hs.162:X16302
 F-PLACE1005763//ESTs, Highly similar to S-ACYL FATTY ACID SYNTHASE THIO
 ESTERASE, MEDIUM CHAIN [Rattus norvegicus]//5.7e-49:252:88//Hs.24309:AI1
 25696
 F-PLACE1005799//ESTs//5.2e-13:392:58//Hs.110530:AA191493
 F-PLACE1005802
 F-PLACE1005803
 F-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds
 //4.5e-128:636:96//Hs.125315:AF027156
 F-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//
 8.4e-156:739:98//Hs.11183:AF065482
 F-PLACE1005828//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
 RY !!!! [H.sapiens]//4.1e-42:327:81//Hs.138404:R70986
 F-PLACE1005834//Retinoblastoma 1 (including osteosarcoma)//0.038:436:58/

/Hs.75770:L41870
 F-PLACE1005845//ESTs//4.8e-50:309:89//Hs.107149:AI379497
 F-PLACE1005850//ESTs//7.1e-40:253:79//Hs.158096:AA186905
 F-PLACE1005851//ESTs//7.6e-93:483:95//Hs.135608:AA732242
 F-PLACE1005876//ESTs//0.97:282:60//Hs.98664:AI381487
 F-PLACE1005884//ESTs//0.070:276:60//Hs.106057:AI031552
 F-PLACE1005890//ESTs//1.5e-91:500:93//Hs.136993:AA843300
 F-PLACE1005898
 F-PLACE1005921
 F-PLACE1005923//ESTs//0.50:308:58//Hs.52489:R61504
 F-PLACE1005925//ESTs//0.024:93:68//Hs.149868:AI288274
 F-PLACE1005932//TYROSINE-PROTEIN KINASE RECEPTOR EPH PRECURSOR//0.97:342
 :57//Hs.89839:M18391
 F-PLACE1005934//ESTs//8.6e-10:74:93//Hs.25092:AA922142
 F-PLACE1005936//DNA excision repair protein ERCC5//1.0:144:63//Hs.48576:
 X69978
 F-PLACE1005951//B94 PROTEIN//0.00025:371:61//Hs.75522:M92357
 F-PLACE1005953//ESTs//2.8e-06:290:61//Hs.140996:R73468
 F-PLACE1005955//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.15:136:
 66//Hs.107747:AI357868
 F-PLACE1005966//Human zinc finger/leucine zipper protein (AF10) mRNA, co
 mplete cds//1.0:215:63//Hs.7885:U13948
 F-PLACE1005968
 F-PLACE1005990
 F-PLACE1006002//Putative mismatch repair/binding protein hMSH3//1.9e-48:
 312:77//Hs.42674:U61981
 F-PLACE1006003//EST//0.00018:171:67//Hs.138882:W73256
 F-PLACE1006011
 F-PLACE1006017//ESTs//3.1e-21:159:88//Hs.142173:AA757743

F-PLACE1006037//Homo sapiens mRNA for KIAA0789 protein, complete cds//0.
021:202:64//Hs.158319:AB018332

F-PLACE1006040//Homo sapiens mRNA for alpha endosulfine//1.1e-148:719:97
//Hs.98782:X99906

F-PLACE1006076//EST//0.29:92:64//Hs.161536:N80395

F-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds//
4.1e-147:679:99//Hs.4976:AF039023

F-PLACE1006129

F-PLACE1006139

F-PLACE1006143//Human mRNA for KIAA0355 gene, complete cds//9.3e-43:357:
79//Hs.153014:AB002353

F-PLACE1006157//ESTs, Weakly similar to ETX1 {alternatively spliced} [H.
sapiens]//2.9e-12:119:84//Hs.23153:R92857

F-PLACE1006159//ESTs//2.3e-87:443:96//Hs.23740:H17868

F-PLACE1006164//ESTs//0.099:223:60//Hs.8108:AA902721

F-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149//1.1e-68:333:9
2//Hs.152894:AC005239

F-PLACE1006170//ESTs//0.081:171:67//Hs.135187:AI074005

F-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds//1.2e-150:694:
99//Hs.30464:AF091433

F-PLACE1006195//ESTs//8.9e-14:229:70//Hs.141470:N49608

F-PLACE1006196//ESTs, Weakly similar to protein synthesis initiation fac
tor 4A-II homolog//3.5e-59:369:88//Hs.135623:AA134719

F-PLACE1006205

F-PLACE1006223//ESTs, Weakly similar to TERATOCARCINOMA-DERIVED GROWTH F
ACTOR 1 [H.sapiens]//0.0089:166:63//Hs.127179:AI279486

F-PLACE1006225

F-PLACE1006236//EST//0.060:89:69//Hs.136977:AA830668

F-PLACE1006239//ESTs//0.028:105:66//Hs.142336:AA358185

F-PLACE1006246//ESTs//0.060:330:60//Hs.105695:AI085802
 F-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds//7.3
 e-168:791:98//Hs.31921:AB014548
 F-PLACE1006262
 F-PLACE1006288//Homo sapiens mRNA for Pex3 protein//4.8e-37:186:100//Hs.
 7277:AJ001625
 F-PLACE1006318
 F-PLACE1006325//ESTs//3.7e-25:206:83//Hs.102319:AI246503
 F-PLACE1006335//ESTs//2.0e-27:161:95//Hs.163529:AI361492
 F-PLACE1006357//ESTs//0.013:268:61//Hs.105775:AA526249
 F-PLACE1006360//ESTs//4.8e-27:146:98//Hs.100739:Z98481
 F-PLACE1006368//Homo sapiens clone 24540 mRNA sequence//0.65:272:59//Hs.
 153529:AF070581
 F-PLACE1006371//Homo sapiens jerky gene product homolog mRNA, complete c
 ds//2.6e-07:403:61//Hs.105940:AF004715
 F-PLACE1006382//EST//0.98:77:68//Hs.136933:AA814693
 F-PLACE1006385//Homo sapiens epsin 2b mRNA, complete cds//1.6e-111:539:9
 7//Hs.22396:AF062085
 F-PLACE1006412//Human mRNA for KIAA0298 gene, complete cds//1.0e-36:424:
 74//Hs.21560:AB002296
 F-PLACE1006414//Homo sapiens PCAF associated factor 65 alpha mRNA, compl
 ete cds//4.3e-111:525:98//Hs.131846:AF069735
 F-PLACE1006438//Homo sapiens mRNA for KIAA0557 protein, partial cds//2.2
 e-24:531:65//Hs.101414:AB011129
 F-PLACE1006445//Homo sapiens chromosome 16 zinc finger protein ZNF200 (Z
 NF200) mRNA, complete cds//1.0:248:60//Hs.88219:AF060866
 F-PLACE1006469//Human SA mRNA for SA gene product, complete cds//0.24:21
 0:62//Hs.89659:AC004381
 F-PLACE1006470

F-PLACE1006482//Homo sapiens basic-leucine zipper transcription factor MafK (MAFK) mRNA, complete cds//5.0e-46:520:71//Hs.131953:AF059194

F-PLACE1006488//ESTs//6.2e-47:239:97//Hs.158161:AA312511

F-PLACE1006492//ESTs//0.82:37:100//Hs.160417:AA488493

F-PLACE1006506//HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDING PROTEIN 2//0.98:505:56//Hs.75063:AL023584

F-PLACE1006521//ESTs//0.032:222:63//Hs.23171:AA706542

F-PLACE1006531//EST//2.1e-53:258:100//Hs.117316:AA699358

F-PLACE1006534//EST//1.8e-07:78:89//Hs.157551:AI356219

F-PLACE1006540//Homo sapiens mRNA for cadherin-6, complete cds//0.96:383:58//Hs.32963:D31784

F-PLACE1006552//Human (clone N5-4) protein p84 mRNA, complete cds//0.058:464:57//Hs.1540:L36529

F-PLACE1006598//Homo sapiens mRNA for KIAA0737 protein, complete cds//4.1e-17:372:65//Hs.17630:AB018280

F-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//2.2e-168:781:99//Hs.155377:U97670

F-PLACE1006617//ESTs//6.0e-08:354:60//Hs.42624:H99088

F-PLACE1006626//NUCLEOLIN//0.0044:186:66//Hs.79110:M60858

F-PLACE1006629//Homo sapiens (clone s22i71) mRNA fragment//0.097:229:63//Hs.26956:L40396

F-PLACE1006640//ESTs//0.00019:380:59//Hs.13672:AI131473

F-PLACE1006673//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]//1.6e-12:113:83//Hs.3385:N25917

F-PLACE1006678

F-PLACE1006704//Homo sapiens ALR mRNA, complete cds//0.16:284:60//Hs.153638:AF010403

F-PLACE1006731//Homo sapiens SOX22 protein (SOX22) mRNA, complete cds//1.6e-05:382:63//Hs.43627:U35612

F-PLACE1006754//Biliary glycoprotein//8.9e-27:305:72//Hs.50964:X16354
 F-PLACE1006760//ESTs//0.10:207:62//Hs.152589:AA954152
 F-PLACE1006779//Kallmann syndrome 1 sequence//0.00025:251:64//Hs.89591:M
 97252
 F-PLACE1006782//ESTs//1.2e-90:423:100//Hs.132826:AI075783
 F-PLACE1006792//ESTs//1.5e-10:439:58//Hs.138501:AI051228
 F-PLACE1006795//TYROSINE-PROTEIN KINASE RECEPTOR ETK1 PRECURSOR//4.5e-10
 :84:95//Hs.123642:M83941
 F-PLACE1006800//ESTs//0.00068:360:61//Hs.157876:AI422017
 F-PLACE1006805//ESTs//4.6e-103:491:98//Hs.140465:AA769892
 F-PLACE1006815//Homo sapiens mRNA for KIAA0618 protein, complete cds//0.
 47:403:56//Hs.15832:AB014518
 F-PLACE1006819//Human Line-1 repeat mRNA with 2 open reading frames//3.7
 e-103:619:87//Hs.23094:M19503
 F-PLACE1006829//ESTs//1.5e-22:141:94//Hs.142988:AA142876
 F-PLACE1006860//EST//0.0062:206:65//Hs.158793:AI376773
 F-PLACE1006867//ESTs//0.068:218:62//Hs.91166:AA551273
 F-PLACE1006878//Homo sapiens mRNA for KIAA0711 protein, complete cds//1.
 0:268:58//Hs.5333:AB018254
 F-PLACE1006883//ESTs//1.6e-75:398:94//Hs.119544:T95601
 F-PLACE1006901//ESTs//1.9e-13:87:96//Hs.134737:AI089187
 F-PLACE1006904//EST//1.0:91:70//Hs.148270:AA906443
 F-PLACE1006917
 F-PLACE1006932//ESTs//0.98:110:70//Hs.100855:AI423913
 F-PLACE1006935//EST//1.0:92:65//Hs.124554:AA847211
 F-PLACE1006956//PERIPHERIN//0.13:443:57//Hs.37044:L14565
 F-PLACE1006958//Heat shock 70kD protein 4//6.4e-40:456:70//Hs.127:L12723
 F-PLACE1006961//ESTs, Highly similar to RSP5 PROTEIN [Saccharomyces cer
 evisiae]//3.2e-07:67:98//Hs.21806:AA630312

F-PLACE1006962//H.sapiens irlB mRNA//2.3e-16:202:71//Hs.135202:X63417
 F-PLACE1006966//Homo sapiens syntaxin 4 binding protein.UNC-18c (UNC-18c) mRNA, complete cds//0.14:191:67//Hs.8813:AF032922
 F-PLACE1006989//Cyclin B1//0.99:224:59//Hs.23960:M25753
 F-PLACE1007014//Homo sapiens NBMPR-insensitive nucleoside transporter ei (ENT2) mRNA, complete cds//3.1e-05:594:58//Hs.32951:AF034102
 F-PLACE1007021//ESTs//7.2e-89:446:96//Hs.7111:U55971
 F-PLACE1007045//Human Line-1 repeat mRNA with 2 open reading frames//1.0 e-117:775:84//Hs.23094:M19503
 F-PLACE1007053//Homo sapiens mRNA for ARNO3 protein//0.35:63:82//Hs.1298 11:AJ223957
 F-PLACE1007068//Polycystic kidney disease 1 (autosomal dominant)//0.22:3 61:60//Hs.75813:L33243
 F-PLACE1007097//ESTs//2.9e-25:197:83//Hs.105665:H78987
 F-PLACE1007105//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glyco gen debranching enzyme, glycogen storage disease type III)//0.18:268:63/ /Hs.904:U84010
 F-PLACE1007111//EST//0.0066:260:60//Hs.147903:AI223385
 F-PLACE1007112
 F-PLACE1007132//ESTs//3.1e-30:195:76//Hs.46158:AI160121
 F-PLACE1007140//TRANSCRIPTION ELONGATION FACTOR S-II//0.13:302:60//Hs.78 869:M81601
 F-PLACE1007178//ESTs//9.6e-54:289:95//Hs.12251:H12965
 F-PLACE1007226//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.00090 :412:59//Hs.8546:U97669
 F-PLACE1007238//Human plectin (PLEC1) mRNA, complete cds//1.4e-07:492:64 //Hs.79706:U53204
 F-PLACE1007239//Human mRNA for transcription elongation factor S-II, hS- II-T1, complete cds//2.0e-58:405:87//Hs.80598:D50495

F-PLACE1007242//EST//0.014:55:89//Hs.88432:AA262141
 F-PLACE1007243//ESTs//2.0e-43:227:97//Hs.124775:AA648467
 F-PLACE1007257//Homo sapiens mRNA for dia-156 protein//3.7e-144:677:98//
 Hs.121556:Y15909
 F-PLACE1007274
 F-PLACE1007276//ATPase, Cu++ transporting, alpha polypeptide (Menkes syn
 drome)//0.94:167:64//Hs.606:L06133
 F-PLACE1007282
 F-PLACE1007286//ESTs//1.0e-25:333:71//Hs.134860:AI091436
 F-PLACE1007301//EST//0.78:171:61//Hs.160990:H52412
 F-PLACE1007317//Homo sapiens oxysterol 7alpha-hydroxylase (CYP7b1) mRNA,
 complete cds//0.88:298:58//Hs.144877:AF029403
 F-PLACE1007342
 F-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mR
 NA, complete cds//1.7e-121:567:98//Hs.76596:AF096870
 F-PLACE1007367//H.sapiens mRNA for MACH-alpha-2 protein//2.2e-55:532:77/
 /Hs.19949:X98173
 F-PLACE1007375
 F-PLACE1007386//ESTs//0.00066:61:91//Hs.149318:AI248642
 F-PLACE1007402//EST//1.7e-06:193:65//Hs.132124:AI041287
 F-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, par
 tial sequence//3.8e-18:128:92//Hs.14387:AF093771
 F-PLACE1007416
 F-PLACE1007450//ESTs//2.6e-36:194:97//Hs.22359:AI024436
 F-PLACE1007452//EST//1.8e-34:197:94//Hs.134795:AI090359
 F-PLACE1007454//Homo sapiens (clone s153) mRNA fragment//2.6e-53:317:93/
 /Hs.6445:L40391
 F-PLACE1007460//ESTs//0.0012:168:64//Hs.151708:AA554714
 F-PLACE1007478//ESTs//1.0e-42:440:74//Hs.141722:AA769103

F-PLACE1007484//ESTs//7.1e-18:127:91//Hs.100251:AA535975
 F-PLACE1007488
 F-PLACE1007507//ESTs//1.2e-99:274:98//Hs.123462:AA903385
 F-PLACE1007511//Keratin 19//4.2e-31:586:64//Hs.23761:Y00503
 F-PLACE1007524//ESTs//6.8e-71:356:97//Hs.163067:AA897296
 F-PLACE1007525//ESTs//0.073:242:59//Hs.128711:AA856979
 F-PLACE1007537//Homo sapiens PYRIN (MEFV) mRNA, complete cds//0.93:468:5
 7//Hs.113283:AF018080
 F-PLACE1007544//ESTs//1.7e-74:360:98//Hs.128632:AI076755
 F-PLACE1007547//Homo sapiens mRNA for KIAA0661 protein, complete cds//1.
 0e-70:733:71//Hs.65238:AB014561
 F-PLACE1007557//EST//0.58:80:72//Hs.130267:AI001863
 F-PLACE1007583//ESTs//1.8e-46:234:98//Hs.155071:AA584257
 F-PLACE1007598//ESTs//1.7e-83:400:99//Hs.120206:AI089163
 F-PLACE1007618//Homo sapiens mRNA for KIAA0633 protein, partial cds//7.2
 e-12:778:56//Hs.33010:AB014533
 F-PLACE1007621
 F-PLACE1007632//ESTs//1.7e-32:175:97//Hs.122278:AA781867
 F-PLACE1007645
 F-PLACE1007649
 F-PLACE1007677//ESTs//3.0e-13:125:82//Hs.143382:AA476266
 F-PLACE1007688//ESTs//6.8e-06:311:61//Hs.132926:AI027055
 F-PLACE1007690//ESTs//1.9e-13:83:98//Hs.150088:AI348503
 F-PLACE1007697//TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR//0.99:216:63
 //Hs.1103:X02812
 F-PLACE1007705//Human mRNA for RTP, complete cds//4.8e-58:637:70//Hs.757
 89:D87953
 F-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds/
 /4.1e-149:709:97//Hs.4812:AF061243

F-PLACE1007725//ESTs, Weakly similar to No definition line found [C.elegans] //4.5e-36:233:89//Hs.108797:AA476815

F-PLACE1007729//ESTs, Moderately similar to RETROVIRUS-RELATED PROTEASE [H.sapiens] //0.00033:270:64//Hs.104129:AA923278

F-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.6e-156:728:98//Hs.153121:AB014585

F-PLACE1007737//Coagulation factor II (thrombin) receptor//1.1e-18:364:68//Hs.159347:M62424

F-PLACE1007743//ESTs//0.029:421:58//Hs.106090:AA457030

F-PLACE1007746//ESTs//6.7e-55:330:89//Hs.153392:AI089469

F-PLACE1007791//EST//0.39:261:62//Hs.145991:AI277656

F-PLACE1007807//ESTs//2.0e-54:385:83//Hs.163930:AA640504

F-PLACE1007810//ESTs//6.1e-53:416:81//Hs.152395:AA533107

F-PLACE1007829//EST//0.28:271:61//Hs.125514:AA883841

F-PLACE1007843//EST//0.020:307:59//Hs.145535:AI261635

F-PLACE1007846//Human Line-1 repeat mRNA with 2 open reading frames//6.3e-38:396:77//Hs.23094:M19503

F-PLACE1007852

F-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//1.3e-190:894:98//Hs.28020:AB018309

F-PLACE1007866//ESTs//3.0e-50:333:86//Hs.15792:AI038387

F-PLACE1007877

F-PLACE1007897//EST//1.0:59:72//Hs.138770:N70943

F-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//7.3e-156:755:97//Hs.92381:AB007956

F-PLACE1007946//ESTs//8.9e-16:250:68//Hs.88527:N24002

F-PLACE1007954//ESTs//1.6e-05:76:90//Hs.63314:AA056538

F-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds//8.9e-173:813:98//Hs.5671:AF084530

F-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B)
mRNA, partial cds//8.2e-155:730:98//Hs.78106:AF079529

F-PLACE1007969//ESTs, Weakly similar to hnRNA-binding protein M4 [H.sapi
ens]//5.1e-45:264:92//Hs.42222:W28567

F-PLACE1007990//ESTs//1.2e-104:493:99//Hs.118445:AI097043

F-PLACE1008000//Homo sapiens veli 1 mRNA, complete cds//5.7e-63:578:74//
Hs.150380:AF087693

F-PLACE1008002//ESTs//0.52:236:59//Hs.134292:AA603031

F-PLACE1008044

F-PLACE1008045//COL10A1//0.29:221:58//Hs.37075:X60382

F-PLACE1008080//Human homeodomain protein (Prox 1) mRNA, complete cds//0
.00037:151:71//Hs.159437:U44060

F-PLACE1008095//Human hybrid receptor gp250 precursor mRNA, complete cds
//1.0:461:58//Hs.155494:U60975

F-PLACE1008111//Homo sapiens B lymphocyte chemoattractant BLC mRNA, comp
lete cds//0.034:497:58//Hs.100431:AF044197

F-PLACE1008122//ESTs//0.95:198:60//Hs.126776:N28769

F-PLACE1008129//ESTs//1.1e-99:499:96//Hs.131807:AA778874

F-PLACE1008132//EST//3.3e-27:218:83//Hs.145258:AI218683

F-PLACE1008177//ESTs, Moderately similar to meiosis-specific nuclear str
uctural protein 1 [M.musculus]//5.1e-20:124:95//Hs.146238:AI263135

F-PLACE1008181//ESTs//0.018:285:61//Hs.88843:AA281427

F-PLACE1008198//ESTs//5.9e-07:410:60//Hs.63348:AA643524

F-PLACE1008201

F-PLACE1008209

F-PLACE1008231//ESTs//0.40:188:61//Hs.130266:AI001856

F-PLACE1008244//Miller-Dieker syndrome chromosome region//0.22:247:61//H
s.77318:L13385

F-PLACE1008273

F-PLACE1008275//EST//0.77:74:71//Hs.145907:AI275113

F-PLACE1008280//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//2.6e-25:389:70//Hs.159897:AB007970

F-PLACE1008309//Homo sapiens serine phosphatase FCP1a (FCP1) mRNA, complete cds//0.16:263:63//Hs.4076:AF081287

F-PLACE1008329//EST//1.3e-09:94:85//Hs.144135:R82071

F-PLACE1008330//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.5e-45:291:83//Hs.101414:AB011129

F-PLACE1008331//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//5.4e-74:356:98//Hs.105382:AA496362

F-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds//3.4e-139:659:98//Hs.5734:AB014579

F-PLACE1008368//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//0.011:355:60//Hs.122967:AF059569

F-PLACE1008369//ESTs//0.00074:443:61//Hs.102756:AA526911

F-PLACE1008392//EST//7.4e-08:324:60//Hs.149930:AI289171

F-PLACE1008398

F-PLACE1008401//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//2.5e-09:461:62//Hs.25674:AF072242

F-PLACE1008402//Homo sapiens mRNA for p115, complete cds//1.4e-149:711:98//Hs.7763:D86326

F-PLACE1008405//ESTs//2.8e-102:529:95//Hs.116278:AA628943

F-PLACE1008424//Human DNA sequence from clone 753P9 on chromosome Xq25-26.1. Contains the gene coding for Aminopeptidase P (EC 3.4.11.9, XAA-Pro/X-Pro/Proline/Aminoacylproline Aminopeptidase) and a novel gene. Contains ESTs, STSS, GSSs and a gaaa repeat polymorphism//0.98:113:67//Hs.57922:AL023653

F-PLACE1008426//ESTs//3.2e-77:393:95//Hs.37585:W28499

F-PLACE1008429//Orf1 5' to PD-ECGF/TP...orf2 5' to PD-ECGF/TP [human, ep

idermoid carcinoma cell line A431, mRNA, 3 genes, 1718 nt]//0.019:530:58
 //Hs.72248:S72487
 F-PLACE1008437
 F-PLACE1008455//ESTs//0.51:279:61//Hs.122319:AA782335
 F-PLACE1008457//ESTs//3.0e-30:229:75//Hs.60740:AA053901
 F-PLACE1008465//Human mRNA for KIAA0383 gene, partial cds//0.0084:210:63
 //Hs.27590:AB002381
 F-PLACE1008488//Human density enhanced phosphatase-1 mRNA, complete cds/
 /6.8e-07:469:60//Hs.1177:U10886
 F-PLACE1008524//Homo sapiens TWIK-related acid-sensitive K⁺ channel (TAS
 K) mRNA, complete cds//1.0:304:60//Hs.24040:AF006823
 F-PLACE1008531//ESTs//1.1e-17:190:76//Hs.156041:AI274697
 F-PLACE1008532//Thromboxane A2 receptor//5.6e-17:231:71//Hs.89887:D38081
 F-PLACE1008533//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter//1.1e-
 45:507:71//Hs.8003:AC004997
 F-PLACE1008568//Homo sapiens mRNA for neuronatin alpha, complete cds//1.
 0:95:71//Hs.117546:U31767
 F-PLACE1008584//ESTs//1.4e-13:252:68//Hs.153429:AI283069
 F-PLACE1008603//Homo sapiens mRNA for KIAA0791 protein, complete cds//3.
 9e-175:812:98//Hs.23255:AB018334
 F-PLACE1008621//ESTs, Weakly similar to reverse transcriptase [H.sapiens
]//1.2e-15:350:66//Hs.151087:AA649326
 F-PLACE1008625//ESTs//0.86:269:57//Hs.94998:N26794
 F-PLACE1008626//ESTs//0.55:69:71//Hs.92096:F10560
 F-PLACE1008627//ESTs//3.0e-62:302:99//Hs.120766:H82458
 F-PLACE1008629//EST//0.0012:174:67//Hs.121195:AA757211
 F-PLACE1008630//ESTs//4.5e-77:371:99//Hs.132960:AA252394
 F-PLACE1008643//Human mRNA for PK-120//4.7e-25:299:64//Hs.76415:D38535
 F-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, compl

ete cds//3.5e-135:622:99//Hs.147967:AF044333

F-PLACE1008693//EST//0.19:36:94//Hs.138817:N93728

F-PLACE1008696//Human mitochondrial NADH dehydrogenase-ubiquinone Fe-S protein 8, 23 kDa subunit precursor (NDUFS8) nuclear mRNA encoding mitochondrial protein, complete cds//8.3e-25:137:97//Hs.90443:AF038406

F-PLACE1008715//Homo sapiens mRNA for matrilin-3//0.99:183:63//Hs.119534:AJ224741

F-PLACE1008748//ESTs//0.88:204:63//Hs.15139:AA527080

F-PLACE1008757//ESTs, Weakly similar to unknown protein [R.norvegicus]//4.3e-17:285:69//Hs.35460:H65503

F-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds//1.4e-121:503:97//Hs.6458:AF060543

F-PLACE1008798//ESTs, Weakly similar to putative p150 [H.sapiens]//0.30:127:68//Hs.111380:AA258772

F-PLACE1008807//ESTs//0.81:346:58//Hs.116901:AA663542

F-PLACE1008808//Homo sapiens putative checkpoint control protein HRAD1 mRNA, complete cds//6.7e-104:376:98//Hs.7179:AF011905

F-PLACE1008813//Glutamate decarboxylase 1 (brain, 67kD)//0.17:318:61//Hs.75668:M81883

F-PLACE1008851//ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 2 HOMOLOG [Plasmodium falciparum (isolate k1 / thailand)]//0.73:354:59//Hs.26322:AA156858

F-PLACE1008854//ESTs//3.0e-26:391:66//Hs.133260:AI052728

F-PLACE1008867//ESTs//5.9e-08:64:93//Hs.91115:AI221563

F-PLACE1008887//Human Line-1 repeat mRNA with 2 open reading frames//5.5e-51:701:68//Hs.23094:M19503

F-PLACE1008902//EST//0.85:425:60//Hs.140573:AA826323

F-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds//2.1e-159:753:98//Hs.62318:AB018308

F-PLACE1008925//ESTs//0.025:133:67//Hs.103218:W84771
 F-PLACE1008934//ESTs//0.27:307:59//Hs.135168:AI394026
 F-PLACE1008941//ESTs//3.3e-53:266:98//Hs.108677:AA488937
 F-PLACE1008947//Human TBP-associated factor (hTAFII130) mRNA, partial cds//2.4e-13:625:58//Hs.24644:U75308
 F-PLACE1009020//ESTs//3.3e-11:122:81//Hs.131777:AI024950
 F-PLACE1009027//Homo sapiens mRNA for doublecortin//1.2e-151:763:96//Hs.34780:AJ003112
 F-PLACE1009039//EST//0.76:111:63//Hs.160997:H55762
 F-PLACE1009045//ESTs//2.2e-76:399:95//Hs.114919:AA457689
 F-PLACE1009048//GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR//2.6e-16:93:100//Hs.119689:S70585
 F-PLACE1009050//ESTs//1.4e-92:451:98//Hs.66373:AI239698
 F-PLACE1009060//ESTs//1.4e-14:86:100//Hs.131725:AI090525
 F-PLACE1009090//ESTs//2.7e-20:198:78//Hs.110044:AA181800
 F-PLACE1009091//ESTs//0.99:342:57//Hs.46903:AI093091
 F-PLACE1009094//ESTs//1.0:225:63//Hs.120374:AI337031
 F-PLACE1009099//H.sapiens ZNF81 gene//2.2e-79:733:74//Hs.104020:X68011
 F-PLACE1009110//ESTs//2.6e-91:453:96//Hs.143756:AI040890
 F-PLACE1009111//ESTs//2.7e-15:159:77//Hs.146811:AA410788
 F-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//1.1e-139:671:97//Hs.99742:AF035586
 F-PLACE1009130//Human mRNA for KIAA0032 gene, complete cds//1.1e-24:718:59//Hs.35804:D25215
 F-PLACE1009150//Human HsLIM15 mRNA for HsLim15, complete cds//1.7e-50:440:78//Hs.37181:D64108
 F-PLACE1009155//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.0e-46:440:69//Hs.158095:AB007953
 F-PLACE1009158//Human growth/differentiation factor 1 (GDF-1) mRNA, comp

lete cds//0.28:245:61//Hs.92614:M62302
 F-PLACE1009166//EST//0.98:114:67//Hs.137706:AA977250
 F-PLACE1009172//EST//6.2e-34:257:84//Hs.161081:N22770
 F-PLACE1009174//ESTs//6.0e-24:234:77//Hs.155196:AI282821
 F-PLACE1009183//EST//0.021:261:62//Hs.144222:N90100
 F-PLACE1009186//ESTs, Weakly similar to No definition line found [C.elegans] //3.6e-117:588:95//Hs.54943:Z78396
 F-PLACE1009190//EST//0.046:95:70//Hs.131646:AI025689
 F-PLACE1009200//EST//2.5e-41:195:78//Hs.162404:AA573131
 F-PLACE1009230//CARCINOEMBRYONIC ANTIGEN PRECURSOR//5.3e-29:157:77//Hs.146403:M29540
 F-PLACE1009246//EST//0.13:178:62//Hs.23298:R22575
 F-PLACE1009298//ESTs, Highly similar to VACUOLAR SORTING PROTEIN 35 [Saccharomyces cerevisiae] //1.9e-21:121:98//Hs.124768:AA307735
 F-PLACE1009308//SERUM PROTEIN MSE55//0.44:195:62//Hs.148101:M88338
 F-PLACE1009319//Homo sapiens post-synaptic density protein 95 (PSD95) mRNA, complete cds//9.7e-08:411:59//Hs.23731:U83192
 F-PLACE1009328//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-91:594:86//Hs.23094:M19503
 F-PLACE1009335//EST//0.037:169:63//Hs.148875:AI240767
 F-PLACE1009338//ESTs//5.7e-22:123:98//Hs.66783:AA059473
 F-PLACE1009368
 F-PLACE1009375
 F-PLACE1009388//Homo sapiens KIAA0395 mRNA, partial cds//1.7e-41:317:81//Hs.43681:AL022394
 F-PLACE1009398//Zinc finger protein 84 (HPF2)//1.4e-79:730:74//Hs.9450:M27878
 F-PLACE1009404//MICROTUBULE-ASSOCIATED PROTEIN TAU//0.099:207:61//Hs.101174:AF047863

F-PLACE1009410//Homo sapiens BAF57 (BAF57) gene, complete cds//1.4e-27:2
10:86//Hs.3404:AF035262

F-PLACE1009434//Human mRNA for KIAA0005 gene, complete cds//2.8e-45:599:
68//Hs.155291:D13630

F-PLACE1009443//H.sapiens 5T4 gene for 5T4 Oncofetal antigen//0.11:350:5
8//Hs.82128:AJ012159

F-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//1.5e-22:146:93//Hs.
76987:AF012872

F-PLACE1009459//H.sapiens gap gene mRNA, complete CDS//1.0:241:60//Hs.1
51641:Z24680

F-PLACE1009468//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERAS
E BETA 2//0.00039:347:60//Hs.994:M95678

F-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1//4.
1e-91:464:96//Hs.155049:AC004531

F-PLACE1009477//ESTs//0.30:221:61//Hs.107287:AI308839

F-PLACE1009493//Homo sapiens mRNA for LAK-4p, complete cds//1.6e-30:608:
63//Hs.16165:AB002405

F-PLACE1009524//Human Sec7p-like protein mRNA, partial cds//2.3e-68:526:
78//Hs.8517:U70728

F-PLACE1009539//ESTs//3.3e-18:186:83//Hs.71922:AA148417

F-PLACE1009542//EST//7.8e-11:265:65//Hs.159692:AI416956

F-PLACE1009571//ESTs//6.1e-15:94:97//Hs.151458:AA600866

F-PLACE1009581//Microtubule-associated protein 1A//1.0:196:59//Hs.147918
:U38291

F-PLACE1009595//EST//1.8e-28:179:92//Hs.60090:AA004806

F-PLACE1009596//ESTs, Weakly similar to LIS-1 protein [H.sapiens]//4.1e-
16:281:66//Hs.13889:AI341394

F-PLACE1009607//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.9e-52:31
3:79//Hs.113283:AF018080

F-PLACE1009613//ESTs//0.50:297:60//Hs.25114:AI074011
 F-PLACE1009621//ESTs//1.4e-98:470:98//Hs.124695:AI094085
 F-PLACE1009622//ESTs//9.8e-14:94:93//Hs.117227:AA682773
 F-PLACE1009637//ESTs//4.9e-92:440:98//Hs.126587:AA917087
 F-PLACE1009639
 F-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds//4.4e-173:816:98//Hs.21862:AB011159
 F-PLACE1009665//ESTs//9.1e-45:383:79//Hs.61199:AA024494
 F-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//8.1e-149:701:98//Hs.109590:AF062534
 F-PLACE1009708//ESTs, Weakly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN HXT14-PHA2 INTERGENIC REGION [S.cerevisiae]//7.5e-51:295:92//Hs.48541:AA827926
 F-PLACE1009721//EST//0.18:467:58//Hs.124358:AA830650
 F-PLACE1009731//ESTs//1.0:207:63//Hs.60440:AA195789
 F-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds//1.3e-126:602:98//Hs.154320:AF046024
 F-PLACE1009794//ESTs//4.0e-41:252:91//Hs.42927:N20989
 F-PLACE1009798//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs and GSSs//5.5e-130:600:95//Hs.16411:AL030996
 F-PLACE1009845
 F-PLACE1009861
 F-PLACE1009879//ESTs//6.3e-12:293:66//Hs.147071:AI200021
 F-PLACE1009886

F-PLACE1009888//EST//0.044:255:58//Hs.160695:AI282889
 F-PLACE1009908
 F-PLACE1009921//Apoptosis (APO-1) antigen 1//0.62:407:57//Hs.82359:X6371
 7
 F-PLACE1009924//EST//2.9e-29:155:99//Hs.162937:AA634379
 F-PLACE1009925
 F-PLACE1009935//CATHEPSIN K PRECURSOR//0.43:153:66//Hs.83942:X82153
 F-PLACE1009947//ESTs//1.8e-07:56:100//Hs.149940:AI306446
 F-PLACE1009971//Acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain//0.89:243:61//Hs.127610:Z80345
 F-PLACE1009992//ESTs//0.99:123:68//Hs.91202:AI139114
 F-PLACE1009995//ESTs, Weakly similar to C01A2.4 [C.elegans]//3.3e-24:174:88//Hs.11449:AI201540
 F-PLACE1009997//Homo sapiens mRNA for KIAA0629 protein, partial cds//3.7e-36:196:96//Hs.153545:AB014529
 F-PLACE1010023
 F-PLACE1010031//ESTs//1.3e-16:132:87//Hs.46847:W02878
 F-PLACE1010053//ESTs, Moderately similar to M-phase phosphoprotein 4 [H.sapiens]//5.2e-63:312:98//Hs.142151:AA984061
 F-PLACE1010069//ESTs//6.6e-33:171:98//Hs.128844:AA977596
 F-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//5.9e-168:792:98//Hs.11183:AF065482
 F-PLACE1010076//ESTs//0.88:379:55//Hs.5884:N21424
 F-PLACE1010083//Homo sapiens mRNA for KIAA0456 protein, partial cds//9.6e-154:727:98//Hs.5003:AB007925
 F-PLACE1010089//ESTs, Highly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE [Mus musculus]//1.8e-38:212:95//Hs.98067:AA236822
 F-PLACE1010096//ESTs, Highly similar to hypothetical protein, 100K [R.novvegicus]//1.8e-08:100:89//Hs.11469:U69567

F-PLACE1010102//Homo sapiens stimulator of Fe transport mRNA, complete cds//0.0035:339:60//Hs.129683:AF020761

F-PLACE1010105//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//1.2e-26:728:60//Hs.122967:AF059569

F-PLACE1010106//EST//8.5e-28:394:70//Hs.142044:AA166682

F-PLACE1010134//H.sapiens hbrm mRNA//1.2e-14:380:64//Hs.77590:X72889

F-PLACE1010148//Human trans-Golgi p230 mRNA, complete cds//0.26:708:57//Hs.158245:U41740

F-PLACE1010152

F-PLACE1010181//EST//1.3e-21:312:71//Hs.141501:N50792

F-PLACE1010194//ESTs//2.6e-55:284:97//Hs.155940:AA459582

F-PLACE1010202//ESTs, Weakly similar to No definition line found [C.elegans]//2.3e-72:391:94//Hs.35225:H69637

F-PLACE1010231

F-PLACE1010261//Homo sapiens mRNA for KIAA0448 protein, complete cds//1.9e-146:693:97//Hs.27349:AB007917

F-PLACE1010270//ESTs//2.0e-104:514:98//Hs.124062:H04590

F-PLACE1010274//ESTs, Weakly similar to C01A2.4 [C.elegans]//6.8e-25:149:93//Hs.11449:AI201540

F-PLACE1010293//EST//4.5e-36:358:74//Hs.162398:AA572813

F-PLACE1010310//HOMEBOX/POU DOMAIN PROTEIN RDC-1//2.1e-10:352:62//Hs.74095:L20433

F-PLACE1010321//Human hSIAH2 mRNA, complete cds//0.071:604:58//Hs.20191:U76248

F-PLACE1010324//ESTs//0.22:286:58//Hs.130853:AI367875

F-PLACE1010329//EST//5.7e-05:351:60//Hs.120644:AA742659

F-PLACE1010341//EST//4.5e-16:255:72//Hs.141206:H53117

F-PLACE1010362//ESTs//1.9e-41:246:92//Hs.128771:AA236855

F-PLACE1010364//EST//0.11:292:58//Hs.135771:AI005648

F-PLACE1010383//EST//6.1e-08:107:76//Hs.136441:AA564986
 F-PLACE1010401
 F-PLACE1010481//Human BLu protein (BLu) mRNA, complete cds//0.94:254:61/
 /Hs.125257:U70824
 F-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete c
 ds//7.2e-152:702:99//Hs.13313:AF039081
 F-PLACE1010492//ESTs//1.0:201:60//Hs.146036:AI038500
 F-PLACE1010522//ESTs//3.9e-52:263:97//Hs.125149:AI302100
 F-PLACE1010529//Homo sapiens chromodomain-helicase-DNA-binding protein m
 RNA, complete cds//1.0:175:64//Hs.159273:AF054177
 F-PLACE1010547//ESTs//0.96:288:57//Hs.87156:AA233472
 F-PLACE1010562//EST//1.0:164:66//Hs.147868:AI222979
 F-PLACE1010579//EST//0.39:279:58//Hs.158960:AI380148
 F-PLACE1010580//ESTs, Moderately similar to PUTATIVE ATP-DEPENDENT RNA
 HELICASE C12C2.06 [Schizosaccharomyces pombe]//3.8e-31:193:91//Hs.145229
 :N44661
 F-PLACE1010599//Homo sapiens peroxisomal membrane anchor protein HsPex14
 p (PEX14) mRNA, complete cds//9.9e-148:707:97//Hs.19851:AF045186
 F-PLACE1010616//EST//3.1e-43:213:100//Hs.128215:AA972394
 F-PLACE1010622//NUCLEOLIN//0.00040:282:60//Hs.79110:M60858
 F-PLACE1010624//Homo sapiens Jagged 2 mRNA, complete cds//1.2e-05:516:61
 //Hs.106387:AF029778
 F-PLACE1010628//EST, Weakly similar to line-1 protein ORF2 [H.sapiens]//
 0.012:258:62//Hs.144375:AA484200
 F-PLACE1010629//EST//8.3e-23:218:79//Hs.161975:AA501461
 F-PLACE1010630//EST//0.29:319:58//Hs.137277:N62225
 F-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds//9.5
 e-66:363:95//Hs.10801:AB011102
 F-PLACE1010661//ESTs//3.9e-89:504:92//Hs.122666:W27076

F-PLACE1010662

F-PLACE1010702//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//1.1e-74:697:74//Hs.37138:U35376

F-PLACE1010714//EST//0.018:253:59//Hs.148028:AI270027

F-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//6.1e-77:393:96//Hs.50758:AF092564

F-PLACE1010739//Homo sapiens mRNA for Sec24 protein (Sec24A isoform), partial//0.97:314:59//Hs.14574:AJ131244

F-PLACE1010743//Human myosin-IXb mRNA, complete cds//2.4e-56:409:86//Hs.159629:U42391

F-PLACE1010761//ESTs, Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD [*Xenopus laevis*]//5.1e-80:407:96//Hs.80965:AA493284

F-PLACE1010771//ESTs, Highly similar to TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP [*Mus musculus*]//6.0e-45:251:94//Hs.11379:AA594140

F-PLACE1010786

F-PLACE1010800

F-PLACE1010802//EST//0.94:128:64//Hs.120366:AA719157

F-PLACE1010811//ESTs//0.89:339:59//Hs.127314:N48085

F-PLACE1010833//ESTs, Weakly similar to allograft inflammatory factor-1 [*H.sapiens*]//2.9e-28:245:79//Hs.132736:AA583494

F-PLACE1010856//ESTs//1.5e-06:95:87//Hs.17401:W81048

F-PLACE1010857//ESTs, Weakly similar to KIAA0157 gene product is novel. [*H.sapiens*]//5.8e-67:336:97//Hs.130135:AA905493

F-PLACE1010870//Zinc finger protein 43 (HTF6)//9.7e-40:498:69//Hs.74107:X59244

F-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds//3.7e-149:694:98//Hs.118087:AB011182

F-PLACE1010891//ESTs//6.9e-54:377:87//Hs.24453:R31671

F-PLACE1010896//Human homologue of yeast sec7 mRNA, complete cds//0.64:1

67:65//Hs.1050:M85169
 F-PLACE1010900
 F-PLACE1010916//EST//0.55:151:66//Hs.145800:AI269981
 F-PLACE1010917
 F-PLACE1010925//ESTs//2.6e-81:437:94//Hs.5876:H26537
 F-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//3.1
 e-139:653:98//Hs.74750:AB011126
 F-PLACE1010942//Homo sapiens intersectin short form mRNA, complete cds//
 2.9e-91:437:98//Hs.66392:AF064244
 F-PLACE1010944//ESTs//1.3e-17:117:91//Hs.29444:W30985
 F-PLACE1010947//EST//0.97:93:72//Hs.162299:AA555154
 F-PLACE1010954//Apolipoprotein B (including Ag(x) antigen)//0.28:444:59/
 /Hs.585:X04506
 F-PLACE1010960//ESTs//0.98:238:60//Hs.163674:AA506632
 F-PLACE1010965//ESTs//3.1e-74:376:96//Hs.115679:AI379721
 F-PLACE1011026//EST//0.022:222:60//Hs.47154:N50931
 F-PLACE1011032//EST//1.1e-05:88:79//Hs.118024:N34032
 F-PLACE1011041//Human density enhanced phosphatase-1 mRNA, complete cds/
 /0.28:179:67//Hs.1177:U10886
 F-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERAS
 E BETA 2//6.2e-11:207:68//Hs.994:M95678
 F-PLACE1011054//H.sapiens OBF-1 mRNA for octamer binding factor 1//6.1e-
 35:310:78//Hs.2407:Z49194
 F-PLACE1011056//Human putative serine/threonine protein kinase PRK (prk)
 mRNA, complete cds//0.74:228:61//Hs.153640:U56998
 F-PLACE1011057//EST//2.5e-80:388:98//Hs.126466:AA913320
 F-PLACE1011090//ESTs//1.4e-94:469:97//Hs.106448:R76663
 F-PLACE1011109//ESTs//0.13:303:62//Hs.49294:AA418037
 F-PLACE1011114//ESTs//5.8e-12:75:100//Hs.147422:AI214317

F-PLACE1011133//ESTs//0.17:225:62//Hs.132853:AI370857
 F-PLACE1011143//ESTs//0.013:264:63//Hs.115368:AA629949
 F-PLACE1011160
 F-PLACE1011165//Galactokinase 2//2.7e-32:194:92//Hs.129228:M84443
 F-PLACE1011185//EST//1.4e-34:261:83//Hs.140250:AA708114
 F-PLACE1011203//Homo sapiens chromosome 18q11 beta-1,4-galactosyltransfe
 rase mRNA, complete cds//6.9e-124:576:99//Hs.159140:AF038664
 F-PLACE1011214//ESTs, Weakly similar to B0035.14 [C.elegans] //9.7e-101:4
 69:99//Hs.8241:AA283057
 F-PLACE1011219//ESTs, Weakly similar to coded for by C. elegans cDNA CEE
 SL70F [C.elegans] //2.6e-62:221:88//Hs.101821:W27452
 F-PLACE1011221//ESTs//0.46:238:62//Hs.32853:AA015751
 F-PLACE1011229//Homo sapiens mRNA for KIAA0529 protein, partial cds//1.4
 e-147:675:99//Hs.23168:AB011101
 F-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21//5.9e-71:350:9
 8//Hs.15144:AC005014
 F-PLACE1011273//ESTs//1.0:222:59//Hs.35274:AA495803
 F-PLACE1011291//Homo sapiens clone 24712 unknown mRNA, partial cds//3.4e
 -09:191:65//Hs.140950:AF070637
 F-PLACE1011296//ESTs//0.019:137:63//Hs.140654:AA865915
 F-PLACE1011310//EST//0.066:336:58//Hs.162529:AA584160
 F-PLACE1011325//ESTs//7.4e-43:229:96//Hs.21081:H08310
 F-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA,
 complete cds//4.8e-151:696:99//Hs.5819:AF102265
 F-PLACE1011340//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
 0501//1.5e-20:120:81//Hs.159897:AB007970
 F-PLACE1011371//Human mRNA for PK-120//9.5e-35:684:63//Hs.76415:D38535
 F-PLACE1011375//ESTs, Moderately similar to potassium channel protein Ra
 w3 [R.norvegicus] //6.7e-68:325:99//Hs.107245:AA627053

F-PLACE1011399//ESTs//8.6e-05:285:61//Hs.130105:AA904868
 F-PLACE1011419//ESTs//0.70:240:62//Hs.159650:N95552
 F-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds//1.5
 e-158:743:98//Hs.10801:AB011102
 F-PLACE1011452//Human Line-1 repeat mRNA with 2 open reading frames//1.9
 e-53:557:72//Hs.23094:M19503
 F-PLACE1011465//EST//3.1e-58:380:85//Hs.131605:AI025204
 F-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds//1.
 5e-152:703:99//Hs.111138:AB018255
 F-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//
 1.7e-146:675:99//Hs.11183:AF065482
 F-PLACE1011492//ESTs//2.0e-35:186:98//Hs.125886:AA884264
 F-PLACE1011503//EST//0.67:149:65//Hs.149774:AI285997
 F-PLACE1011520//ESTs//0.00014:213:64//Hs.119889:AA705319
 F-PLACE1011563//ESTs//2.2e-61:394:86//Hs.117718:AA883476
 F-PLACE1011567//Homo sapiens DEC-205 mRNA, complete cds//3.1e-46:325:84/
 /Hs.153563:AF011333
 F-PLACE1011576//Homo sapiens hematopoietic cell derived zinc finger prot
 ein mRNA, complete cds//4.3e-67:268:86//Hs.86371:AF054180
 F-PLACE1011586//Homo sapiens hLRp105 mRNA for LDL receptor related prote
 in 105, complete cds//0.98:153:65//Hs.143641:AB009462
 F-PLACE1011635//Homo sapiens Jagged 2 mRNA, complete cds//0.00029:585:57
 //Hs.106387:AF029778
 F-PLACE1011641
 F-PLACE1011643//Homo sapiens mRNA for KIAA0293 gene, partial cds//0.0005
 8:499:58//Hs.12784:AB006631
 F-PLACE1011646//EST//3.2e-26:201:68//Hs.140349:AA757661
 F-PLACE1011649//ESTs//0.25:145:64//Hs.23033:R46086
 F-PLACE1011650//ESTs//0.041:96:77//Hs.119351:AA447745

F-PLACE1011664//Human mRNA for stac, complete cds//1.0:245:60//Hs.56045:
D86640

F-PLACE1011675//Cell division cycle 27//0.098:448:57//Hs.73151:S78234

F-PLACE1011682//EST//9.6e-06:119:72//Hs.93664:N23366

F-PLACE1011719//Human mRNA for KIAA0352 gene, complete cds//0.92:365:60/
/Hs.17262:AB002350

F-PLACE1011725

F-PLACE1011729//EST//0.56:304:58//Hs.86378:AA210853

F-PLACE1011749//ESTs//4.3e-88:443:96//Hs.132850:AA779891

F-PLACE1011762//ESTs//0.012:149:68//Hs.145075:AI208240

F-PLACE1011778//ESTs//0.00016:199:64//Hs.160395:AI393693

F-PLACE1011783//EST//1.0:119:66//Hs.162191:AA534660

F-PLACE1011858//Human novel homeobox mRNA for a DNA binding protein//8.9
e-05:477:59//Hs.37035:U07664

F-PLACE1011874//EST//0.20:118:66//Hs.127351:AA954775

F-PLACE1011875//Homo sapiens mRNA for KIAA0580 protein, partial cds//5.3
e-110:526:98//Hs.22572:AB011152

F-PLACE1011891//ESTs//1.8e-58:397:88//Hs.84698:AA725913

F-PLACE1011896//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//9.4e-09:4
78:56//Hs.107747:AI357868

F-PLACE1011922//ESTs//0.49:249:62//Hs.152627:AA595817

F-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds//
3.7e-140:664:98//Hs.3838:AF059617

F-PLACE1011962//EST//1.7e-07:81:85//Hs.104333:AA250763

F-PLACE1011964//EST//6.6e-38:412:74//Hs.140562:AA826514

F-PLACE1011982//ESTs//0.40:405:60//Hs.127743:AI261591

F-PLACE1011995//ESTs//1.7e-22:486:64//Hs.105157:AA527514

F-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds//4.0
e-148:690:98//Hs.88756:AB018256

F-PLACE2000003//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0487//6.5e-54:290:81//Hs.92381:AB007956

F-PLACE2000006//ESTs//0.067:224:62//Hs.144100:AI205503

F-PLACE2000007//ESTs//8.1e-23:147:91//Hs.128530:AA325330

F-PLACE2000011//Interleukin 10//4.2e-42:362:78//Hs.2180:M57627

F-PLACE2000014//EST//0.10:214:61//Hs.160247:AI138831

F-PLACE2000015//Interleukin 10//1.4e-44:393:78//Hs.2180:M57627

F-PLACE2000017

F-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose
polymerase mRNA, partial cds//5.7e-85:844:72//Hs.7928:AF082557

F-PLACE2000030

F-PLACE2000033//Human adhesion molecule ninjurin mRNA, complete cds//0.8
5:234:66//Hs.11342:U91512

F-PLACE2000034//Homo sapiens mRNA for KIAA0607 protein, partial cds//0.0
58:348:62//Hs.94653:AB011179

F-PLACE2000039//Human plectin (PLEC1) mRNA, complete cds//0.0058:473:59/
/Hs.79706:U53204

F-PLACE2000047//ESTs//4.9e-32:328:75//Hs.141024:H07128

F-PLACE2000050//ESTs//3.0e-36:270:83//Hs.155512:AA663966

F-PLACE2000061

F-PLACE2000062//Human membrane-associated lectin type-C mRNA//2.9e-114:6
62:86//Hs.23759:M98457

F-PLACE2000072//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//7
.1e-135:631:98//Hs.9443:AF027219

F-PLACE2000097//ESTs//0.021:117:70//Hs.132811:AI034333

F-PLACE2000100

F-PLACE2000103//ESTs//1.1e-56:284:98//Hs.144786:AI219219

F-PLACE2000111//H.sapiens mRNA for 1-acylglycerol-3-phosphate O-acyltran
sferase//0.76:215:65//Hs.6587:U56417

F-PLACE2000115

F-PLACE2000124//Human mRNA for KIAA0355 gene, complete cds//2.8e-49:400:
79//Hs.153014:AB002353

F-PLACE2000132

F-PLACE2000136//ESTs, Moderately similar to hypothetical protein [H.sapi
ens]//1.2e-08:245:64//Hs.140343:AA718911

F-PLACE2000140//Adenylate kinase 2 (adk2)//3.7e-24:162:90//Hs.83833:U546
45

F-PLACE2000164

F-PLACE2000170

F-PLACE2000172//ESTs//0.64:239:62//Hs.31175:AI219179

F-PLACE2000176

F-PLACE2000187

F-PLACE2000216

F-PLACE2000223//EST//0.0092:171:60//Hs.162830:AA643933

F-PLACE2000235//Human mRNA for KIAA0298 gene, complete cds//1.6e-38:792:
63//Hs.21560:AB002296

F-PLACE2000246//Homo sapiens mRNA for KIAA0795 protein, partial cds//1.5
e-74:367:98//Hs.22926:AB018338

F-PLACE2000264//Homo sapiens mRNA for KIAA0792 protein, complete cds//2.
0e-29:366:73//Hs.119387:AB007958

F-PLACE2000274//Homo sapiens mRNA for dynein heavy chain//1.0e-23:650:62
//Hs.144672:AJ000522

F-PLACE2000302//ESTs//1.7e-05:66:89//Hs.55572:W37560

F-PLACE2000305//ESTs//1.6e-78:382:98//Hs.136731:AA745869

F-PLACE2000317

F-PLACE2000335//Fc fragment of IgE, high affinity I, receptor for; beta
polypeptide//6.1e-24:295:76//Hs.30:M89796

F-PLACE2000341//Human sodium iodide symporter mRNA, complete cds//6.8e-2

1:593:61//Hs.103983:U66088

F-PLACE2000342//Centromere protein B (80kD)//1.4e-06:326:61//Hs.85004:X0
5299

F-PLACE2000347//ESTs, Moderately similar to F18547_1 [H.sapiens]//3.7e-1
6:139:82//Hs.28209:AI073817

F-PLACE2000359//ESTs//5.0e-19:251:71//Hs.58272:W76645

F-PLACE2000366//ESTs//1.7e-37:399:75//Hs.136646:AA748045

F-PLACE2000371//EST//0.65:107:65//Hs.157677:AI358861

F-PLACE2000373//ESTs//0.30:207:59//Hs.143902:AI131032

F-PLACE2000379//ESTs//1.3e-64:402:87//Hs.146307:AA584638

F-PLACE2000394//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0484//1.0e-87:694:80//Hs.158095:AB007953

F-PLACE2000398

F-PLACE2000399

F-PLACE2000404

F-PLACE2000411

F-PLACE2000419//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.0e-52:46
3:74//Hs.113283:AF018080

F-PLACE2000425//EST//0.44:168:62//Hs.44677:N34966

F-PLACE2000427

F-PLACE2000433//ESTs//4.7e-18:213:74//Hs.110187:AA699719

F-PLACE2000435//EST//4.7e-05:159:64//Hs.123604:AA815257

F-PLACE2000438//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalact
osaminyltransferase (T2)//1.9e-20:418:64//Hs.130181:X85019

F-PLACE2000450//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.0e-83:32
4:81//Hs.113283:AF018080

F-PLACE2000455//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNIN
G ENTRY !!!! [H.sapiens]//4.0e-05:100:73//Hs.104239:AA488082

F-PLACE2000458//H.sapiens mRNA for hFat protein//0.0010:545:57//Hs.91107

:X87241

F-PLACE2000465//ESTs//4.4e-38:377:75//Hs.55855:AA621381

F-PLACE2000477//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.8e-68:52
0:81//Hs.113283:AF018080

F-PLACE3000004//Human EYA3 homolog (EYA3) mRNA, complete cds//3.9e-14:20
4:73//Hs.46925:Y10262

F-PLACE3000009//Human mRNA for KIAA0386 gene, complete cds//4.8e-59:696:
69//Hs.101359:AB002384

F-PLACE3000020//Prostaglandin I2 (prostacyclin) receptor (IP)//0.00081:5
00:61//Hs.393:D38128

F-PLACE3000029

F-PLACE3000059//ESTs//0.0026:49:100//Hs.42913:AI082248

F-PLACE3000070//ESTs//5.6e-15:202:74//Hs.154993:AA142842

F-PLACE3000103//Homo sapiens cofactor of initiator function (CIF150) mRN
A, complete cds//1.0:186:62//Hs.122752:AF026445

F-PLACE3000119//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.8
e-48:283:83//Hs.23711:AB018295

F-PLACE3000121

F-PLACE3000124//Thromboxane A2 receptor//1.1e-55:195:83//Hs.89887:D38081

F-PLACE3000136//Homo sapiens mRNA for KIAA0703 protein, complete cds//1.
0:194:59//Hs.6168:AB014603

F-PLACE3000142//EST//0.41:179:59//Hs.137438:AA282243

F-PLACE3000145//ESTs//3.5e-25:145:96//Hs.163950:AA683016

F-PLACE3000147//EST//5.0e-43:285:86//Hs.160895:AI365871

F-PLACE3000148

F-PLACE3000155//Homo sapiens mRNA for KIAA0672 protein, complete cds//5..
6e-80:382:99//Hs.6336:AB014572

F-PLACE3000156//ESTs//0.00015:277:62//Hs.156834:AI336023

F-PLACE3000157//Calcium channel, voltage-dependent, P/Q type, alpha 1A s

ubunit//0.54:320:60//Hs.96253:U79666

F-PLACE3000158//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.

9e-66:319:88//Hs.153468:AB011147

F-PLACE3000160

F-PLACE3000169//Small inducible cytokine A5 (RANTES)//1.3e-64:501:80//Hs

.155464:AF088219

F-PLACE3000194

F-PLACE3000197

F-PLACE3000199//EST//1.0:108:68//Hs.98488:AA426546

F-PLACE3000207//EST//1.0e-32:184:75//Hs.160146:AI049975

F-PLACE3000208//CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN PRECU

RSOR//1.0:271:61//Hs.77522:X62744

F-PLACE3000218//EST//1.3e-46:317:84//Hs.162197:AA535216

F-PLACE3000220//EST//9.3e-95:443:99//Hs.112702:AA609377

F-PLACE3000221//Homo sapiens DNA fragmentation factor 40 kDa subunit (DF

F40) mRNA, complete cds//9.2e-56:200:85//Hs.133089:AF064019

F-PLACE3000226

F-PLACE3000230//EST//6.1e-16:173:72//Hs.148578:AI201568

F-PLACE3000242//Human DNA sequence from clone 1409 on chromosome Xp11.1-

11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a

alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6

-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. C

ontains ESTs, STSs and genomic marker DXS8032//1.2e-54:434:80//Hs.4943:Z

98046

F-PLACE3000244

F-PLACE3000254//NUCLEOLIN//2.6e-05:445:60//Hs.79110:M60858

F-PLACE3000271//ESTs//1.6e-25:195:72//Hs.108452:H78650

F-PLACE3000276//ESTs//1.0e-13:274:66//Hs.28589:AI004944

F-PLACE3000304//EST//0.043:210:61//Hs.132378:AI026770

F-PLACE3000310

F-PLACE3000320//EST//1.2e-12:188:70//Hs.145771:AI269586

F-PLACE3000322//Small inducible cytokine A5 (RANTES)//4.7e-29:252:80//Hs.
.155464:AF088219

F-PLACE3000331

F-PLACE3000339//Homo sapiens mRNA for KIAA0645 protein, complete cds//0.
91:222:61//Hs.155987:AB014545

F-PLACE3000341//EST//1.8e-05:394:58//Hs.112894:AA620741

F-PLACE3000350//ESTs, Highly similar to SERINE/THREONINE-PROTEIN KINASE
SULU [Caenorhabditis elegans]//2.9e-59:474:77//Hs.125850:AA885355

F-PLACE3000352//H.sapiens OBF-1 mRNA for octamer binding factor 1//2.5e-
48:442:78//Hs.2407:Z49194

F-PLACE3000353//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylglact
osaminyltransferase (T1)//0.78:234:63//Hs.7498:U41514

F-PLACE3000362//EST//6.5e-25:302:73//Hs.140504:AA810441

F-PLACE3000363

F-PLACE3000365//ESTs//0.81:200:60//Hs.141556:N49928

F-PLACE3000373//ESTs//0.0071:82:73//Hs.136310:AA442641

F-PLACE3000388//ESTs//7.9e-16:235:71//Hs.44701:AA830432

F-PLACE3000399//Clathrin, light polypeptide (Lcb)//5.2e-70:391:81//Hs.73
919:X81637

F-PLACE3000400//ESTs//0.53:162:66//Hs.49303:AA810785

F-PLACE3000401//EST//2.3e-35:178:100//Hs.162851:AA632270

F-PLACE3000402//ESTs//2.4e-84:425:96//Hs.148962:AI219715

F-PLACE3000405//EST//2.1e-39:452:73//Hs.140414:AA778541

F-PLACE3000406//Homo sapiens apoptotic protease activating factor 1 (Apa
f-1) mRNA, complete cds//1.9e-07:116:78//Hs.77579:AF013263

F-PLACE3000413//ESTs, Weakly similar to methyl sterol oxidase [H.sapiens
]//1.6e-51:260:98//Hs.122512:H61502

F-PLACE3000416//Homo sapiens mRNA for KIAA0801 protein, complete cds//0.00020:630:57//Hs.17585:AB018344

F-PLACE3000425//EST//3.8e-34:286:79//Hs.135301:AI039161

F-PLACE3000455//Homo sapiens mRNA for cytochrome b small subunit of complex II, complete cds//3.6e-32:183:93//Hs.108326:AB006202

F-PLACE3000475//ESTs//1.9e-09:422:61//Hs.145783:AA081874

F-PLACE3000477//H.sapiens mRNA for chemokine receptor D6//1.0:426:54//Hs.117572:U94888

F-PLACE4000009//TRICHOHYALIN//3.1e-09:692:60//Hs.82276:L09190

F-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds//3.6e-118:331:100//Hs.105399:AB018352

F-PLACE4000034//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//1.1e-06:244:63//Hs.154050:AC004131

F-PLACE4000049//Homo sapiens clone 24619 mRNA sequence//4.3e-45:371:79//Hs.139088:AF070533

F-PLACE4000052//Human ATP binding cassette transporter (ABCR) mRNA, complete cds//1.4e-53:669:67//Hs.40993:AF000148

F-PLACE4000063

F-PLACE4000089//ESTs//2.2e-10:121:85//Hs.49391:W00713

F-PLACE4000093//ESTs//0.0053:273:60//Hs.136952:AA825819

F-PLACE4000100//ESTs//8.0e-21:246:73//Hs.140207:N32058

F-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds//3.8e-147:684:99//Hs.129937:AB007931

F-PLACE4000128//Homo sapiens ES/130 mRNA, complete cds//0.23:398:60//Hs.98614:AF006751

F-PLACE4000129

F-PLACE4000131//ESTs//2.4e-13:194:72//Hs.41418:H90627

F-PLACE4000147//ESTs//0.0060:324:60//Hs.85640:AA535856

F-PLACE4000156//Zinc finger protein 136 (clone pHZ-20)//2.3e-89:764:76//

Hs.69740:U09367
 F-PLACE4000192
 F-PLACE4000211
 F-PLACE4000222//EST//1.9e-15:317:66//Hs.149206:AI246594
 F-PLACE4000230//Human mRNA for KIAA0331 gene, complete cds//0.0048:258:6
 0//Hs.146395:AB002329
 F-PLACE4000233//ESTs//4.4e-38:240:80//Hs.114605:AI304317
 F-PLACE4000247//Homo sapiens mitochondrial outer membrane protein (TOM40
) mRNA, nuclear gene encoding mitochondrial protein, complete cds//0.009
 5:156:69//Hs.30928:AF043250
 F-PLACE4000250//ESTs//3.8e-72:377:94//Hs.124234:T89609
 F-PLACE4000252//ESTs//1.0:196:64//Hs.144869:AA493886
 F-PLACE4000259//Homo sapiens mRNA for KIAA0788 protein, partial cds//6.2
 e-27:191:87//Hs.2397:Z70200
 F-PLACE4000261
 F-PLACE4000269//ESTs, Weakly similar to coded for by C. elegans cDNA yk5
 2b10.3 [C.elegans]//9.5e-41:202:100//Hs.118849:AA215645
 F-PLACE4000270
 F-PLACE4000300
 F-PLACE4000320//FKBP-RAPAMYCIN ASSOCIATED PROTEIN//4.5e-23:135:96//Hs.15
 5952:U88966
 F-PLACE4000323//EST//6.7e-09:180:68//Hs.116769:AA630365
 F-PLACE4000326//ESTs//2.1e-94:453:98//Hs.103177:W72798
 F-PLACE4000344//EST//6.4e-05:135:67//Hs.146729:AI147292
 F-PLACE4000367
 F-PLACE4000369
 F-PLACE4000379//EST//3.9e-42:381:79//Hs.162335:AA564256
 F-PLACE4000387//ESTs//0.19:93:69//Hs.154173:AI379823
 F-PLACE4000392//ESTs//0.0015:381:59//Hs.120172:AA709046

F-PLACE4000401//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.1
e-47:605:71//Hs.153026:AB014540

F-PLACE4000411//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//
4.7e-33:159:81//Hs.154257:AI275982

F-PLACE4000431//Homo sapiens mRNA for KIAA0788 protein, partial cds//1.3
e-45:263:92//Hs.2397:Z70200

F-PLACE4000445

F-PLACE4000450

F-PLACE4000465//ESTs//1.5e-11:273:65//Hs.145783:AA081874

F-PLACE4000487//Sialophorin (gPL115, leukosialin, CD43)//3.0e-14:189:71/
/Hs.80738:X52075

F-PLACE4000489//ESTs//0.94:104:68//Hs.125119:R38951

F-PLACE4000494//ESTs//1.0:185:60//Hs.143053:AI126289

F-PLACE4000521//ESTs//0.0027:161:70//Hs.135740:AA651731

F-PLACE4000522//ESTs, Highly similar to NEUROGENIC LOCUS NOTCH PROTEIN
HOMOLOG 1 PRECURSOR [Homo sapiens]//0.047:119:65//Hs.129053:AA767022

F-PLACE4000548

F-PLACE4000558//Homo sapiens mRNA for DFFRY protein, abundant transcript
//0.0035:510:59//Hs.39163:AF000986

F-PLACE4000581

F-PLACE4000590//ESTs, Highly similar to POL POLYPROTEIN [Friend murine
leukemia virus (isolate 57)]//3.4e-13:275:68//Hs.113980:AI034080

F-PLACE4000593//ESTs, Weakly similar to F25D7.1 [C.elegans]//5.2e-28:239
:79//Hs.109084:AI004675

F-PLACE4000612//Keratin 9//0.27:207:64//Hs.2783:Z29074

F-PLACE4000638//Homo sapiens mRNA from chromosome 5q21-22, clone:sF2//3.
5e-47:562:69//Hs.129685:AB002446

F-PLACE4000650

F-PLACE4000654

F-PLACE4000670//ESTs//6.1e-88:411:100//Hs.130688:AI028132

F-SKNMC1000011//Centromere protein B (80kD)//0.0013:243:62//Hs.85004:X05
299

F-SKNMC1000013//ESTs, Highly similar to MULTIDRUG RESISTANCE PROTEIN HO
MOLOG 50 [*Drosophila melanogaster*]//2.5e-36:197:96//Hs.118634:U66688

F-SKNMC1000046//Homo sapiens mRNA for KIAA0654 protein, partial cds//2.5
e-148:706:98//Hs.109299:AB014554

F-SKNMC1000050//Calpain, large polypeptide L2//4.1e-53:330:90//Hs.76288:
M23254

F-SKNMC1000091//ESTs//3.3e-64:420:88//Hs.90997:AA946877

F-THYRO1000017//Human mRNA for KIAA0315 gene, partial cds//1.0:310:60//H
s.3989:AB002313

F-THYRO1000026//H.sapiens OBF-1 mRNA for octamer binding factor 1//2.9e-
35:299:81//Hs.2407:Z49194

F-THYRO1000034

F-THYRO1000035//ESTs//4.1e-37:317:79//Hs.141254:AI334099

F-THYRO1000040//ESTs//0.30:331:59//Hs.87176:AI148326

F-THYRO1000070//Human mRNA for KIAA0347 gene, complete cds//0.069:278:63
//Hs.101996:AB002345

F-THYRO1000072//Homo sapiens clone 23584 mRNA sequence//8.7e-86:722:77//
Hs.6654:AB014557

F-THYRO1000085

F-THYRO1000092//ESTs//3.1e-100:469:99//Hs.132207:AI148065

F-THYRO1000107

F-THYRO1000111//Human Line-1 repeat mRNA with 2 open reading frames//6.8
e-106:690:86//Hs.23094:M19503

F-THYRO1000121

F-THYRO1000124//Human mRNA for alanine aminotransferase//0.0026:420:58//
Hs.103502:U70732

F-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds//2.8e-155:732:98//Hs.87619:AF087142

F-THYRO1000132//ESTs//1.9e-35:164:79//Hs.139179:AA650203

F-THYRO1000156//EST//0.32:102:68//Hs.139634:AA478416

F-THYRO1000163//Small inducible cytokine A5 (RANTES)//5.2e-50:331:85//Hs.155464:AF088219

F-THYRO1000173//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//1.1e-05:261:61//Hs.152936:D63475

F-THYRO1000186//H.sapiens mRNA for phosphoinositide 3-kinase//3.7e-41:270:87//Hs.101238:Y11312

F-THYRO1000187//EST//0.11:227:62//Hs.101773:H23270

F-THYRO1000190//ESTs//0.82:194:63//Hs.128818:AA976883

F-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease//2.4e-175:805:99//Hs.43445:AJ005698

F-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds//4.0e-88:616:84//Hs.79672:AB014552

F-THYRO1000206//EST//0.96:291:61//Hs.104962:AA443848

F-THYRO1000221//Human clone 23589 mRNA sequence//0.035:242:62//Hs.11506:U79297

F-THYRO1000241//EST//0.48:102:69//Hs.160764:AI313322

F-THYRO1000242//Zinc finger protein 84 (HPF2)//1.2e-42:534:64//Hs.9450:M27878

F-THYRO1000253//Homo sapiens mRNA for KIAA0690 protein, partial cds//0.61:211:64//Hs.60103:AB014590

F-THYRO1000270

F-THYRO1000279//ESTs//0.0020:104:72//Hs.121476:AI215500

F-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds//1.3e-180:848:98//Hs.25846:AB016068

F-THYRO1000320//ESTs, Weakly similar to Similar to glutamate decarboxyla

se [C.elegans] //7.6e-92:431:99//Hs.122719:AA777803
 F-THYRO1000327//Autocrine motility factor receptor//2.8e-52:290:93//Hs.8
 0731:M63175
 F-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds//7.2
 e-164:763:98//Hs.12002:AB018333
 F-THYRO1000358//Human selenium-binding protein (hsBP) mRNA, complete cds
 //6.9e-34:177:84//Hs.7833:U29091
 F-THYRO1000368//ESTs//0.0011:55:96//Hs.34994:AA252919
 F-THYRO1000381//Homo sapiens mRNA for KIAA0562 protein, complete cds//0.
 081:240:62//Hs.118401:AB011134
 F-THYRO1000387//EST//3.6e-14:197:71//Hs.139399:AA416855
 F-THYRO1000394//ESTs, Weakly similar to No definition line found [C.eleg
 ans] //5.8e-39:245:91//Hs.119095:T79413
 F-THYRO1000395//EST//5.8e-69:333:99//Hs.156524:AA724572
 F-THYRO1000401//ESTs//1.8e-24:132:98//Hs.54852:W26238
 F-THYRO1000438//EST//1.9e-05:217:63//Hs.115930:AA579773
 F-THYRO1000452//B cell lymphoma protein 6 (zinc finger protein 51)//0.09
 6:306:60//Hs.155024:U00115
 F-THYRO1000471//Tyrosine aminotransferase//5.6e-44:403:77//Hs.2999:X5252
 0
 F-THYRO1000484//EST, Weakly similar to putative p150 [H.sapiens]//8.9e-2
 2:248:76//Hs.162011:AA513663
 F-THYRO1000488
 F-THYRO1000501//H.sapiens Staf50 mRNA//3.2e-75:615:77//Hs.68054:X82200
 F-THYRO1000502//ESTs//1.0:350:57//Hs.119749:AA689298
 F-THYRO1000505//Interleukin 13//0.95:245:60//Hs.845:U31120
 F-THYRO1000558//EST//1.3e-24:351:64//Hs.142326:AA351877
 F-THYRO1000569//Homo sapiens mRNA for dihydropyrimidinase related protei
 n 4, complete cds//0.28:229:61//Hs.100058:AB006713

F-THYRO1000570//EST//0.80:171:61//Hs.112790:AA609949
 F-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete
 cds//2.4e-168:808:97//Hs.151411:AF075587
 F-THYRO1000596//EST//9.5e-94:461:96//Hs.135397:AI056322
 F-THYRO1000602//EST//4.9e-06:80:80//Hs.162135:AA526331
 F-THYRO1000605//Guanylate cyclase 1, soluble, alpha 2//0.44:182:62//Hs.2
 685:Z50053
 F-THYRO1000625//Thromboxane A2 receptor//4.5e-45:323:82//Hs.89887:D38081
 F-THYRO1000637//ESTs//4.4e-24:255:75//Hs.101014:AA194941
 F-THYRO1000641//ESTs//0.00017:375:58//Hs.32703:AA054125
 F-THYRO1000658//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA,
 3429 nt]//1.8e-09:127:77//Hs.116007:S79267
 F-THYRO1000662
 F-THYRO1000666//ESTs//1.9e-28:149:99//Hs.105187:AI394157
 F-THYRO1000676//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA,
 3429 nt]//5.7e-49:281:77//Hs.116007:S79267
 F-THYRO1000684//ESTs, Weakly similar to band-6-protein [H.sapiens]//0.46
 :368:57//Hs.26557:AA480380
 F-THYRO1000699//ESTs//1.6e-10:314:65//Hs.139212:AA243452
 F-THYRO1000712//ESTs//3.3e-42:211:99//Hs.69330:AI056324
 F-THYRO1000715//Human plectin (PLEC1) mRNA, complete cds//2.9e-06:631:59
 //Hs.79706:U53204
 F-THYRO1000734//ESTs//8.4e-08:226:64//Hs.125754:AA806085
 F-THYRO1000748//Homo sapiens KIAA0411 mRNA, complete cds//3.1e-35:339:74
 //Hs.7977:AB007871
 F-THYRO1000756//Homo sapiens protocadherin (PCDH8) mRNA, complete cds//1
 .0:209:62//Hs.19492:AF061573
 F-THYRO1000777//Human mRNA for KIAA0147 gene, partial cds//0.00069:636:5
 7//Hs.158132:D63481

F-THYRO1000783//Homo sapiens Arp2/3 protein complex subunit p41-Arc (ARC
41) mRNA, complete cds//0.70:452:58//Hs.11538:AF006084

F-THYRO1000787

F-THYRO1000793

F-THYRO1000796

F-THYRO1000805//Homo sapiens mRNA from chromosome 5q21-22, clone:sF2//9.
4e-36:561:68//Hs.129685:AB002446

F-THYRO1000815//Human mRNA for KIAA0118 gene, partial cds//1.2e-45:465:7
5//Hs.154326:D42087

F-THYRO1000829//ESTs//1.7e-66:361:95//Hs.7906:H16339

F-THYRO1000843

F-THYRO1000852//ESTs//6.2e-23:204:81//Hs.144452:AA838788

F-THYRO1000855//ESTs//0.049:159:64//Hs.163532:A1424170

F-THYRO1000865//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
RY !!!! [H.sapiens]//3.0e-33:190:75//Hs.133526:N21103

F-THYRO1000895//ESTs//3.8e-24:191:84//Hs.132722:AA618531

F-THYRO1000916//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0487//1.8e-43:318:79//Hs.92381:AB007956

F-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B)
mRNA, partial cds//3.0e-179:839:98//Hs.78106:AF079529

F-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE//1.1e-33:759:63//Hs.79
217:M77836

F-THYRO1000951//MUELLERIAN INHIBITING FACTOR PRECURSOR//0.055:662:56//Hs
.112432:AC005263

F-THYRO1000952//Human mRNA for KIAA0208 gene, complete cds//0.98:177:65/
/Hs.83558:D86963

F-THYRO1000974//Homo sapiens putative ATP-dependent mitochondrial RNA he
licase (SUV3) mRNA, nuclear gene encoding mitochondrial protein, complet
e cds//2.7e-15:123:90//Hs.106469:AF042169

F-THYRO1000975//EST//0.45:172:62//Hs.105449:AA513907
 F-THYRO1000983
 F-THYRO1000984//EST//0.0075:119:65//Hs.150347:AA984646
 F-THYRO1000988//ESTs//0.056:99:71//Hs.153409:AI224307
 F-THYRO1001003
 F-THYRO1001031//Thiopurine S-methyltransferase//3.8e-44:568:71//Hs.51124
 :AF019369
 F-THYRO1001033//H.sapiens mRNA for cyclin II//0.0061:287:60//Hs.3232:Z4
 6788
 F-THYRO1001062//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.2e-45:394:79//Hs.
 51048:X68830
 F-THYRO1001093//Human mRNA for KIAA0355 gene, complete cds//3.4e-33:421:
 72//Hs.153014:AB002353
 F-THYRO1001100//Human DNA-binding protein mRNA, 3' end//2.1e-74:741:74//H
 s.159249:Z99130
 F-THYRO1001120//Homo sapiens deltex (Dx) mRNA, complete cds//4.5e-18:447
 :62//Hs.124024:AF053700
 F-THYRO1001121//ESTs//0.92:257:61//Hs.118246:N95416
 F-THYRO1001133//EST//1.1e-38:367:75//Hs.144175:H70425
 F-THYRO1001134//ESTs//1.4e-28:186:91//Hs.109468:W52074
 F-THYRO1001142//ESTs//1.8e-44:332:82//Hs.146811:AA410788
 F-THYRO1001173
 F-THYRO1001177//ESTs//7.7e-40:240:84//Hs.155384:Z78385
 F-THYRO1001189//ESTs//2.1e-36:323:76//Hs.120206:AI089163
 F-THYRO1001204
 F-THYRO1001213//Small inducible cytokine A5 (RANTES)//3.1e-43:256:81//Hs
 .155464:AF088219
 F-THYRO1001262//ESTs//7.9e-44:279:87//Hs.138856:H47461
 F-THYRO1001271//Homo sapiens mRNA for synaptogyrin 3//0.0045:273:60//Hs.

6467:AJ002309

F-THYRO1001287//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds
//0.014:178:66//Hs.125315:AF027156

F-THYRO1001290//ESTs//3.9e-43:145:99//Hs.147797:AA069836

F-THYRO1001313//ESTs//1.0:244:61//Hs.127488:AA528182

F-THYRO1001320//ESTs//0.062:126:67//Hs.133296:AI311872

F-THYRO1001321//Homo sapiens DEC-205 mRNA, complete cds//2.5e-35:560:68/
/Hs.153563:AF011333

F-THYRO1001322//ESTs//0.12:238:61//Hs.29169:N66545

F-THYRO1001347//ESTs//7.5e-61:293:99//Hs.129962:AA927207

F-THYRO1001363//ESTs//1.0e-16:178:78//Hs.163954:N57939

F-THYRO1001365//Homo sapiens KIAA0417 mRNA, complete cds//3.6e-18:187:79
//Hs.12385:AB007877

F-THYRO1001374//Homo sapiens mRNA for KIAA0707 protein, partial cds//7.4
e-157:740:97//Hs.138488:AB014607

F-THYRO1001401//EST//4.6e-14:171:76//Hs.157587:AI356993

F-THYRO1001403//ESTs//2.2e-50:464:79//Hs.118046:N49946

F-THYRO1001405//ESTs//1.7e-44:226:98//Hs.156667:AI347694

F-THYRO1001406//Hydroxysteroid (17-beta) dehydrogenase 3//2.8e-20:459:62
//Hs.477:U05659

F-THYRO1001411//ESTs//1.9e-41:342:78//Hs.146811:AA410788

F-THYRO1001426//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' f
lanking sequence//4.6e-33:153:81//Hs.102877:U41315

F-THYRO1001434//ESTs//1.1e-07:274:60//Hs.151093:AI224099

F-THYRO1001458//Myosin, heavy polypeptide 9, non-muscle//6.2e-60:653:71/
/Hs.44782:Z82215

F-THYRO1001480//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.3e-42:370:78//Hs.
51048:X68830

F-THYRO1001487//EST//1.0:88:71//Hs.160760:AI311943

F-THYRO1001534//ESTs//1.2e-94:457:98//Hs.125523:AA883904
 F-THYRO1001537//ESTs//3.5e-94:469:97//Hs.106448:R76663
 F-THYRO1001541//EST//1.4e-10:158:65//Hs.145159:AI150211
 F-THYRO1001559//ESTs//1.4e-07:91:81//Hs.43507:N24046
 F-THYRO1001570//ESTs//2.3e-41:280:80//Hs.119752:AA703335
 F-THYRO1001573//Homo sapiens clone 24778 unknown mRNA//2.7e-105:546:95//
 Hs.25306:AF070572
 F-THYRO1001584//Human RGP3 mRNA, complete cds//0.14:335:58//Hs.82294:U27
 655
 F-THYRO1001595//Human RSU-1/RSP-1 mRNA, complete cds//3.6e-35:165:84//Hs
 .75551:L12535
 F-THYRO1001602//ESTs//3.1e-42:350:80//Hs.138384:R72849
 F-THYRO1001605//EST//0.11:426:57//Hs.151206:AI126071
 F-THYRO1001617//ESTs//5.2e-43:345:81//Hs.8710:W07046
 F-THYRO1001637//ESTs, Weakly similar to anion exchanger [H.sapiens]//5.2
 e-13:108:86//Hs.141045:AA191659
 F-THYRO1001656//Solute carrier family 2 (facilitated glucose transporter
), member 4//0.099:540:55//Hs.95958:M91463
 F-THYRO1001661//ESTs//0.12:53:92//Hs.151586:W45568
 F-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59
 kDa isoform//8.0e-166:780:98//Hs.118633:AJ225089
 F-THYRO1001673//Von Hippel-Lindau syndrome//4.6e-25:212:73//Hs.78160:AF0
 10238
 F-THYRO1001703//Homo sapiens clone 24767 mRNA sequence//0.27:421:57//Hs.
 122908:AF070552
 F-THYRO1001706//ESTs//1.8e-24:142:95//Hs.112536:AI147691
 F-THYRO1001721//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila
 melanogaster]//2.5e-51:296:92//Hs.3826:U69560
 F-THYRO1001738//EST//6.9e-30:180:94//Hs.58641:W81229

F-THYRO1001745//ESTs//6.1e-49:244:98//Hs.97534:AA398813
 F-THYRO1001746//EST//0.96:119:63//Hs.144107:AI053590
 F-THYRO1001772//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
 RY !!!! [H.sapiens]//2.2e-21:182:81//Hs.118053:N75725
 F-THYRO1001793//ESTs//1.9e-93:439:99//Hs.150116:AI299324
 F-THYRO1001809//Human mRNA for KIAA0297 gene, partial cds//0.47:168:67//
 Hs.11711:AB002295
 F-THYRO1001828
 F-THYRO1001854//EST//0.038:128:67//Hs.160649:AI241823
 F-THYRO1001895//Intercellular adhesion molecule 1 (CD54), human rhinovir
 us receptor//9.6e-13:288:65//Hs.51061:M24283
 F-THYRO1001907//EST//1.9e-12:126:80//Hs.139296:AA350198
 F-VESEN1000122
 F-Y79AA1000013//ESTs//1.7e-72:369:96//Hs.97176:AA447885
 F-Y79AA1000033
 F-Y79AA1000037//Murine leukemia viral (bmi-1) oncogene homolog//7.8e-21:
 230:66//Hs.431:L13689
 F-Y79AA1000059//Homo sapiens immunophilin homolog ARA9 mRNA, complete cd
 s//7.3e-40:629:64//Hs.75305:U78521
 F-Y79AA1000065//CD81 ANTIGEN//0.0050:241:60//Hs.54457:M33680
 F-Y79AA1000131//Guanylate cyclase 1, soluble, alpha 2//0.078:477:58//Hs.
 2685:Z50053
 F-Y79AA1000181//Fatty acid synthase {3' region} [human, breast and HepG2
 cells, mRNA Partial, 2237 nt]//0.0022:684:58//Hs.83190:U29344
 F-Y79AA1000202//ESTs//2.5e-17:143:86//Hs.76925:AA211860
 F-Y79AA1000214//Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, comple
 te cds//3.9e-73:345:100//Hs.9242:AF081192
 F-Y79AA1000230//Polymeric immunoglobulin receptor//0.98:335:59//Hs.842:X
 73079

F-Y79AA1000231//ESTs//0.11:209:66//Hs.132184:AI278623
F-Y79AA1000258//Homo sapiens metase (MET-1) mRNA, complete cds//0.30:444
:61//Hs.99941:L23134
F-Y79AA1000268//Human mRNA for KIAA0367 gene, partial cds//9.1e-11:300:6
4//Hs.23311:AB002365
F-Y79AA1000313//Human mRNA for KIAA0129 gene, complete cds//0.89:744:56/
/Hs.44361:D50919
F-Y79AA1000328
F-Y79AA1000342//Homo sapiens OPA-containing protein mRNA, complete cds//
8.4e-15:223:75//Hs.85313:AF071309
F-Y79AA1000346
F-Y79AA1000349//ALPHA-2C-1 ADRENERGIC RECEPTOR//8.3e-06:180:73//Hs.12302
2:J03853
F-Y79AA1000355
F-Y79AA1000368//ESTs//0.0062:235:64//Hs.114777:AA782908
F-Y79AA1000405//ESTs//0.76:244:62//Hs.153027:AA648897
F-Y79AA1000410//Small inducible cytokine A5 (RANTES)//8.1e-31:229:83//Hs
.155464:AF088219
F-Y79AA1000420//ESTs//1.1e-53:271:87//Hs.13056:AA181018
F-Y79AA1000469//Homo sapiens I-1 receptor candidate protein mRNA, comple
te cds//0.0047:315:66//Hs.26285:AF082516
F-Y79AA1000480
F-Y79AA1000538//ESTs//5.7e-09:110:77//Hs.98790:AA284871
F-Y79AA1000539//ESTs//2.6e-52:412:77//Hs.81648:W26521
F-Y79AA1000540//Homo sapiens chromosome 7q22 sequence//0.70:133:69//Hs.1
51555:AF053356
F-Y79AA1000560//Homo sapiens gamma2-adaptin (G2AD) mRNA, complete cds//1
.2e-07:371:63//Hs.8991:AF068706
F-Y79AA1000574//Human mRNA for GC box bindig protein, complete cds//0.95

:258:62//Hs.150557:D31716

F-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence//
2.8e-154:755:97//Hs.21811:AF091080

F-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete
cds//1.7e-136:644:98//Hs.60580:AF060503

F-Y79AA1000705//Homo sapiens CHD1 mRNA, complete cds//0.0023:523:59//Hs.
22670:AF006513

F-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA
, complete cds//1.6e-181:850:98//Hs.83023:AF093670

F-Y79AA1000748//ESTs//4.2e-12:95:90//Hs.33687:R85969

F-Y79AA1000752//ESTs//8.1e-114:551:97//Hs.153471:AI198377

F-Y79AA1000774//ESTs//2.9e-59:296:98//Hs.150536:W20067

F-Y79AA1000782//EST//0.97:78:69//Hs.147351:AI208468

F-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds//1.1e-
178:847:97//Hs.5151:AF098799

F-Y79AA1000794//G-rich RNA sequence binding factor 1//0.83:228:61//Hs.79
295:U07231

F-Y79AA1000800//Homo sapiens GABA-B receptor mRNA, complete cds//0.12:24
4:60//Hs.12307:AF056085

F-Y79AA1000802//Homo sapiens actin binding protein MAYVEN mRNA, complete
cds//0.87:466:59//Hs.122967:AF059569

F-Y79AA1000805

F-Y79AA1000824//Titin//1.0:437:58//Hs.83049:X90568

F-Y79AA1000827//Fatty acid synthase [3' region] [human, breast and HepG2
cells, mRNA Partial, 2237 nt]//0.0048:630:57//Hs.83190:U29344

F-Y79AA1000833//TUBULIN ALPHA-4 CHAIN//6.9e-107:603:90//Hs.75318:X06956

F-Y79AA1000850//ESTs, Weakly similar to T22C1.7 [C.elegans]//6.0e-77:368
:99//Hs.86660:AA398644

F-Y79AA1000962//Homo sapiens orphan nuclear hormone receptor BD73 mRNA,

3' end//0.14:499:58//Hs.37288:D16815
 F-Y79AA1000966//ESTs//0.80:52:86//Hs.6671:AI341699
 F-Y79AA1000968//ESTs, Moderately similar to initiation factor eIF-2B gamma subunit [R.norvegicus]//6.9e-69:310:94//Hs.76822:AI359536
 F-Y79AA1000969//LYMPHOTOXIN-BETA RECEPTOR PRECURSOR//1.0:150:64//Hs.1116:L04270
 F-Y79AA1000976//Arachidonate 15-lipoxygenase//0.87:174:66//Hs.73809:M23892
 F-Y79AA1000985//Human plectin (PLEC1) mRNA, complete cds//0.091:385:58//Hs.79706:U53204
 F-Y79AA1001023
 F-Y79AA1001041//Human mutY homolog (hMYH) gene, complete cds//0.99:37:100//Hs.78489:U63329
 F-Y79AA1001048//Acyl-Coenzyme A dehydrogenase, very long chain//8.7e-30:772:60//Hs.82208:L46590
 F-Y79AA1001061//ESTs//6.3e-41:303:84//Hs.55855:AA621381
 F-Y79AA1001068//EST//3.0e-23:165:90//Hs.157607:AI357511
 F-Y79AA1001077//ESTs//4.9e-40:237:94//Hs.11197:AA309047
 F-Y79AA1001078
 F-Y79AA1001105//Homo sapiens homeodomain protein (OG12) mRNA, complete cds//6.5e-11:247:66//Hs.55967:AF022654
 F-Y79AA1001145//ESTs//1.3e-20:234:75//Hs.55855:AA621381
 F-Y79AA1001167//Homo sapiens mRNA for KIAA0750 protein, complete cds//1.0:155:63//Hs.5444:AB018293
 F-Y79AA1001177//Human hSIAH2 mRNA, complete cds//6.5e-09:299:65//Hs.20191:U76248
 F-Y79AA1001185//ESTs//1.7e-56:318:93//Hs.102991:AA639646
 F-Y79AA1001211//ESTs//9.1e-108:503:99//Hs.100605:AA305965
 F-Y79AA1001216//Peroxisome receptor 1//0.00028:458:57//Hs.158084:Z48054

F-Y79AA1001228//Fragile X mental retardation 2//0.040:207:64//Hs.54472:U
48436

F-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1//6.5e-25:731:60//Hs.85
279:U34879

F-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequ
ence (clone IMAGE 34581 and IMAGE 45355 and LLNLc1101133Q7 (RZPD Berlin)
)//4.0e-135:441:97//Hs.23170:AJ005892

F-Y79AA1001281//ESTs//2.7e-21:157:88//Hs.163825:AI393240

F-Y79AA1001299//Human Inil mRNA, complete cds//2.2e-116:323:93//Hs.15562
6:U04847

F-Y79AA1001312//ESTs//3.7e-95:448:99//Hs.104469:W38395

F-Y79AA1001323//ESTs//8.9e-50:340:86//Hs.144198:AI017555

F-Y79AA1001384

F-Y79AA1001391//Human Hoxb-13 mRNA, complete cds//8.6e-42:505:70//Hs.667
31:U81599

F-Y79AA1001394//ESTs, Weakly similar to F54B3.3 [C.elegans]//1.5e-90:424
:96//Hs.154221:H23167

F-Y79AA1001402//ESTs//1.0:245:62//Hs.134695:AI088489

F-Y79AA1001493//SRY (sex determining region Y)-box 4//0.38:311:61//Hs.83
484:X70683

F-Y79AA1001511//ESTs//9.9e-105:487:99//Hs.153581:AA630465

F-Y79AA1001533//ESTs, Highly similar to RETROVIRUS-RELATED POL POLYPROT
EIN [Homo sapiens]//0.95:256:63//Hs.29974:AI360447

F-Y79AA1001541//EST//0.96:202:61//Hs.99141:AA447744

F-Y79AA1001548//ESTs//2.6e-25:166:90//Hs.164036:AA845659

F-Y79AA1001555//ESTs//1.6e-35:191:97//Hs.52885:H29851

F-Y79AA1001581//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//2.5e-0
5:272:64//Hs.106070:U22398

F-Y79AA1001585//ESTs//1.1e-84:473:93//Hs.42547:AA210783

F-Y79AA1001594//ESTs//1.7e-08:169:71//Hs.97366:AA393109
 F-Y79AA1001603//ESTs//4.6e-07:429:59//Hs.160422:AI363426
 F-Y79AA1001613//Homo sapiens mRNA for KIAA0683 protein, complete cds//0.
 00078:520:57//Hs.12334:AB014583
 F-Y79AA1001647//ESTs, Weakly similar to ZK1058.5 [C.elegans]//9.4e-79:42
 1:94//Hs.107039:W27244
 F-Y79AA1001665//VON WILLEBRAND FACTOR PRECURSOR//1.0:386:60//Hs.110802:X
 04385
 F-Y79AA1001679//Guanine nucleotide binding protein (G protein), beta pol
 ypeptide 1//0.88:243:61//Hs.3620:X04526
 F-Y79AA1001692//Insulin-like growth factor binding protein 2//1.9e-06:42
 6:59//Hs.162:X16302
 F-Y79AA1001696//ESTs//2.3e-44:249:94//Hs.163665:AA250877
 F-Y79AA1001705//Homo sapiens interleukin-1 receptor-associated kinase (I
 RAK) mRNA, complete cds//0.19:609:58//Hs.77297:L76191
 F-Y79AA1001711//ESTs//5.2e-29:224:83//Hs.100461:AI018620
 F-Y79AA1001781//Homo sapiens KIAA0443 mRNA, complete cds//0.49:183:66//H
 s.113082:AB007903
 F-Y79AA1001805//ESTs//1.1e-62:315:98//Hs.16141:W56079
 F-Y79AA1001827//ESTs, Weakly similar to Similar to S.cerevisiae YD9335.0
 3c protein [H.sapiens]//2.9e-62:313:98//Hs.15709:W81213
 F-Y79AA1001846//ESTs//9.4e-16:146:82//Hs.140588:H60533
 F-Y79AA1001848//ESTs, Weakly similar to KIAA0390 [H.sapiens]//1.6e-19:14
 2:90//Hs.103349:AI141124
 F-Y79AA1001866//Homo sapiens mRNA for zinc finger protein 10//5.1e-09:21
 5:67//Hs.104115:X52332
 F-Y79AA1001874//Homo sapiens Jagged 2 mRNA, complete cds//5.4e-06:412:62
 //Hs.106387:AF029778
 F-Y79AA1001875//ESTs//6.8e-09:198:67//Hs.138036:AI343173

F-Y79AA1001923//Homo sapiens growth-arrest-specific protein (gas) mRNA,
complete cds//0.98:430:58//Hs.78501:L13720

F-Y79AA1001963//ESTs//8.1e-131:642:97//Hs.54971:AI424382

F-Y79AA1002027//ESTs//0.00042:58:91//Hs.5375:AA620611

F-Y79AA1002083//ESTs//2.5e-51:285:95//Hs.117205:W88943

F-Y79AA1002089//ESTs, Weakly similar to putative p150 [H.sapiens]//8.3e-
53:348:88//Hs.18122:AI338045

F-Y79AA1002093

F-Y79AA1002103//ESTs//1.5e-15:223:71//Hs.97427:AA411865

F-Y79AA1002115

F-Y79AA1002125//ESTs//6.5e-41:206:99//Hs.159257:N40395

F-Y79AA1002139//ESTs, Weakly similar to B0035.14 [C.elegans]//1.2e-24:16
5:90//Hs.6473:AA853955

F-Y79AA1002204//Homo sapiens mRNA for KIAA0638 protein, partial cds//9.5
e-05:393:62//Hs.77864:AB014538

F-Y79AA1002208//ESTs//2.7e-13:211:69//Hs.112469:AA598515

F-Y79AA1002209//ESTs, Weakly similar to TYROSYL-TRNA SYNTHETASE [Bacillu
s caldotenax]//2.3e-113:568:96//Hs.111637:AA305890

F-Y79AA1002210//ESTs, Weakly similar to D2045.8 [C.elegans]//8.6e-33:338
:73//Hs.26662:U55984

F-Y79AA1002211//ESTs//2.6e-15:121:75//Hs.159584:AA524477

F-Y79AA1002220//EST//0.010:360:60//Hs.136341:AA482508

F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds//0.0041:203:6
3//Hs.1560:D42045

F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//4.1
e-176:821:98//Hs.100729:AB014592

F-Y79AA1002246//Human involucrin mRNA//5.6e-05:525:59//Hs.157091:M13903

F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.2
e-160:748:98//Hs.96731:AB014555

F-Y79AA1002298//ESTs//2.5e-05:115:77//Hs.87164:T84489
 F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//2.1
 e-130:622:97//Hs.30898:AB014534
 F-Y79AA1002311//ESTs//4.9e-19:126:94//Hs.58595:AA830999
 F-Y79AA1002351//Human high conductance inward rectifier potassium channe
 l alpha subunit mRNA, complete cds//0.028:587:58//Hs.2363:L36069
 F-Y79AA1002361//ESTs//8.7e-29:149:100//Hs.156074:AA824377
 F-Y79AA1002399
 F-Y79AA1002407//ESTs//1.5e-25:183:89//Hs.110031:T52569
 F-Y79AA1002416//CTP synthetase//9.1e-51:489:72//Hs.84112:X52142
 F-Y79AA1002431
 F-Y79AA1002433//EST//0.0037:94:71//Hs.136780:AA772318
 F-Y79AA1002472//Homo sapiens DNA from chromosome 19, BAC 33152//1.1e-37:
 263:69//Hs.55452:AC003973
 F-Y79AA1002482//ESTs//1.4e-49:313:80//Hs.132590:AI160765
 F-Y79AA1002487//Insulin-like growth factor binding protein 2//0.43:249:6
 1//Hs.162:X16302

【 0 2 9 5 】

3'末端クローン配列に対するHuman Unigene相同性検索結果データ

各データは、

クローン配列名、

トップヒットデータのTitle、

P値:比較配列の長さ (base):相同性(%)、

トップヒットデータのAccession No.の順に//で区切って記載した。

なお、同一クローンで5'末端配列に対応する3'末端配列が決定されていないものは空欄とした。相同性のスコアのP値が1より大であった場合はデータは示さない。

R-HEMBA1000005//ESTs, Highly similar to HYPOTHETICAL 31.6 KD PROTEIN F5
 4F2.9 IN CHROMOSOME III [Caenorhabditis elegans]//5.6e-93:501:93//Hs.130

15:AA628434

R-HEMBA1000030//Human POU domain protein (Brn-3b) mRNA, complete cds//0.83:314:61//Hs.266:U06233

R-HEMBA1000042//Archain//1.4e-45:282:89//Hs.33642:X81198

R-HEMBA1000046//Human mRNA for KIAA0118 gene, partial cds//8.3e-52:528:72//Hs.154326:D42087

R-HEMBA1000050//EST//0.043:155:63//Hs.149031:AI243340

R-HEMBA1000076//ESTs//3.1e-77:394:97//Hs.111742:R39329

R-HEMBA1000111//ESTs//1.7e-33:228:85//Hs.146811:AA410788

R-HEMBA1000129//ESTs, Weakly similar to contains similarity to helicases [C.elegans]//4.4e-90:502:90//Hs.55918:AA151667

R-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.1e-100:514:94//Hs.27197:AB018340

R-HEMBA1000150//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.1e-45:435:77//Hs.153026:AB014540

R-HEMBA1000156//ESTs, Moderately similar to The KIAA0138 gene product is novel. [H.sapiens]//7.7e-92:428:100//Hs.126925:AA931237

R-HEMBA1000158

R-HEMBA1000168//ESTs, Weakly similar to F13B12.1 [C.elegans]//1.3e-05:58:91//Hs.5570:AI377863

R-HEMBA1000180//ESTs//7.7e-90:461:95//Hs.159200:N50545

R-HEMBA1000185//ESTs//1.3e-72:371:96//Hs.134506:AA308366

R-HEMBA1000193//ESTs//4.2e-103:481:99//Hs.143251:AA769927

R-HEMBA1000201//Human Inil mRNA, complete cds//3.0e-25:137:99//Hs.155626:U04847

R-HEMBA1000213//ESTs//5.4e-85:465:94//Hs.23412:AA133311

R-HEMBA1000216//ESTs//3.0e-37:311:79//Hs.137875:AA993532

R-HEMBA1000227//EST//2.2e-100:498:96//Hs.161570:W80404

R-HEMBA1000231//Homo sapiens KIAA0414 mRNA, partial cds//2.7e-34:287:70/

/Hs.127649:AB007874

R-HEMBA1000243//Homo sapiens mRNA for KIAA0475 protein, complete cds//1.

3e-23:276:75//Hs.5737:AB007944

R-HEMBA1000244//ESTs//2.3e-88:455:96//Hs.8929:AA719019

R-HEMBA1000251//ESTs//0.96:411:56//Hs.120277:AI243808

R-HEMBA1000264//ESTs//3.7e-97:487:96//Hs.29258:W37424

R-HEMBA1000280//ESTs, Moderately similar to ovarian-specific protein [R. norvegicus] //4.9e-14:208:73//Hs.93332:AA811920

R-HEMBA1000282//ESTs//2.5e-38:216:94//Hs.120757:R92485

R-HEMBA1000288//ESTs//2.6e-43:289:86//Hs.151365:AA643962

R-HEMBA1000290//ESTs//5.1e-110:543:96//Hs.139068:AA516409

R-HEMBA1000302//Homo sapiens mRNA for KIAA0527 protein, partial cds//1.0 :122:67//Hs.129748:AB011099

R-HEMBA1000303//ESTs//7.4e-76:386:97//Hs.22276:AA191323

R-HEMBA1000304//Human Ca²⁺-dependent activator protein for secretion mRNA, complete cds//8.8e-30:160:98//Hs.151301:U36448

R-HEMBA1000307//ESTs, Highly similar to 8A-2V protein [M.musculus]//1.1e -103:489:99//Hs.108881:AI018024

R-HEMBA1000333//ESTs//9.3e-99:472:98//Hs.163512:AA903238

R-HEMBA1000338//EST//5.1e-49:278:92//Hs.150815:AI302560

R-HEMBA1000351//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//1.1e-42:270:88//Hs.73614:U83460

R-HEMBA1000355//ESTs//1.0e-105:531:96//Hs.61762:AI422243

R-HEMBA1000357//Human kpni repeat mRNA (cdna clone pcd-kpni-4), 3' end// 9.4e-89:432:87//Hs.139107:K00629

R-HEMBA1000366//ESTs//1.1e-99:524:95//Hs.11785:T65857

R-HEMBA1000369//ESTs//6.5e-70:355:96//Hs.124847:AA843938

R-HEMBA1000376//Human mRNA for KIAA0205 gene, complete cds//3.6e-44:388: 77//Hs.3610:D86960

R-HEMBA1000387//Human high-affinity copper uptake protein (hCTR1) mRNA,
complete cds//5.5e-47:337:83//Hs.73614:U83460

R-HEMBA1000390//Oxytocin receptor//2.4e-16:428:62//Hs.2820:X64878

R-HEMBA1000392//ESTs//3.9e-105:531:96//Hs.130661:AI340248

R-HEMBA1000396//ESTs, Weakly similar to line-1 protein ORF2 [H.sapiens] /
/1.1e-44:447:75//Hs.42849:N31920

R-HEMBA1000411//ESTs, Weakly similar to ankyrin 3, long form [H.sapiens]
//6.1e-92:373:99//Hs.48675:AI005282

R-HEMBA1000418//ESTs//3.1e-66:315:100//Hs.94133:AI270700

R-HEMBA1000422//ESTs//1.6e-99:464:99//Hs.33024:AA002140

R-HEMBA1000428//Homo sapiens mRNA for oligophrenin 1//4.9e-85:535:87//Hs
.158122:AJ001189

R-HEMBA1000434//ESTs//3.7e-53:266:99//Hs.22782:Z38143

R-HEMBA1000442//ESTs//0.93:322:57//Hs.144763:AI218014

R-HEMBA1000456//ESTs//4.1e-48:277:93//Hs.6937:AA524349

R-HEMBA1000459//ESTs//0.010:184:63//Hs.128797:AI246316

R-HEMBA1000460

R-HEMBA1000464//EST//0.082:87:70//Hs.147977:AI262370

R-HEMBA1000469//Small inducible cytokine A5 (RANTES)//1.4e-65:494:81//Hs
.155464:AF088219

R-HEMBA1000488//ESTs, Weakly similar to The KIAA0132 gene product is rel
ated to Drosophila melanogaster ring canel protein. [H.sapiens]//1.1e-31
:181:94//Hs.61454:AA312449

R-HEMBA1000490//ESTs//6.4e-17:132:86//Hs.32855:N25528

R-HEMBA1000491//ESTs//2.2e-22:171:85//Hs.8035:AA195087

R-HEMBA1000504//ESTs//0.016:282:58//Hs.130778:AI077571

R-HEMBA1000505//EST//6.1e-15:116:87//Hs.162783:AA627318

R-HEMBA1000508//ESTs//1.1e-28:244:81//Hs.132722:AA618531

R-HEMBA1000518//EST//0.60:141:60//Hs.97831:AA400885

R-HEMBA1000519//ESTs//2.8e-64:334:96//Hs.97885:AA402414
 R-HEMBA1000520//ESTs//6.9e-104:503:97//Hs.18370:AA947280
 R-HEMBA1000523//Cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD
 //4.0e-55:203:92//Hs.155510:U15782
 R-HEMBA1000531//ESTs, Weakly similar to HEAT SHOCK 70 KD PROTEIN 1 [H.sapiens] //1.3e-117:550:99//Hs.99722:AI422277
 R-HEMBA1000540//ESTs//4.7e-72:350:98//Hs.109755:AA180809
 R-HEMBA1000545//Homo sapiens clone 23892 mRNA sequence//3.7e-68:549:80//
 Hs.91916:AF035317
 R-HEMBA1000555//ESTs//2.3e-66:342:97//Hs.71916:AA219699
 R-HEMBA1000557//EST//1.5e-49:297:90//Hs.149580:AI281881
 R-HEMBA1000561//ESTs, Moderately similar to zinc finger protein [R.novgicus] //1.8e-108:550:96//Hs.26799:W74481
 R-HEMBA1000563//Adenosine kinase//0.16:367:58//Hs.94382:U50196
 R-HEMBA1000568//ESTs//5.1e-42:321:82//Hs.141024:H07128
 R-HEMBA1000569
 R-HEMBA1000575//ESTs//3.8e-45:352:80//Hs.146811:AA410788
 R-HEMBA1000588//ESTs//0.18:122:67//Hs.140507:AA761944
 R-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein//3.9e-113:591:94//Hs.155218:AJ007509
 R-HEMBA1000592//TYROSINE-PROTEIN KINASE ITK/TSK//0.024:309:61//Hs.89519:L10717
 R-HEMBA1000594//ESTs//8.6e-07:172:68//Hs.160289:AI168041
 R-HEMBA1000604//Human telomerase-associated protein TP-1 mRNA, complete cds//1.5e-19:129:93//Hs.158334:U86136
 R-HEMBA1000608//ESTs//2.2e-95:506:94//Hs.6103:AA496424
 R-HEMBA1000622//ESTs//3.8e-10:440:61//Hs.137538:AA769438
 R-HEMBA1000636//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli] //1.4e-86:422:97//Hs.26252:AA643235

R-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds//3.7e-99:443:97//Hs.60103:AB014590

R-HEMBA1000655//Human mRNA for KIAA0392 gene, partial cds//1.3e-50:426:79//Hs.40100:AB002390

R-HEMBA1000657//ESTs//3.0e-74:419:93//Hs.109477:AA477929

R-HEMBA1000662//EST//1.1e-90:425:99//Hs.122144:AA780136

R-HEMBA1000673//ESTs//1.2e-101:473:99//Hs.138215:AI123922

R-HEMBA1000682//ESTs, Weakly similar to putative p150 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403

R-HEMBA1000686//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//6.8e-18:137:86//Hs.7049:AI141736

R-HEMBA1000702//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//7.4e-52:345:84//Hs.144563:AF057280

R-HEMBA1000705//EST//0.21:139:63//Hs.132687:AI033672

R-HEMBA1000719//ESTs//8.4e-90:484:94//Hs.29005:AA477213

R-HEMBA1000722//ESTs, Weakly similar to similar to enoyl-CoA hydratases/isomerases [C.elegans]//7.2e-113:572:95//Hs.28644:AI018612

R-HEMBA1000726//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//2.8e-40:449:75//Hs.74478:U33931

R-HEMBA1000727//ESTs//0.0047:267:60//Hs.133095:AA927777

R-HEMBA1000747//EST//3.9e-20:160:85//Hs.99048:AA446110

R-HEMBA1000749//Small inducible cytokine A5 (RANTES)//4.7e-37:286:82//Hs.155464:AF088219

R-HEMBA1000752//EST//0.041:39:94//Hs.127772:AA961131

R-HEMBA1000769//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.6e-32:309:75//Hs.10458:AF088219

R-HEMBA1000773//EST//7.5e-05:201:63//Hs.122887:AA767612

R-HEMBA1000774//Kangai 1 (suppression of tumorigenicity 6, prostate; CD8 2 antigen (R2 leukocyte antigen, antigen detected by monoclonal and anti

body IA4))//1.3e-48:284:90//Hs.103458:X53795
R-HEMBA1000791//Human mRNA for KIAA0118 gene, partial cds//1.2e-45:291:87//Hs.154326:D42087
R-HEMBA1000817//ESTs//8.3e-95:445:99//Hs.107357:AA983939
R-HEMBA1000822//ESTs//1.1e-107:522:97//Hs.92832:AA631027
R-HEMBA1000827//Homo sapiens Ser/Arg-related nuclear matrix protein (SRM160) mRNA, complete cds//2.2e-44:228:98//Hs.18192:AF048977
R-HEMBA1000843//Homo sapiens LIM protein mRNA, complete cds//6.6e-46:410:77//Hs.154103:AF061258
R-HEMBA1000851
R-HEMBA1000852//Aldehyde dehydrogenase 10 (fatty aldehyde dehydrogenase)//3.7e-33:284:80//Hs.159608:U46689
R-HEMBA1000867//EST//2.0e-17:211:74//Hs.145670:AI265794
R-HEMBA1000869//ESTs//3.1e-16:237:71//Hs.116518:AA653202
R-HEMBA1000870//ESTs//1.6e-43:222:98//Hs.69564:AA203608
R-HEMBA1000872//ESTs//1.9e-93:453:98//Hs.152622:AA594951
R-HEMBA1000876//Small inducible cytokine A5 (RANTES)//3.0e-41:329:79//Hs.155464:AF088219
R-HEMBA1000908//ESTs//1.6e-51:291:92//Hs.12247:AI203154
R-HEMBA1000910//EST//0.98:139:64//Hs.132687:AI033672
R-HEMBA1000918//EST//9.6e-30:152:84//Hs.162136:AA526508
R-HEMBA1000919
R-HEMBA1000934//ESTs//4.1e-38:254:89//Hs.87784:AA460597
R-HEMBA1000942//ESTs//3.5e-20:172:69//Hs.160065:AI018619
R-HEMBA1000943//Homo sapiens mRNA for KIAA0748 protein, complete cds//1.3e-44:281:78//Hs.33187:AB018291
R-HEMBA1000946//ESTs//1.6e-68:352:96//Hs.21331:H93074
R-HEMBA1000960//Homo sapiens tapasin (NGS-17) mRNA, complete cds//4.0e-61:347:81//Hs.5247:AF029750

R-HEMBA1000968//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0508//6.8e-51:362:84//Hs.159187:AB007977

R-HEMBA1000971//ESTs//2.8e-41:246:91//Hs.104287:AI363498

R-HEMBA1000972//Homo sapiens mRNA for XPR2 protein//7.3e-44:341:81//Hs.4
4766:AJ007590

R-HEMBA1000974//ESTs//1.4e-32:166:100//Hs.149274:AI018170

R-HEMBA1000975//Oxytocin receptor//2.7e-46:563:73//Hs.2820:X64878

R-HEMBA1000985//ESTs//4.4e-05:125:69//Hs.147434:AI214464

R-HEMBA1000986//ESTs//7.8e-44:266:84//Hs.163784:N54902

R-HEMBA1000991//EST//1.4e-42:162:86//Hs.149580:AI281881

R-HEMBA1001007

R-HEMBA1001008//ESTs//2.3e-82:463:92//Hs.10339:AA058764

R-HEMBA1001009//ESTs, Weakly similar to non-lens beta gamma-crystallin l
ike protein [H.sapiens]//2.6e-58:280:100//Hs.128738:AA970836

R-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds//3.
3e-115:587:95//Hs.158287:AB007937

R-HEMBA1001019//Cell division cycle 2, G1 to S and G2 to M//1.1e-24:140:
95//Hs.58393:X05360

R-HEMBA1001020//ESTs//0.52:86:72//Hs.69683:AA115292

R-HEMBA1001022//ESTs//3.4e-18:102:100//Hs.63243:AI123912

R-HEMBA1001024//ESTs//1.9e-07:262:61//Hs.124399:AA832336

R-HEMBA1001026//ESTs//0.0017:142:67//Hs.144109:AI345543

R-HEMBA1001043//Ankyrin G//0.23:244:60//Hs.75893:U13616

R-HEMBA1001051//Homo sapiens mRNA for KIAA0621 protein, partial cds//6.4
e-21:186:79//Hs.132942:AB014521

R-HEMBA1001052//ESTs//5.4e-107:497:99//Hs.121773:AI357886

R-HEMBA1001060//ESTs//1.1e-31:298:80//Hs.24821:AA044813

R-HEMBA1001071//Alpha-1 type 3 collagen//9.1e-34:179:98//Hs.119571:X1442

0

R-HEMBA1001077//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0492//2.7e-21:417:64//Hs.127338:AB007961

R-HEMBA1001080

R-HEMBA1001085//ESTs//1.9e-47:385:79//Hs.146811:AA410788

R-HEMBA1001088//ESTs//2.8e-102:548:93//Hs.127273:AA522674

R-HEMBA1001094

R-HEMBA1001099//ESTs//0.24:41:97//Hs.18612:T99245

R-HEMBA1001109//Small inducible cytokine A5 (RANTES)//2.4e-46:396:80//Hs
.155464:AF088219

R-HEMBA1001121//ESTs//1.7e-15:216:71//Hs.141605:H92974

R-HEMBA1001122//ESTs//2.0e-90:474:94//Hs.107884:AA131320

R-HEMBA1001123//B-CELL GROWTH FACTOR PRECURSOR//2.7e-45:319:84//Hs.99879
:M15530

R-HEMBA1001133//ESTs//1.2e-92:443:99//Hs.99626:AA632341

R-HEMBA1001137//ESTs//2.0e-86:426:97//Hs.157103:W60265

R-HEMBA1001140//Small inducible cytokine A5 (RANTES)//2.9e-45:323:83//Hs
.155464:AF088219

R-HEMBA1001172//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING
ENTRY !!!! [H.sapiens]//1.1e-39:309:82//Hs.96337:AA225358

R-HEMBA1001174//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0492//0.21:238:60//Hs.127338:AB007961

R-HEMBA1001197//ESTs//0.010:388:61//Hs.14881:R91896

R-HEMBA1001208//ESTs, Highly similar to Similar to S.cerevisiae hypothet
ical protein 5 [H.sapiens]//0.27:305:62//Hs.100238:U69194

R-HEMBA1001226//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.0e-54:33
3:81//Hs.113283:AF018080

R-HEMBA1001235//EST//2.3e-07:42:92//Hs.141620:N63316

R-HEMBA1001247//ESTs, Weakly similar to WWP2 [H.sapiens]//2.9e-20:160:87
//Hs.103102:W55932

R-HEMBA1001257//ESTs//3.3e-112:544:97//Hs.128749:AA779728
 R-HEMBA1001265//ESTs//8.7e-116:564:98//Hs.155150:AI061435
 R-HEMBA1001281//ESTs, Weakly similar to Lpa8p [S.cerevisiae]//2.4e-35:23
 9:87//Hs.103919:AA159181
 R-HEMBA1001286//ESTs//1.4e-97:507:95//Hs.26244:AI352674
 R-HEMBA1001289//ESTs//8.2e-44:122:96//Hs.76267:AA877534
 R-HEMBA1001294//ESTs//1.0:140:65//Hs.149638:AI298324
 R-HEMBA1001299//Small inducible cytokine A5 (RANTES)//1.1e-45:307:84//Hs
 .155464:AF088219
 R-HEMBA1001302//Homo sapiens mRNA for APC 2 protein, complete cds//0.53:
 89:68//Hs.20912:AB012162
 R-HEMBA1001303//EST//0.00053:271:60//Hs.156148:AI333214
 R-HEMBA1001310//ESTs//1.4e-91:486:93//Hs.86228:AA206019
 R-HEMBA1001319//ESTs//0.051:228:61//Hs.99404:AA953977
 R-HEMBA1001323//ESTs//6.2e-83:401:98//Hs.47343:AI282950
 R-HEMBA1001326//ESTs, Weakly similar to HYPOTHETICAL 55.1 KD PROTEIN IN
 FAB1-PES4 INTERGENIC REGION [S.cerevisiae]//1.3e-77:458:92//Hs.9398:N418
 38
 R-HEMBA1001327//ESTs//0.60:251:58//Hs.117162:AA701259
 R-HEMBA1001330//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-46:24
 9:78//Hs.113283:AF018080
 R-HEMBA1001351//ESTs//0.13:230:57//Hs.138510:R94816
 R-HEMBA1001361//ESTs//3.5e-107:570:94//Hs.7727:AA142837
 R-HEMBA1001375//ESTs//1.1e-96:454:99//Hs.59584:AA587334
 R-HEMBA1001377//ESTs//8.5e-91:459:95//Hs.61859:AA628550
 R-HEMBA1001383//ESTs//0.077:381:58//Hs.163093:AA745458
 R-HEMBA1001387//ESTs//2.0e-85:405:99//Hs.152127:AI246482
 R-HEMBA1001388//ESTs//1.5e-83:395:99//Hs.105191:AA133439
 R-HEMBA1001391//ESTs//7.7e-90:455:96//Hs.120905:R22204

R-HEMBA1001398//Thromboxane A2 receptor//4.0e-46:279:89//Hs.89887:D38081
 R-HEMBA1001405//ESTs//1.2e-98:485:97//Hs.73287:W16714
 R-HEMBA1001407//ESTs//2.2e-76:365:99//Hs.110128:AA584364
 R-HEMBA1001411//ESTs//1.2e-102:476:100//Hs.143162:AI380343
 R-HEMBA1001413//ESTs//3.7e-66:321:98//Hs.152472:AA041199
 R-HEMBA1001415
 R-HEMBA1001432//Putative mismatch repair/binding protein hMSH3//7.9e-42:
 183:82//Hs.42674:U61981
 R-HEMBA1001433//ESTs//1.4e-34:240:77//Hs.95611:U51704
 R-HEMBA1001435//ESTs//5.6e-23:292:70//Hs.116315:AA629263
 R-HEMBA1001442//ESTs//0.76:414:58//Hs.156189:AI419982
 R-HEMBA1001446//ESTs//2.2e-95:447:99//Hs.154091:AA767546
 R-HEMBA1001450//ESTs//1.0e-93:491:94//Hs.16130:AA195077
 R-HEMBA1001454//Human Line-1 repeat mRNA with 2 open reading frames//1.7
 e-47:304:88//Hs.23094:M19503
 R-HEMBA1001455//ESTs//7.1e-103:482:99//Hs.97407:AI417220
 R-HEMBA1001463
 R-HEMBA1001476//Human mRNA for KIAA0186 gene, complete cds//2.0e-25:409:
 66//Hs.36232:D80008
 R-HEMBA1001478
 R-HEMBA1001497
 R-HEMBA1001510//ESTs//3.3e-44:381:78//Hs.139882:AA864426
 R-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frames//5.9
 e-79:528:84//Hs.23094:M19503
 R-HEMBA1001517//ESTs//5.8e-32:272:81//Hs.119512:AA487269
 R-HEMBA1001522//ESTs//1.7e-84:364:95//Hs.117858:AA702493
 R-HEMBA1001526//ESTs//1.8e-93:527:93//Hs.10624:N64723
 R-HEMBA1001533//ESTs//1.9e-42:211:100//Hs.55830:AA580270
 R-HEMBA1001557//ESTs//4.2e-83:413:97//Hs.47546:AA181348

R-HEMBA1001566//Small inducible cytokine A5 (RANTES)//3.4e-50:304:88//Hs.155464:AF088219

R-HEMBA1001569//POU domain, class 3, transcription factor 4//2.3e-06:259:62//Hs.2229:X82324

R-HEMBA1001570//Homo sapiens pendrin (PDS) mRNA, complete cds//3.5e-47:456:77//Hs.159275:AF030880

R-HEMBA1001579//ESTs//0.11:299:60//Hs.106090:AA457030

R-HEMBA1001581//ESTs//0.016:350:61//Hs.124664:AI015652

R-HEMBA1001585//Human mRNA for KIAA0331 gene, complete cds//0.30:251:63//Hs.146395:AB002329

R-HEMBA1001589

R-HEMBA1001595//ESTs, Weakly similar to SEPTIN 2 [D.melanogaster]//6.9e-71:431:88//Hs.26625:W25874

R-HEMBA1001608//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//1.3e-73:533:82//Hs.103948:K00627

R-HEMBA1001620//ESTs, Highly similar to MYO-INOSITOL-1-PHOSPHATE SYNTHASE [Arabidopsis thaliana]//4.5e-93:537:90//Hs.20218:AA628530

R-HEMBA1001635//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.054:362:60//Hs.132206:AF039694

R-HEMBA1001636//ESTs//4.9e-53:267:97//Hs.47459:AA700158

R-HEMBA1001640//ESTs//2.9e-27:299:72//Hs.65236:AA927623

R-HEMBA1001651//ESTs, Weakly similar to Mi-2 protein [H.sapiens]//1.2e-86:442:95//Hs.63888:AA203398

R-HEMBA1001655//ESTs//1.5e-101:516:95//Hs.86541:AA214554

R-HEMBA1001658

R-HEMBA1001661//Homo sapiens protocadherin 68 (PCH68) mRNA, complete cds//1.3e-16:427:61//Hs.106511:AF029343

R-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//1.4e-93:493:92//Hs.107254:AC005943

R-HEMBA1001675

R-HEMBA1001678//Homo sapiens voltage dependent anion channel protein mRNA, complete cds//4.2e-103:534:94//Hs.7381:AF038962

R-HEMBA1001681//ESTs//6.0e-49:292:92//Hs.65588:AA523424

R-HEMBA1001702//ESTs//9.0e-98:478:97//Hs.28661:AA805916

R-HEMBA1001709//Homo sapiens mRNA for KIAA0698 protein, complete cds//6.3e-98:483:96//Hs.31720:AB014598

R-HEMBA1001711//ESTs//5.8e-83:398:98//Hs.34804:AA514960

R-HEMBA1001712//ESTs//0.028:202:63//Hs.105790:AA528095

R-HEMBA1001714//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]//1.8e-46:236:98//Hs.132948:AA194452

R-HEMBA1001718//Small inducible cytokine A5 (RANTES)//8.6e-43:166:88//Hs.155464:AF088219

R-HEMBA1001723//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION [Saccharomyces cerevisiae]//7.1e-88:431:96//Hs.29203:AI344105

R-HEMBA1001731//EST//0.25:100:68//Hs.149171:AI245712

R-HEMBA1001734//Human mRNA for KIAA0355 gene, complete cds//2.6e-39:366:77//Hs.153014:AB002353

R-HEMBA1001744

R-HEMBA1001745//ESTs//6.6e-05:244:62//Hs.157663:AI358623

R-HEMBA1001746//EST//4.9e-65:409:88//Hs.124673:AA858162

R-HEMBA1001761//ESTs//1.9e-44:315:84//Hs.159510:AA297145

R-HEMBA1001781//ESTs//3.0e-98:462:99//Hs.60059:AI057306

R-HEMBA1001784//EST//1.0e-12:250:68//Hs.152366:AA486721

R-HEMBA1001791//EST//1.4e-47:292:89//Hs.163333:AA879053

R-HEMBA1001800//ESTs//8.4e-37:314:79//Hs.105151:AA970243

R-HEMBA1001803//ESTs//4.5e-99:465:99//Hs.135159:AI095823

R-HEMBA1001804//Zinc finger protein 148 (pHZ-52)//0.78:232:57//Hs.112180

:AF039019

R-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0500//9.0e-114:548:98//Hs.118164:AB007969

R-HEMBA1001809//EST//3.8e-63:292:89//Hs.158591:AI369334

R-HEMBA1001815//Calcium modulating ligand//1.1e-47:299:87//Hs.13572:AF06
8179

R-HEMBA1001819//ZINC FINGER PROTEIN HF.12//1.2e-16:259:69//Hs.155470:X07
290

R-HEMBA1001820//ESTs//2.6e-86:404:100//Hs.112881:AA620707

R-HEMBA1001822//ESTs//2.2e-101:480:99//Hs.159940:AA971578

R-HEMBA1001824//ESTs, Weakly similar to MATRIN 3 [H.sapiens]//6.2e-27:14
7:97//Hs.23476:AA401210

R-HEMBA1001835//EST//0.79:216:64//Hs.47437:N52250

R-HEMBA1001844//ESTs//4.7e-62:319:95//Hs.55200:N98513

R-HEMBA1001847//ESTs//2.3e-102:522:95//Hs.20879:AA845446

R-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds//1.
1e-109:553:96//Hs.78946:AB014517

R-HEMBA1001864//ESTs//7.4e-94:449:99//Hs.132776:AI142853

R-HEMBA1001866//Myelin oligodendrocyte glycoprotein {alternative product
s} //1.9e-37:357:76//Hs.53217:Z48051

R-HEMBA1001869//ESTs, Weakly similar to trithorax homolog HTX, version 2
[H.sapiens]//2.3e-32:193:94//Hs.9489:R84329

R-HEMBA1001888//H.sapiens mRNA for urea transporter//2.0e-47:425:78//Hs.
66710:X96969

R-HEMBA1001896//ESTs//3.5e-56:274:99//Hs.129018:H03128

R-HEMBA1001910

R-HEMBA1001912//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
RY !!!! [H.sapiens]//1.5e-73:347:100//Hs.30991:AA994438

R-HEMBA1001913//ESTs, Highly similar to GCN20 PROTEIN [Saccharomyces ce

revisiae]//5.1e-57:320:91//Hs.91251:U66685
 R-HEMBA1001915//ESTs//4.9e-88:459:95//Hs.122810:AI273706
 R-HEMBA1001918//ESTs//1.2e-106:505:99//Hs.98518:AI027125
 R-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds//5.5e-107:534:96//Hs.154934:AF000145
 R-HEMBA1001939//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.9e-99:482:98//Hs.96849:AA879470
 R-HEMBA1001940//Human mRNA for KIAA0392 gene, partial cds//5.6e-45:336:82//Hs.40100:AB002390
 R-HEMBA1001942//EST//2.6e-84:397:99//Hs.145444:AI203668
 R-HEMBA1001945//ESTs//1.4e-92:437:99//Hs.144565:AI192452
 R-HEMBA1001950//ESTs//3.9e-43:280:88//Hs.84429:N28866
 R-HEMBA1001960//ESTs//0.040:243:62//Hs.29567:AA640421
 R-HEMBA1001962//ESTs//0.0071:113:69//Hs.49792:N70048
 R-HEMBA1001964//ESTs//3.0e-38:239:87//Hs.158126:W26825
 R-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isoform of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs//1.8e-106:517:97//Hs.11050:AL031178
 R-HEMBA1001979//EST//0.039:167:63//Hs.129451:AA993932
 R-HEMBA1001987//ESTs//3.1e-44:320:83//Hs.136839:H93717
 R-HEMBA1001991//Human mRNA for KIAA0355 gene, complete cds//9.5e-47:303:88//Hs.153014:AB002353
 R-HEMBA1002003//Homo sapiens mRNA for protein phosphatase 2C (beta)//1.6e-91:448:97//Hs.5687:AJ005801
 R-HEMBA1002008//ESTs//9.2e-47:297:87//Hs.142314:AA347930
 R-HEMBA1002018//ESTs//9.4e-21:118:97//Hs.7871:AI041837
 R-HEMBA1002022//Human mRNA for KIAA0075 gene, partial cds//0.25:196:63//Hs.1189:D38550

R-HEMBA1002035//ESTs//7.7e-101:475:99//Hs.8858:AI131538
R-HEMBA1002039//H.sapiens mRNA for phosphoinositide 3-kinase//0.68:256:6
4//Hs.101238:Y11312
R-HEMBA1002049//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.
4e-51:254:85//Hs.15731:AB011135
R-HEMBA1002084//EST//0.31:219:60//Hs.162396:AA572764
R-HEMBA1002092//EST//6.4e-72:342:99//Hs.148533:AI200996
R-HEMBA1002100//EST//5.6e-38:258:85//Hs.103094:W52354
R-HEMBA1002102//Thiopurine S-methyltransferase//1.4e-46:403:79//Hs.51124
:AF019369
R-HEMBA1002113//Prostaglandin I2 (prostacyclin) synthase //1.4e-76:280:9
0//Hs.61333:D83402
R-HEMBA1002119//Homo sapiens OR7E12P pseudogene, complete sequence//1.4e
-87:362:94//Hs.103443:AF065854
R-HEMBA1002125//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//1.7e-16:9
4:100//Hs.107747:AI357868
R-HEMBA1002139//H.sapiens mRNA for nebulin//0.0019:68:88//Hs.83870:X8395
7
R-HEMBA1002144//ESTs//3.1e-30:259:72//Hs.141575:AA211734
R-HEMBA1002150//ESTs//7.1e-105:543:95//Hs.32275:AA595199
R-HEMBA1002151//ESTs//2.2e-35:178:100//Hs.77703:W19642
R-HEMBA1002153//EST//4.5e-49:458:77//Hs.141708:W44337
R-HEMBA1002160//Homo sapiens nephrocystin (NPHP1) mRNA, partial cds//1.4
e-36:400:75//Hs.75474:AF023674
R-HEMBA1002161//Homo sapiens EVI5 homolog mRNA, complete cds//1.9e-33:29
4:77//Hs.26929:AF008915
R-HEMBA1002162//ESTs//1.0e-47:317:85//Hs.48919:N64043
R-HEMBA1002166//Thromboxane A2 receptor//6.8e-46:296:81//Hs.89887:D38081
R-HEMBA1002177//EST//2.6e-42:215:99//Hs.116880:AA662457

R-HEMBA1002185//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//6.0e-42:419:73//Hs.159523:AF001622

R-HEMBA1002189//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.4e-29:244:72//Hs.119387:AB007958

R-HEMBA1002191//ESTs//2.6e-31:275:66//Hs.133852:AI076357

R-HEMBA1002199//Human Line-1 repeat mRNA with 2 open reading frames//4.3e-84:557:84//Hs.23094:M19503

R-HEMBA1002204//EST//0.00057:113:71//Hs.144868:AI202342

R-HEMBA1002212//ESTs//1.5e-48:277:93//Hs.104741:AI393315

R-HEMBA1002215//ESTs//1.1e-23:158:90//Hs.152529:AA897151

R-HEMBA1002226//Homo sapiens mRNA for KIAA0706 protein, complete cds//5.1e-21:230:75//Hs.139648:AB014606

R-HEMBA1002229//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//1.5e-47:238:98//Hs.25664:AF089814

R-HEMBA1002237//ESTs//6.9e-35:357:76//Hs.116518:AA653202

R-HEMBA1002253//EST//6.0e-19:125:81//Hs.140596:AA829426

R-HEMBA1002257

R-HEMBA1002267//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]//1.3e-31:201:91//Hs.114673:W72675

R-HEMBA1002270//ESTs//4.6e-100:483:97//Hs.34940:AI264314

R-HEMBA1002321//ESTs//2.3e-85:403:99//Hs.120388:AA723595

R-HEMBA1002328//ESTs//1.3e-90:423:100//Hs.117936:AI280818

R-HEMBA1002337//ESTs//8.7e-24:147:93//Hs.9893:AA007679

R-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds//7.8e-130:642:96//Hs.6162:AB018314

R-HEMBA1002348//ESTs//5.0e-71:387:93//Hs.30494:H04822

R-HEMBA1002349//ESTs//9.7e-88:420:98//Hs.132972:AA543094

R-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mR

NA, complete cds//3.9e-123:661:93//Hs.119023:AF092563
 R-HEMBA1002381//ESTs//1.3e-73:352:99//Hs.56121:AA781435
 R-HEMBA1002389//EST//2.3e-05:132:69//Hs.37558:H58237
 R-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784//3.9e-63:358:9
 1//Hs.25527:AC005954
 R-HEMBA1002419//ESTs, Weakly similar to APK1 antigen [H.sapiens]//5.6e-8
 7:429:96//Hs.13209:AI417849
 R-HEMBA1002430//ESTs//0.10:388:57//Hs.119238:AA476267
 R-HEMBA1002439//Human mRNA for KIAA0080 gene, partial cds//2.0e-22:181:8
 0//Hs.74554:D38522
 R-HEMBA1002458//ESTs//1.8e-88:448:95//Hs.97914:AA769069
 R-HEMBA1002460//Catalase//0.67:314:60//Hs.76359:X04085
 R-HEMBA1002462//EST//0.032:44:88//Hs.161536:N80395
 R-HEMBA1002475//ESTs, Weakly similar to F08G12.1 [C.elegans]//5.4e-95:48
 8:95//Hs.108115:AA582193
 R-HEMBA1002477//Homo sapiens KIAA0395 mRNA, partial cds//2.5e-37:281:80/
 /Hs.43681:AL022394
 R-HEMBA1002486//Small inducible cytokine A5 (RANTES)//1.1e-49:311:88//Hs
 .155464:AF088219
 R-HEMBA1002495//ESTs//1.2e-94:457:98//Hs.42140:AI188995
 R-HEMBA1002498//ESTs//1.7e-35:240:78//Hs.119871:AA705133
 R-HEMBA1002503//ESTs//2.3e-14:64:85//Hs.140190:AA701449
 R-HEMBA1002508//ESTs//0.00057:160:62//Hs.149661:AA872990
 R-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (
 JN21)//2.3e-113:456:92//Hs.6764:AJ011972
 R-HEMBA1002515//EST//1.0:153:63//Hs.118045:N51715
 R-HEMBA1002538//Homo sapiens mRNA for KIAA0454 protein, partial cds//5.1
 e-106:564:93//Hs.129928:AB007923
 R-HEMBA1002542//ESTs//1.0e-101:539:93//Hs.93872:AA524700

R-HEMBA1002547//EST//8.7e-27:151:96//Hs.132145:AI041804
R-HEMBA1002552//EST//5.9e-49:335:85//Hs.149580:AI281881
R-HEMBA1002555//ESTs//1.1e-77:461:91//Hs.38750:N30012
R-HEMBA1002558//Homo sapiens 4F5S mRNA, complete cds//1.3e-42:264:89//Hs
.32567:AF073519
R-HEMBA1002561//Small inducible cytokine A5 (RANTES)//6.4e-40:196:78//Hs
.155464:AF088219
R-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete
cds//1.4e-120:587:97//Hs.151411:AF075587
R-HEMBA1002583//ESTs//7.1e-79:410:95//Hs.21599:AA478904
R-HEMBA1002590//EST//3.3e-54:278:97//Hs.138637:N20838
R-HEMBA1002592//ESTs//2.6e-44:500:74//Hs.110934:N26055
R-HEMBA1002621
R-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds//2.
2e-77:380:97//Hs.91338:AB018351
R-HEMBA1002628//ESTs//0.0020:167:66//Hs.140605:AA830881
R-HEMBA1002629//ESTs//0.00014:50:100//Hs.119132:AA398715
R-HEMBA1002645//EST//2.1e-37:285:82//Hs.141728:W73041
R-HEMBA1002651//EST//2.2e-23:374:69//Hs.139357:AA420970
R-HEMBA1002659//Human 53K isoform of Type II phosphatidylinositol-4-phos
phate 5-kinase (PIPK) mRNA, complete cds//1.5e-53:406:81//Hs.108966:U486
96
R-HEMBA1002661//Homo sapiens mRNA for KIAA0764 protein, complete cds//1.
1e-41:296:84//Hs.6232:AB018307
R-HEMBA1002666//EST//4.4e-09:79:88//Hs.72015:AA151945
R-HEMBA1002678//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING
ENTRY !!!! [H.sapiens]//7.6e-104:560:92//Hs.161748:T64896
R-HEMBA1002679//EST//0.15:136:69//Hs.129570:AA995396
R-HEMBA1002688//T-CELL SURFACE PROTEIN TACTILE PRECURSOR//0.16:247:62//H

s.142023:M88282
R-HEMBA1002696//ESTs//3.5e-94:529:92//Hs.16725:AA196477
R-HEMBA1002712//Homo sapiens mRNA for KIAA0772 protein, complete cds//6.
0e-46:302:86//Hs.15519:AB018315
R-HEMBA1002716//ESTs//1.3e-109:555:96//Hs.9812:AA147884
R-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds//3.8
e-37:287:81//Hs.132942:AB014521
R-HEMBA1002730//ESTs//1.2e-95:488:95//Hs.22030:AA521168
R-HEMBA1002742//ESTs//1.0e-91:437:99//Hs.139987:AA652163
R-HEMBA1002746//ESTs//4.4e-97:468:98//Hs.129903:AA576526
R-HEMBA1002748//ESTs//5.0e-98:475:98//Hs.125461:AI375792
R-HEMBA1002750//ESTs//1.6e-42:223:97//Hs.40460:N36090
R-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//4.0
e-106:545:95//Hs.74750:AB011126
R-HEMBA1002770//EST//0.34:294:59//Hs.43091:N22127
R-HEMBA1002777//ESTs//3.0e-85:316:98//Hs.17537:C06491
R-HEMBA1002779//Human mRNA for KIAA0013 gene, complete cds//0.25:342:58/
/Hs.48824:D87717
R-HEMBA1002780//Homo sapiens DEC-205 mRNA, complete cds//4.2e-46:449:75/
/Hs.153563:AF011333
R-HEMBA1002794//ESTs//1.2e-115:559:97//Hs.79741:AI279709
R-HEMBA1002801//EST//0.00049:287:60//Hs.126466:AA913320
R-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cd
s//1.4e-116:559:97//Hs.28307:AF071185
R-HEMBA1002816//Human plectin (PLEC1) mRNA, complete cds//0.28:281:62//H
s.79706:U53204
R-HEMBA1002826//EST//6.7e-25:134:99//Hs.134683:AI092013
R-HEMBA1002833//ESTs, Highly similar to ribosome-binding protein p34 [R.
norvegicus]//4.3e-25:137:98//Hs.5337:AA243757

R-HEMBA1002850//ESTs//0.010:323:57//Hs.18282:W67514
 R-HEMBA1002863//ESTs//1.1e-67:359:94//Hs.124699:W27830
 R-HEMBA1002876//ESTs//0.72:202:62//Hs.144816:AI220827
 R-HEMBA1002886//EST//3.2e-85:401:99//Hs.96580:AA405670
 R-HEMBA1002896//Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds//1.2e-107:541:95//Hs.33787:AF037261
 R-HEMBA1002921//Human mRNA for KIAA0189 gene, complete cds//0.84:103:71//Hs.95140:D80011
 R-HEMBA1002924//ESTs//3.5e-86:423:98//Hs.27513:N34820
 R-HEMBA1002934//Human mRNA for KIAA0118 gene, partial cds//2.1e-50:308:88//Hs.154326:D42087
 R-HEMBA1002935//ESTs//1.0e-73:384:95//Hs.118193:N74481
 R-HEMBA1002937//ESTs//0.052:167:65//Hs.145504:AI254165
 R-HEMBA1002939//ESTs//1.6e-94:467:97//Hs.9893:AA007679
 R-HEMBA1002944//ESTs//2.7e-17:176:80//Hs.143768:AA229732
 R-HEMBA1002951//ESTs//3.7e-119:565:98//Hs.16218:AI190892
 R-HEMBA1002954//EST//0.076:285:58//Hs.98706:AA431085
 R-HEMBA1002968//Thiopurine S-methyltransferase//1.9e-46:314:85//Hs.51124:AF019369
 R-HEMBA1002970//EST//0.00050:164:64//Hs.129630:AI000405
 R-HEMBA1002971//Homo sapiens mRNA for KIAA0679 protein, partial cds//2.3e-30:162:99//Hs.5734:AB014579
 R-HEMBA1002973//Small inducible cytokine A5 (RANTES)//5.7e-42:318:81//Hs.155464:AF088219
 R-HEMBA1002997//ESTs//3.2e-18:102:100//Hs.146255:AA197064
 R-HEMBA1002999//ESTs, Moderately similar to lamina associated polypeptide 1C [R.norvegicus]//7.9e-113:560:96//Hs.125749:AI377682
 R-HEMBA1003021//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.3e-42:290:85//Hs.113283:AF018080

R-HEMBA1003033//ESTs//2.8e-77:417:94//Hs.138860:W47480
R-HEMBA1003034//ESTs//3.7e-42:429:74//Hs.132818:AI038577
R-HEMBA1003035//ESTs//0.025:156:64//Hs.8473:T40827
R-HEMBA1003037//ESTs//0.69:381:57//Hs.47312:AI240366
R-HEMBA1003041//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4.4 IN CHROMOSOME II PRECURSOR [Caenorhabditis elegans]//5.6e-34:280:79//Hs.114905:AA088442
R-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds//1.3e-119:578:97//Hs.44097:AF054182
R-HEMBA1003064//ESTs//7.8e-85:419:96//Hs.87020:AA706627
R-HEMBA1003067//Von Hippel-Lindau syndrome//2.0e-30:299:75//Hs.78160:AF010238
R-HEMBA1003071//ESTs//2.3e-74:360:98//Hs.17270:AA701903
R-HEMBA1003077//ESTs, Weakly similar to KIAA0405 [H.sapiens]//1.1e-90:434:99//Hs.14146:W92235
R-HEMBA1003078//ESTs//5.9e-16:156:77//Hs.142684:AA902402
R-HEMBA1003079//ESTs//0.16:341:58//Hs.95923:AI075249
R-HEMBA1003083//Small inducible cytokine A5 (RANTES)//1.9e-39:284:83//Hs.155464:AF088219
R-HEMBA1003086//EST//1.0e-48:372:82//Hs.161917:AA483223
R-HEMBA1003096//ESTs, Weakly similar to Mouse 19.5 mRNA, complete cds [M.musculus]//4.2e-100:531:94//Hs.104800:AA709155
R-HEMBA1003098//ESTs//4.2e-107:537:96//Hs.107213:AA121624
R-HEMBA1003117//ESTs//2.4e-67:331:97//Hs.157158:AI150058
R-HEMBA1003129//Human nucleolar fibrillar center protein (ASE-1) mRNA, complete cds//2.1e-13:109:88//Hs.118717:U86751
R-HEMBA1003133//ESTs//1.1e-34:180:98//Hs.159387:AI370845
R-HEMBA1003136//ESTs, Weakly similar to MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE [Saccharomyces cerevisiae]//9.2e-114:577:95//Hs.27059:AI088615

R-HEMBA1003142//Small inducible cytokine A5 (RANTES)//1.1e-45:285:88//Hs.155464:AF088219

R-HEMBA1003148//Homo sapiens mRNA for dachshund protein//3.6e-118:586:96//Hs.63931:AJ005670

R-HEMBA1003166//ESTs//1.6e-96:479:96//Hs.119940:AA705933

R-HEMBA1003175//ESTs//2.7e-74:407:92//Hs.139167:AA715389

R-HEMBA1003197//ESTs//1.6e-68:384:94//Hs.120969:W92000

R-HEMBA1003199//Sjogren syndrome antigen B (autoantigen La)//0.19:328:57//Hs.83715:X69804

R-HEMBA1003202//Homo sapiens mRNA for KIAA0640 protein, partial cds//1.3e-40:290:83//Hs.153026:AB014540

R-HEMBA1003204//ESTs//1.1e-34:215:91//Hs.108090:AA424943

R-HEMBA1003212//ESTs//1.9e-81:441:93//Hs.28471:W20265

R-HEMBA1003220//ESTs, Weakly similar to MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S28 PRECURSOR [S.cerevisiae]//1.6e-40:232:93//Hs.107707:N32817

R-HEMBA1003222//ESTs, Weakly similar to weak similarity to HSP90 [C.elegans]//1.1e-42:310:85//Hs.23294:W27666

R-HEMBA1003229//ESTs//4.8e-18:133:90//Hs.61763:AA035305

R-HEMBA1003235//ESTs//7.7e-35:201:78//Hs.163979:AA828834

R-HEMBA1003250//Homo sapiens p21-activated kinase 3 (PAK3) mRNA, complete cds//7.4e-05:534:58//Hs.152663:AF068864

R-HEMBA1003257//EST//1.4e-95:473:97//Hs.32443:H28929

R-HEMBA1003273//Small inducible cytokine A5 (RANTES)//2.6e-38:253:86//Hs.155464:AF088219

R-HEMBA1003276//ESTs//7.6e-55:269:99//Hs.23817:AA526392

R-HEMBA1003278//ESTs//2.6e-45:301:71//Hs.51652:AI084785

R-HEMBA1003281

R-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds//9.7e-117:551:99//Hs.12836:AB011109

R-HEMBA1003296//ESTs//4.8e-17:210:72//Hs.44451:AA203266
 R-HEMBA1003304//ESTs//2.8e-98:468:98//Hs.120849:AI148353
 R-HEMBA1003309//ESTs//1.8e-97:455:99//Hs.11571:AA713504
 R-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds//8.9e-113:545:97//Hs.124224:AB001872
 R-HEMBA1003322//ESTs//4.9e-79:419:95//Hs.138760:N66869
 R-HEMBA1003327//Homo sapiens clone 23622 mRNA sequence//1.4e-16:177:78//Hs.151608:AF052119
 R-HEMBA1003328//H.sapiens mRNA for MACH-alpha-2 protein//2.1e-43:269:88//Hs.19949:X98173
 R-HEMBA1003330//Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds//0.66:64:76//Hs.117176:AF026029
 R-HEMBA1003348//ESTs//1.4e-35:185:78//Hs.117879:H77357
 R-HEMBA1003369//ESTs, Weakly similar to F59C6.9 [C.elegans]//3.2e-113:553:97//Hs.65539:AI148540
 R-HEMBA1003370//ESTs//2.0e-46:319:86//Hs.37573:H59651
 R-HEMBA1003373//ESTs//1.6e-31:136:81//Hs.114849:AI139588
 R-HEMBA1003376//ESTs//3.0e-47:383:80//Hs.138852:AA284247
 R-HEMBA1003380//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.8e-11:261:65//Hs.87578:AI125363
 R-HEMBA1003384//EST//0.00013:82:75//Hs.141237:H57847
 R-HEMBA1003395//ESTs//5.2e-78:379:98//Hs.162208:AA536127
 R-HEMBA1003402//ESTs//8.6e-14:108:89//Hs.55424:AA774204
 R-HEMBA1003408//ESTs//1.7e-24:188:85//Hs.70266:Z78309
 R-HEMBA1003417//ESTs//4.2e-74:396:94//Hs.55220:D11563
 R-HEMBA1003418//ESTs//3.1e-107:545:95//Hs.3494:AI421013
 R-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//3.2e-115:544:98//Hs.25812:AF058696
 R-HEMBA1003461//ESTs//2.8e-62:304:99//Hs.148747:AI225121

R-HEMBA1003463//ESTs//2.3e-112:549:97//Hs.104627:AA885516
 R-HEMBA1003480//Homo sapiens PYRIN (MEFV) mRNA; complete cds//7.7e-76:52
 9:84//Hs.113283:AF018080
 R-HEMBA1003528//ESTs//2.1e-59:312:96//Hs.22505:R41688
 R-HEMBA1003531//ESTs//2.2e-17:116:93//Hs.140217:AA702760
 R-HEMBA1003538//Complement component C1r//4.7e-25:333:68//Hs.1279:M14058
 R-HEMBA1003545//ESTs//8.7e-89:432:98//Hs.99497:AA776817
 R-HEMBA1003548//EST//0.0091:274:60//Hs.148336:AA911673
 R-HEMBA1003555//ESTs, Weakly similar to NUCLEOTIDE-BINDING PROTEIN [H.sapiens]//2.8e-93:495:93//Hs.91619:AA552351
 R-HEMBA1003556//ESTs//7.1e-44:406:77//Hs.141575:AA211734
 R-HEMBA1003560//ESTs//4.0e-34:182:97//Hs.14811:AA434522
 R-HEMBA1003568//ESTs//2.0e-101:486:98//Hs.118570:AI342058
 R-HEMBA1003569//ESTs, Moderately similar to metastasis-associated gene [H.sapiens]//4.0e-63:343:93//Hs.58598:AA625440
 R-HEMBA1003571//Homo sapiens clone 23632 mRNA sequence//3.7e-47:338:84//
 Hs.46918:AF052099
 R-HEMBA1003579//EST//0.00057:239:60//Hs.162828:AA643892
 R-HEMBA1003581//ESTs//2.6e-10:118:79//Hs.44856:N37065
 R-HEMBA1003591//ESTs//2.4e-96:460:98//Hs.128741:AI244212
 R-HEMBA1003595//Human mRNA for KIAA0118 gene, partial cds//1.7e-48:421:7
 8//Hs.154326:D42087
 R-HEMBA1003597//EST//1.6e-38:313:80//Hs.160911:AI371042
 R-HEMBA1003598//ESTs//0.0085:273:61//Hs.145333:AI251374
 R-HEMBA1003615
 R-HEMBA1003617//ESTs//1.0e-111:574:95//Hs.4552:W68167
 R-HEMBA1003621//EST//1.7e-31:288:78//Hs.140909:R49387
 R-HEMBA1003622//EST//1.1e-46:468:75//Hs.139093:AA166888
 R-HEMBA1003630//ESTs//1.4e-21:411:69//Hs.128729:AA973021

R-HEMBA1003637//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens] //9.3e-24:189:84//Hs.142208:AA209438

R-HEMBA1003640//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.5e-42:332:81//Hs.51048:X68830

R-HEMBA1003645//ESTs//2.4e-77:423:94//Hs.99539:R59010

R-HEMBA1003646//ESTs//2.6e-98:549:91//Hs.96427:AA151783

R-HEMBA1003656//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//5.6e-44:245:77//Hs.67619:AB007957

R-HEMBA1003662//Human TBX2 (TXB2) mRNA, complete cds//2.6e-17:144:84//Hs.32931:U28049

R-HEMBA1003667//Farnesyltransferase, CAAX box, beta//1.3e-22:170:88//Hs.117596:L00635

R-HEMBA1003679//ESTs, Weakly similar to trithorax homolog HTX, version 2 [H.sapiens] //4.1e-87:434:97//Hs.9489:R84329

R-HEMBA1003680//Human DNA-binding protein (HRC1) mRNA, complete cds//0.86:315:61//Hs.72925:M91083

R-HEMBA1003684//ESTs, Highly similar to ZINC FINGER PROTEIN 7 [Homo sapiens] //1.1e-101:528:95//Hs.22934:AA581379

R-HEMBA1003690//ESTs//0.0021:119:69//Hs.98641:AA429916

R-HEMBA1003692//Human cytochrome P450-IIB (hIIB3) mRNA, complete cds//2.0e-43:360:80//Hs.110194:M29873

R-HEMBA1003711//ESTs//1.0e-70:375:94//Hs.150407:AI279064

R-HEMBA1003714//VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR//0.94:367:62//Hs.1139:X77777

R-HEMBA1003715//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.1e-77:299:85//Hs.113283:AF018080

R-HEMBA1003720//Homo sapiens TWIK-related acid-sensitive K⁺ channel (TAS K) mRNA, complete cds//1.2e-33:377:74//Hs.24040:AF006823

R-HEMBA1003725//ESTs//3.8e-103:481:99//Hs.122518:AA778847

R-HEMBA1003729//ESTs//2.5e-51:277:95//Hs.26270:AA258839
 R-HEMBA1003733//ESTs//1.9e-69:350:96//Hs.139278:AA702592
 R-HEMBA1003742//ESTs, Moderately similar to T13H5.2 [C.elegans]//4.6e-70
 :348:96//Hs.11282:AI147040
 R-HEMBA1003758//ESTs//1.7e-52:306:85//Hs.138852:AA284247
 R-HEMBA1003760//ESTs//7.4e-76:420:93//Hs.26501:H05089
 R-HEMBA1003773//ESTs, Highly similar to SIGNAL RECOGNITION PARTICLE REC
 EPTOR BETA SUBUNIT [Mus musculus]//1.9e-77:364:100//Hs.12152:AA156214
 R-HEMBA1003783//ESTs, Weakly similar to C01H6.7 [C.elegans]//2.1e-101:55
 8:93//Hs.18171:AA524327
 R-HEMBA1003784//EST//0.83:127:62//Hs.144002:F01600
 R-HEMBA1003799//EST//9.7e-30:362:71//Hs.156577:AA860236
 R-HEMBA1003803//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//2.8e-16:9
 3:100//Hs.107747:AI357868
 R-HEMBA1003804//Interleukin 15//0.13:227:62//Hs.111867:AB007295
 R-HEMBA1003805//ESTs//0.029:199:65//Hs.91582:T25344
 R-HEMBA1003807//EST//2.4e-13:137:81//Hs.145645:AI264163
 R-HEMBA1003836//Small inducible cytokine A5 (RANTES)//3.2e-39:284:83//Hs
 .155464:AF088219
 R-HEMBA1003838//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE C
 HAIN 2 [Paramecium tetraurelia]//6.5e-71:357:96//Hs.107573:AA524333
 R-HEMBA1003856//ESTs//8.2e-20:266:71//Hs.48312:N68161
 R-HEMBA1003864//ESTs//1.6e-99:528:93//Hs.26890:AA449033
 R-HEMBA1003866//POLYPOSIS LOCUS PROTEIN 1//0.30:146:64//Hs.74648:M73547
 R-HEMBA1003879//EST, Weakly similar to DNA-REPAIR PROTEIN COMPLEMENTING
 XP-A CELLS [Homo sapiens]//2.1e-59:295:98//Hs.161661:AA166911
 R-HEMBA1003880//Homo sapiens clone 24760 mRNA sequence//3.8e-34:286:79//
 Hs.61408:AF070621
 R-HEMBA1003885//ESTs//4.6e-50:293:90//Hs.142314:AA347930

R-HEMBA1003893//Calcium modulating ligand//2.1e-43:294:86//Hs.13572:AF06
8179
R-HEMBA1003902//ESTs//1.8e-43:300:85//Hs.146811:AA410788
R-HEMBA1003908//ESTs//3.5e-91:477:94//Hs.6638:AA536187
R-HEMBA1003926//ESTs//7.9e-44:294:87//Hs.164036:AA845659
R-HEMBA1003937//Homo sapiens mRNA for KIAA0585 protein, partial cds//3.5
e-48:276:81//Hs.72660:AB011157
R-HEMBA1003939
R-HEMBA1003942//ESTs//1.6e-81:428:94//Hs.50418:AA524669
R-HEMBA1003950//ESTs//8.1e-54:283:95//Hs.145528:AI261545
R-HEMBA1003953//ESTs//3.8e-30:194:89//Hs.99681:AA504591
R-HEMBA1003958//ESTs//4.0e-45:394:77//Hs.141602:N63562
R-HEMBA1003959//ESTs//5.2e-28:197:86//Hs.9951:W56253
R-HEMBA1003976//ESTs//2.0e-29:232:84//Hs.133947:AI074525
R-HEMBA1003978//ESTs//3.2e-115:549:98//Hs.76798:AI050882
R-HEMBA1003985//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
RY !!!! [H.sapiens]//2.2e-91:448:97//Hs.117834:AA766771
R-HEMBA1003987//ESTs//8.1e-36:193:88//Hs.151844:N92756
R-HEMBA1003989//Human mRNA for KIAA0241 gene, partial cds//3.6e-43:360:8
1//Hs.150275:D87682
R-HEMBA1004000//EST//5.5e-62:308:97//Hs.50438:N74105
R-HEMBA1004011//ESTs//8.6e-85:431:96//Hs.36185:R99899
R-HEMBA1004012//ESTs//1.3e-40:309:83//Hs.140329:AA714011
R-HEMBA1004015//ESTs//5.1e-97:453:99//Hs.111446:AI333774
R-HEMBA1004024//ESTs//5.2e-19:159:79//Hs.138856:H47461
R-HEMBA1004038//ESTs//1.3e-41:346:79//Hs.146173:AA906191
R-HEMBA1004042//ESTs//0.0012:201:69//Hs.24248:AA528253
R-HEMBA1004045//ESTs, Weakly similar to putative p150 [H.sapiens]//1.5e-
22:365:70//Hs.99692:AA811804

R-HEMBA1004048//ESTs//9.5e-104:497:98//Hs.77735:AI125469
R-HEMBA1004049//HEAT SHOCK 70 KD PROTEIN 1//6.3e-31:176:96//Hs.8997:M117
17
R-HEMBA1004055//ESTs//1.7e-115:577:96//Hs.59503:W63754
R-HEMBA1004056//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.2e-78:57
7:82//Hs.113283:AF018080
R-HEMBA1004074//EST//1.0:152:61//Hs.149093:AI243988
R-HEMBA1004086//ESTs//4.0e-53:266:98//Hs.34658:N98652
R-HEMBA1004097//ESTs//4.4e-46:279:91//Hs.110533:H16251
R-HEMBA1004131//Human mRNA for KIAA0128 gene, partial cds//3.0e-43:534:6
9//Hs.90998:D50918
R-HEMBA1004132//ESTs//4.6e-47:316:86//Hs.141602:N63562
R-HEMBA1004133
R-HEMBA1004138//EST//1.7e-08:211:64//Hs.129189:AA988736
R-HEMBA1004143//ESTs//4.0e-25:137:97//Hs.21307:AA203320
R-HEMBA1004146//Small inducible cytokine A5 (RANTES)//4.1e-27:191:86//Hs
.155464:AF088219
R-HEMBA1004150//GRANALCALCIN//0.99:357:59//Hs.79381:M81637
R-HEMBA1004164//Human mRNA for KIAA0118 gene, partial cds//9.5e-47:313:8
4//Hs.154326:D42087
R-HEMBA1004168//Homo sapiens geminin mRNA, complete cds//7.7e-112:563:96
//Hs.59988:AF067855
R-HEMBA1004199
R-HEMBA1004200//EST//3.1e-89:441:97//Hs.141173:R97701
R-HEMBA1004202//ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea m
ays]//1.7e-107:552:94//Hs.10092:AI189282
R-HEMBA1004203//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.
5e-96:275:98//Hs.15832:AB014518
R-HEMBA1004207//Leptin receptor//1.1e-117:573:97//Hs.54515:U50748

R-HEMBA1004225//EST//9.7e-34:186:95//Hs.137567:R20617
R-HEMBA1004227//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNIN
G ENTRY !!!! [H.sapiens] //4.0e-16:117:91//Hs.92033:AA255832
R-HEMBA1004238//Human mRNA for KIAA0355 gene, complete cds//3.0e-46:338:
83//Hs.153014:AB002353
R-HEMBA1004241//ESTs//1.3e-10:93:87//Hs.137511:AA456389
R-HEMBA1004246//Homo sapiens LIM protein mRNA, complete cds//2.7e-43:511
:72//Hs.154103:AF061258
R-HEMBA1004248//ESTs, Highly similar to INSULIN-INDUCED GROWTH RESPONSE
PROTEIN CL-6 [Rattus norvegicus] //2.1e-61:221:86//Hs.7089:W37284
R-HEMBA1004264//ESTs//1.5e-80:425:95//Hs.107206:AA234962
R-HEMBA1004267//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNIN
G ENTRY !!!! [H.sapiens] //1.4e-89:465:95//Hs.113660:D20018
R-HEMBA1004272//ESTs//4.5e-111:577:94//Hs.115696:N57931
R-HEMBA1004275//Homo sapiens clone 617 unknown mRNA, complete sequence//
1.4e-111:553:96//Hs.93677:AF091081
R-HEMBA1004276//ESTs, Highly similar to BETA-ADAPTIN [Homo sapiens; Rat
tus norvegicus; Bos taurus] //4.4e-92:559:89//Hs.28298:AA203228
R-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA
, complete cds//6.2e-108:538:97//Hs.101766:AF022795
R-HEMBA1004289//Sulfotransferase, dehydroepiandrosterone (DHEA) -preferr
ing//1.7e-34:223:75//Hs.81884:U13061
R-HEMBA1004295//ESTs, Weakly similar to weakly similar to ANK repeat reg
ion of Fowlpox virus BamHI-orf7 protein [C.elegans] //3.6e-93:496:94//Hs.
14337:AA534961
R-HEMBA1004306//ESTs//3.4e-26:363:68//Hs.70279:AA757426
R-HEMBA1004312//ESTs//4.8e-64:351:94//Hs.138611:H82679
R-HEMBA1004321//Zinc finger protein 44 (KOX 7)//2.6e-37:415:64//Hs.51199
:X16281

R-HEMBA1004323//ESTs//2.1e-40:280:70//Hs.153300:AA928904
 R-HEMBA1004327//ESTs//3.8e-72:343:99//Hs.151708:AA554714
 R-HEMBA1004330//ESTs//4.0e-52:270:97//Hs.24654:AA456561
 R-HEMBA1004334//ESTs//1.6e-46:234:98//Hs.47159:AI310231
 R-HEMBA1004335//ESTs//1.9e-25:250:76//Hs.155880:AA703336
 R-HEMBA1004341//ESTs//3.7e-101:480:98//Hs.69321:AA633240
 R-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds//1.3e-75:444:90//Hs.80686:D89667
 R-HEMBA1004354//Human mRNA for KIAA0355 gene, complete cds//5.9e-39:286:83//Hs.153014:AB002353
 R-HEMBA1004356//SINGLE-STRANDED DNA-BINDING PROTEIN MSSP-1//1.3e-107:576:93//Hs.55458:X77494
 R-HEMBA1004366//ESTs//2.3e-94:524:91//Hs.111496:AA652869
 R-HEMBA1004372//EST//0.27:198:60//Hs.162665:AA605057
 R-HEMBA1004389//ESTs//4.1e-102:490:98//Hs.153708:AA687264
 R-HEMBA1004394//ESTs//1.5e-94:471:96//Hs.151647:AA002084
 R-HEMBA1004396//Small inducible cytokine A5 (RANTES)//6.2e-41:285:83//Hs.155464:AF088219
 R-HEMBA1004405//ESTs//2.0e-44:329:83//Hs.136839:H93717
 R-HEMBA1004408//ESTs, Weakly similar to homologous to mouse Rsu-1 [H.sapiens]//6.1e-89:420:99//Hs.88365:AA648933
 R-HEMBA1004429//ESTs, Weakly similar to homeotic protein protein zhx-1 [M.musculus]//3.0e-112:552:96//Hs.12940:AI123518
 R-HEMBA1004433//Human Line-1 repeat mRNA with 2 open reading frames//2.9e-32:463:68//Hs.23094:M19503
 R-HEMBA1004460//ESTs//2.0e-104:574:93//Hs.46848:AA195829
 R-HEMBA1004461//ESTs//2.9e-102:503:98//Hs.16370:AA017033
 R-HEMBA1004479//ELK1, member of ETS oncogene family//1.1e-45:310:75//Hs.116549:AL009172

R-HEMBA1004482//ESTs//9.1e-05:322:62//Hs.34489:AA759306
R-HEMBA1004502//ESTs//6.9e-112:566:96//Hs.93985:N50034
R-HEMBA1004506//EST//5.3e-59:456:80//Hs.72412:AA160941
R-HEMBA1004507
R-HEMBA1004509//ESTs, Moderately similar to HYPOTHETICAL 52.2 KD PROTEIN IN MPR1-GCN20 INTERGENIC REGION [*Saccharomyces cerevisiae*]//2.9e-82:262:99//Hs.12820:AA004271
R-HEMBA1004534//ESTs, Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN IN [*Homo sapiens*]//1.1e-43:281:89//Hs.58414:AA196947
R-HEMBA1004538//EST//3.3e-15:270:71//Hs.136667:AA707972
R-HEMBA1004554
R-HEMBA1004560//ESTs//8.2e-25:179:88//Hs.96560:W22924
R-HEMBA1004573//ESTs, Moderately similar to ALR [*H.sapiens*]//1.0:305:60//Hs.30272:AA134913
R-HEMBA1004577//ESTs//7.9e-50:319:89//Hs.22660:AA582243
R-HEMBA1004586//ESTs//2.6e-73:384:96//Hs.9582:R39769
R-HEMBA1004596//ESTs//6.0e-22:190:82//Hs.42530:N41661
R-HEMBA1004610//ESTs//1.2e-91:438:98//Hs.47823:AA780767
R-HEMBA1004617//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//4.6e-52:327:85//Hs.159897:AB007970
R-HEMBA1004629//ESTs//2.3e-19:215:76//Hs.111995:AI375915
R-HEMBA1004631//ESTs//3.6e-99:470:98//Hs.49303:AA810785
R-HEMBA1004632//ESTs//1.0:128:66//Hs.159182:AA831152
R-HEMBA1004637//ESTs, Highly similar to HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III [*Caenorhabditis elegans*]//4.8e-111:532:98//Hs.12263:AA282393
R-HEMBA1004638//ESTs//1.2e-66:341:95//Hs.122687:AI278454
R-HEMBA1004666//ESTs//2.1e-65:333:96//Hs.98873:AA625442
R-HEMBA1004669//ESTs//0.00039:116:74//Hs.138725:N76348

R-HEMBA1004670//ESTs//1.7e-16:116:89//Hs.56825:AI057560
 R-HEMBA1004672//EST//6.7e-76:315:97//Hs.20821:R19368
 R-HEMBA1004693//ESTs//6.4e-68:327:99//Hs.159066:AI093252
 R-HEMBA1004697//ESTs//9.3e-98:467:98//Hs.62637:AA043562
 R-HEMBA1004705//EST//0.0034:271:58//Hs.112503:AA599042
 R-HEMBA1004709//EST//1.3e-55:392:85//Hs.149580:AI281881
 R-HEMBA1004711//Small inducible cytokine A5 (RANTES)//1.9e-47:449:76//Hs.
 .155464:AF088219
 R-HEMBA1004725//EST//1.8e-71:424:88//Hs.155712:AI309235
 R-HEMBA1004730//Homo sapiens clone 23892 mRNA sequence//2.1e-44:467:73//
 Hs.91916:AF035317
 R-HEMBA1004733//EST//0.99:84:65//Hs.161372:AI423151
 R-HEMBA1004734//ESTs//1.8e-82:421:96//Hs.21275:N73275
 R-HEMBA1004736//Ataxia telangiectasia mutated (includes complementation
 groups A, C and D)//9.5e-39:296:82//Hs.51187:U82828
 R-HEMBA1004748//ESTs//1.7e-43:166:86//Hs.37573:H59651
 R-HEMBA1004751//ESTs//8.0e-23:155:88//Hs.149464:AI279428
 R-HEMBA1004752//Thromboxane A2 receptor//2.7e-45:281:89//Hs.89887:D38081
 R-HEMBA1004753//40S RIBOSOMAL PROTEIN S20//8.3e-67:475:84//Hs.8102:L0649
 8
 R-HEMBA1004756//ESTs//2.0e-81:384:99//Hs.129545:N68679
 R-HEMBA1004758//EST//2.0e-43:367:80//Hs.133006:AI049504
 R-HEMBA1004763//ESTs//2.0e-108:567:94//Hs.3757:W87380
 R-HEMBA1004768//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTE
 IN [Mus musculus]//1.4e-47:379:81//Hs.141273:H66705
 R-HEMBA1004770//ESTs//0.0014:246:61//Hs.124857:AA687092
 R-HEMBA1004771//ESTs//1.1e-12:323:63//Hs.124146:AA699633
 R-HEMBA1004776//ESTs//2.5e-112:567:95//Hs.12680:W74476
 R-HEMBA1004778//ESTs//1.4e-33:272:75//Hs.141123:AA848167

R-HEMBA1004795
 R-HEMBA1004803//ESTs//1.0e-48:319:86//Hs.139231:W87732
 R-HEMBA1004806
 R-HEMBA1004807//ESTs//6.2e-77:362:100//Hs.140945:N47676
 R-HEMBA1004816//EST//4.3e-18:246:72//Hs.150552:AI053784
 R-HEMBA1004820//Human arginine-rich nuclear protein mRNA, complete cds//
 5.0e-14:141:85//Hs.80510:M74002
 R-HEMBA1004847
 R-HEMBA1004850//ESTs//1.2e-83:395:99//Hs.30925:AA577120
 R-HEMBA1004863//ESTs//7.5e-21:204:79//Hs.35036:H95267
 R-HEMBA1004864
 R-HEMBA1004865//EST//6.7e-18:191:75//Hs.129944:AA429362
 R-HEMBA1004880//EST//4.4e-70:346:98//Hs.145094:AA452409
 R-HEMBA1004889//ESTs//4.8e-117:496:97//Hs.15641:W63676
 R-HEMBA1004900//ESTs//1.2e-15:283:68//Hs.157606:AI357470
 R-HEMBA1004909//ESTs//7.3e-44:366:79//Hs.140329:AA714011
 R-HEMBA1004918//Human mRNA for KIAA0392 gene, partial cds//4.6e-50:313:8
 9//Hs.40100:AB002390
 R-HEMBA1004923//ESTs//0.013:162:64//Hs.143655:AI128388
 R-HEMBA1004929//EST//2.3e-48:250:97//Hs.131589:AI025053
 R-HEMBA1004930//Cytochrome P450, subfamily I (aromatic compound-inducibl
 e), polypeptide 2//1.2e-70:547:80//Hs.1361:M55053
 R-HEMBA1004933//ESTs, Weakly similar to R06C7.6 [C.elegans]//5.3e-110:53
 0:98//Hs.18029:AI422883
 R-HEMBA1004934//ESTs//1.3e-103:522:96//Hs.40415:AA037215
 R-HEMBA1004944//ESTs//6.0e-21:97:84//Hs.141973:N21434
 R-HEMBA1004954//ESTs//7.9e-112:596:93//Hs.6226:W61007
 R-HEMBA1004956//ESTs//3.1e-58:280:100//Hs.120750:AA741074
 R-HEMBA1004960//ESTs//6.9e-89:476:93//Hs.163738:AA601040

R-HEMBA1004972//ESTs//3.0e-72:381:95//Hs.55014:AA934035
 R-HEMBA1004973//ESTs//2.7e-91:441:98//Hs.28144:AI292065
 R-HEMBA1004977//ESTs//2.0e-95:446:99//Hs.29690:AI168404
 R-HEMBA1004978//Homo sapiens natural killer cell group 2-F (NKG2-F) mRNA,
 complete cds//0.43:187:67//Hs.129734:AJ001683
 R-HEMBA1004980//Human mRNA for KIAA0331 gene, complete cds//6.4e-53:305:
 91//Hs.146395:AB002329
 R-HEMBA1004983//ESTs//0.16:482:57//Hs.131929:AI021894
 R-HEMBA1004995
 R-HEMBA1005008//EST, Weakly similar to mariner transposase [H.sapiens]//
 6.9e-51:482:78//Hs.141601:N63520
 R-HEMBA1005009//ESTs, Highly similar to ACTIN I [Naegleria fowleri]//3.
 8e-109:551:96//Hs.103180:AI365212
 R-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds//2.0
 e-105:542:94//Hs.31921:AB014548
 R-HEMBA1005029//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOM
 OLOG [Homo sapiens]//8.4e-95:491:94//Hs.16085:AI261382
 R-HEMBA1005035//Human mRNA for KIAA0033 gene, partial cds//2.3e-64:312:8
 5//Hs.22271:D26067
 R-HEMBA1005039//ESTs, Weakly similar to zinc finger protein [H.sapiens]/
 /2.6e-48:443:78//Hs.139019:N99348
 R-HEMBA1005047//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-5A [Can
 is familiaris]//1.2e-87:542:87//Hs.16258:AI376436
 R-HEMBA1005050//ESTs//6.3e-46:311:86//Hs.159510:AA297145
 R-HEMBA1005062//ESTs//1.1e-14:216:68//Hs.129935:AA994451
 R-HEMBA1005066//Human clone 23574 mRNA sequence//2.2e-24:303:73//Hs.7938
 5:U90905
 R-HEMBA1005075//EST//0.65:214:62//Hs.133991:AI075789
 R-HEMBA1005079//Human BENE mRNA, partial cds//1.9e-44:304:83//Hs.85889:U

17077

R-HEMBA1005083//ESTs//2.8e-74:356:98//Hs.132272:AI393958
 R-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete
 cds//1.7e-111:545:96//Hs.11170:AF080561
 R-HEMBA1005113//ESTs//1.1e-101:512:95//Hs.7972:AI052739
 R-HEMBA1005123//Ley I-L//3.6e-58:519:77//Hs.37062:AC005952
 R-HEMBA1005133//H.sapiens mRNA for MACH-alpha-2 protein//8.3e-46:309:85/
 /Hs.19949:X98173
 R-HEMBA1005149//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
 0488//4.7e-36:394:75//Hs.67619:AB007957
 R-HEMBA1005152//Homo sapiens antigen NY-CO-16 mRNA, complete cds//3.6e-3
 2:362:77//Hs.132206:AF039694
 R-HEMBA1005159//EST//7.4e-47:252:94//Hs.134930:AI093397
 R-HEMBA1005185//ESTs//5.2e-48:305:89//Hs.14920:AA910914
 R-HEMBA1005201//ESTs//4.7e-58:293:97//Hs.23752:C05766
 R-HEMBA1005202//ESTs//1.0:169:59//Hs.153423:AI198239
 R-HEMBA1005219//Homo sapiens putative tumor suppressor protein (123F2) m
 RNA, complete cds//0.84:191:61//Hs.26931:AF061836
 R-HEMBA1005223//ESTs//0.75:90:70//Hs.127446:AA167284
 R-HEMBA1005232//EST//0.056:162:67//Hs.65649:F13687
 R-HEMBA1005241//ESTs//3.6e-113:564:96//Hs.12770:W84331
 R-HEMBA1005244//ESTs//6.4e-22:118:100//Hs.21396:AA114834
 R-HEMBA1005251//ESTs//8.5e-36:213:92//Hs.161554:AA393896
 R-HEMBA1005252//Homo sapiens mRNA for KIAA0585 protein, partial cds//6.1
 e-49:277:93//Hs.72660:AB011157
 R-HEMBA1005274//ESTs//3.7e-65:322:98//Hs.105166:AA668862
 R-HEMBA1005275//ESTs//2.1e-29:298:73//Hs.33393:R83391
 R-HEMBA1005293//ESTs//3.5e-93:448:98//Hs.12066:AI208611
 R-HEMBA1005296//ESTs//4.3e-33:168:100//Hs.13916:AI025750

R-HEMBA1005304//Small inducible cytokine A5 (RANTES)//2.8e-50:315:82//Hs.155464:AF088219

R-HEMBA1005311//Homo sapiens 4F5S mRNA, complete cds//1.3e-44:318:83//Hs.32567:AF073519

R-HEMBA1005314//ESTs//3.0e-103:491:98//Hs.41606:AI095046

R-HEMBA1005315//EST//1.9e-29:370:72//Hs.161483:N59169

R-HEMBA1005318//ESTs//3.9e-110:535:97//Hs.26771:AA126472

R-HEMBA1005331//Intercellular adhesion molecule 2//7.6e-39:256:87//Hs.83733:X15606

R-HEMBA1005353//ESTs//1.7e-81:406:96//Hs.155374:AI341467

R-HEMBA1005359//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//4.7e-46:294:81//Hs.129735:AF010144

R-HEMBA1005367//Alcohol dehydrogenase 2 (class I), beta polypeptide//1.0:210:62//Hs.4:X03350

R-HEMBA1005372//ESTs//6.2e-95:451:99//Hs.135219:AI091653

R-HEMBA1005374//ESTs//1.5e-107:502:99//Hs.118208:AA947305

R-HEMBA1005389//Fc fragment of IgA, receptor for//1.0e-39:311:80//Hs.54486:X54150

R-HEMBA1005394//ESTs, Weakly similar to coded for by C. elegans cDNA yk30b3.5 [C.elegans]//4.0e-88:489:92//Hs.43864:AA131568

R-HEMBA1005403//EST//0.0011:78:75//Hs.127061:AA863278

R-HEMBA1005408//ESTs//3.2e-29:395:71//Hs.117532:AA676725

R-HEMBA1005410//ESTs//1.5e-18:271:70//Hs.144604:AI052059

R-HEMBA1005411//ESTs//1.1e-35:335:77//Hs.141181:R98757

R-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds//1.8e-118:453:99//Hs.4854:AF041248

R-HEMBA1005426//Chromosome 1 specific transcript KIAA0491//0.25:264:61//Hs.136309:AB007960

R-HEMBA1005443//Homo sapiens (clone s153) mRNA fragment//1.7e-47:305:87/

/Hs.6445:L40391

R-HEMBA1005447//ESTs//5.7e-83:529:86//Hs.114253:AA745961

R-HEMBA1005468//ESTs//7.3e-23:249:73//Hs.61199:AA024494

R-HEMBA1005469//Human mRNA for KIAA0355 gene, complete cds//4.5e-45:320:85//Hs.153014:AB002353

R-HEMBA1005472//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//8.4e-73:464:87//Hs.103948:K00627

R-HEMBA1005475//ESTs//0.32:192:59//Hs.62694:AA100445

R-HEMBA1005497

R-HEMBA1005500//ESTs//2.2e-43:307:85//Hs.146811:AA410788

R-HEMBA1005506//75 kda infertility-related sperm protein [human, testis, mRNA Partial, 2427 nt]//0.11:295:60//Hs.62608:S58544

R-HEMBA1005508//ESTs//2.8e-55:319:93//Hs.50150:N90870

R-HEMBA1005511//ESTs, Weakly similar to similar to mouse MMR1 [C.elegans]//2.6e-82:387:99//Hs.67466:AI219740

R-HEMBA1005517//ESTs//4.6e-77:469:90//Hs.126787:AA203322

R-HEMBA1005518//ESTs//1.5e-108:561:94//Hs.123167:AA601045

R-HEMBA1005520//Putative mismatch repair/binding protein hMSH3//7.5e-44:179:84//Hs.42674:U61981

R-HEMBA1005526//ESTs//8.7e-46:308:86//Hs.146811:AA410788

R-HEMBA1005528//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//8.6e-115:578:95//Hs.17035:AI080471

R-HEMBA1005530//ESTs//1.5e-110:551:96//Hs.107294:W72350

R-HEMBA1005548//ESTs//1.7e-100:510:96//Hs.9115:N90926

R-HEMBA1005552//Interleukin 10//2.4e-38:306:80//Hs.2180:M57627

R-HEMBA1005558//ESTs, Weakly similar to unknown [S.cerevisiae]//5.3e-77:439:91//Hs.22897:R43193

R-HEMBA1005568//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT RY !!!! [H.sapiens]//3.4e-31:182:76//Hs.133526:N21103

R-HEMBA1005570//ESTs//3.3e-67:411:88//Hs.142245:AA489709
 R-HEMBA1005576//EST//0.91:52:73//Hs.149518:AI280497
 R-HEMBA1005577
 R-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//3.1e-28:561:64
 //Hs.57929:AB011538
 R-HEMBA1005582//ESTs//6.0e-73:371:97//Hs.103758:C06392
 R-HEMBA1005583//ESTs//8.3e-79:413:95//Hs.62348:AA419539
 R-HEMBA1005588//Human c-yes-1 mRNA//2.6e-52:403:83//Hs.75680:M15990
 R-HEMBA1005593//ESTs//3.3e-30:139:80//Hs.142273:W37905
 R-HEMBA1005595//ESTs//1.1e-97:454:100//Hs.27497:AI274820
 R-HEMBA1005606//EST//1.0e-12:313:64//Hs.162402:AA573125
 R-HEMBA1005609//ESTs//0.49:278:58//Hs.76235:W56390
 R-HEMBA1005616//EST//1.3e-98:470:99//Hs.122230:AA781422
 R-HEMBA1005621//ESTs, Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisi
 ae]//2.8e-95:539:92//Hs.19400:AA662845
 R-HEMBA1005627//Human mRNA for adipogenesis inhibitory factor//5.5e-38:3
 17:78//Hs.1721:X58377
 R-HEMBA1005631//Human mRNA for KIAA0393 gene, complete cds//2.3e-11:279:
 65//Hs.15245:AF041081
 R-HEMBA1005632//EST//1.5e-10:181:70//Hs.120259:AA731522
 R-HEMBA1005634//Homo sapiens mRNA for chemokine LEC precursor, complete
 cds//1.4e-25:234:80//Hs.10458:AF088219
 R-HEMBA1005666//ESTs//2.3e-103:534:95//Hs.14512:AA205973
 R-HEMBA1005670//ESTs//2.6e-39:166:81//Hs.139414:AI279477
 R-HEMBA1005679//Esterase D/formylglutathione hydrolase//1.3e-50:322:88//
 Hs.82193:M13450
 R-HEMBA1005680//Homo sapiens LIM protein mRNA, complete cds//3.3e-43:343
 :81//Hs.154103:AF061258
 R-HEMBA1005685//Human homeodomain protein (Prox 1) mRNA, complete cds//0

.0050:235:64//Hs.159437:U44060
R-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (E
plg8) mRNA, complete cds//1.7e-47:376:84//Hs.26988:U66406
R-HEMBA1005705//ESTs//3.0e-53:259:99//Hs.55314:AA772055
R-HEMBA1005717//EST//2.5e-59:287:99//Hs.146870:AI159943
R-HEMBA1005732//Homo sapiens mRNA for cartilage-associated protein (CASP
)//1.2e-45:398:79//Hs.155481:AJ006470
R-HEMBA1005737//ESTs//2.5e-57:416:83//Hs.23245:AA053815
R-HEMBA1005746//EST//0.098:125:68//Hs.136945:AA765672
R-HEMBA1005755//EST//2.2e-22:180:84//Hs.141488:N47096
R-HEMBA1005765//Human peptide transporter (HPEPT1) mRNA, complete cds//3
.9e-47:404:80//Hs.2217:U21936
R-HEMBA1005780//ESTs//1.3e-106:512:97//Hs.11901:AA173974
R-HEMBA1005813//Homo sapiens mRNA for chemokine LEC precursor, complete
cds//2.0e-33:195:84//Hs.10458:AF088219
R-HEMBA1005815//ESTs//7.6e-19:290:71//Hs.112218:AI038601
R-HEMBA1005822//ESTs//5.4e-49:246:98//Hs.34804:AA514960
R-HEMBA1005829//ESTs//2.7e-72:344:99//Hs.54548:AI039201
R-HEMBA1005834//ESTs//1.6e-44:317:82//Hs.157029:AI080618
R-HEMBA1005852//ESTs//1.6e-102:544:93//Hs.9911:AA098911
R-HEMBA1005853//ESTs//1.8e-78:398:95//Hs.140248:AA757917
R-HEMBA1005884//EST//2.6e-18:275:67//Hs.139357:AA420970
R-HEMBA1005891//ESTs//2.1e-89:427:98//Hs.67317:AI022252
R-HEMBA1005894
R-HEMBA1005909//ESTs//2.6e-91:436:99//Hs.147492:AI215686
R-HEMBA1005911//ESTs//1.1e-85:446:95//Hs.134494:AI076363
R-HEMBA1005921//ESTs//1.4e-84:428:95//Hs.127993:AA970632
R-HEMBA1005931//Homo sapiens mRNA for KIAA0526 protein, complete cds//9.
5e-45:446:75//Hs.59403:AB011098

R-HEMBA1005934//ESTs//0.20:142:65//Hs.97079:AA370867
 R-HEMBA1005962//ESTs//1.8e-87:409:100//Hs.161292:AI199418
 R-HEMBA1005963
 R-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//2.2e-113:580:95//Hs.26285:AF082516
 R-HEMBA1005991//Human antiseecretory factor-1 mRNA, complete cds//2.0e-45:551:70//Hs.148495:AF050199
 R-HEMBA1005999//ESTs//7.5e-24:201:69//Hs.157029:AI080618
 R-HEMBA1006002//ESTs//3.1e-112:573:95//Hs.61233:AI379875
 R-HEMBA1006005//EST//1.0:105:63//Hs.145273:AI249436
 R-HEMBA1006031//Homo sapiens mRNA for KIAA0725 protein, partial cds//2.4e-28:444:67//Hs.26450:AB018268
 R-HEMBA1006035//ESTs//4.5e-94:465:97//Hs.44625:N49951
 R-HEMBA1006036//ESTs//6.1e-90:420:100//Hs.126771:AA916508
 R-HEMBA1006042//EST//1.5e-88:424:98//Hs.132551:AA948490
 R-HEMBA1006067
 R-HEMBA1006081//ESTs//7.8e-68:356:95//Hs.27410:N25612
 R-HEMBA1006090//EST//5.1e-66:320:99//Hs.99551:AA461517
 R-HEMBA1006091//ESTs//2.0e-84:441:94//Hs.9658:AA506313
 R-HEMBA1006100//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//3.4e-43:328:82//Hs.73614:U83460
 R-HEMBA1006108//ESTs//1.5e-44:228:98//Hs.26368:AA789297
 R-HEMBA1006121//ESTs//1.6e-116:547:99//Hs.34151:AI279293
 R-HEMBA1006124//EST//1.6e-20:286:64//Hs.148457:AI198931
 R-HEMBA1006130//ESTs//8.8e-47:231:99//Hs.16470:AA121635
 R-HEMBA1006138//Homo sapiens mRNA for KIAA0792 protein, complete cds//8.7e-27:296:73//Hs.119387:AB007958
 R-HEMBA1006142//ESTs//1.5e-27:255:70//Hs.139507:T77542
 R-HEMBA1006155//ESTs//4.9e-64:353:94//Hs.84560:R41212

R-HEMBA1006158//Deoxyuridine triphosphatase//0.99:162:62//Hs.82113:U3193
0

R-HEMBA1006173//ESTs//7.5e-85:462:92//Hs.79092:H29627

R-HEMBA1006182//ESTs//5.5e-29:218:72//Hs.141466:H96906

R-HEMBA1006198//ESTs//2.1e-34:282:82//Hs.142068:AA176125

R-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//6.9e-112:545:97/
/Hs.109268:AF070557

R-HEMBA1006248//ESTs, Highly similar to ZINC FINGER PROTEIN MFG1 [Mus m
usculus] //3.3e-114:581:95//Hs.23617:AA928683

R-HEMBA1006252//Human mRNA for KIAA0080 gene, partial cds//7.0e-48:284:7
6//Hs.74554:D38522

R-HEMBA1006253//Homo sapiens 45kDa splicing factor mRNA, complete cds//5
.7e-30:179:91//Hs.15836:AF083384

R-HEMBA1006259//Homo sapiens KIAA0421 mRNA, partial cds//1.5e-45:326:84/
/Hs.41742:AB007881

R-HEMBA1006268//ESTs, Highly similar to c-Jun leucine zipper interactive
[M.musculus] //1.2e-97:529:93//Hs.10552:AA524401

R-HEMBA1006272//ESTs, Moderately similar to RETROVIRUS-RELATED PROTEASE
[H.sapiens] //2.7e-88:484:92//Hs.104129:AA923278

R-HEMBA1006278//H.sapiens PAP mRNA//5.2e-56:585:71//Hs.49007:X76770

R-HEMBA1006283//ESTs, Weakly similar to NUCLEAR POLYADENYLATED RNA-BINDI
NG PROTEIN NAB2 [S.cerevisiae] //1.6e-66:377:91//Hs.108674:W25821

R-HEMBA1006284//ESTs//3.7e-110:544:96//Hs.55296:AI084735

R-HEMBA1006291//ESTs//2.2e-91:457:96//Hs.114611:N37019

R-HEMBA1006293//ESTs//5.4e-78:370:99//Hs.155111:AI202037

R-HEMBA1006309//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//3.7e-40:16
7:86//Hs.74478:U33931

R-HEMBA1006310//ESTs, Weakly similar to reverse transcriptase [M.musculu
s] //5.6e-76:417:94//Hs.111754:AI204587

R-HEMBA1006328//Small inducible cytokine A5 (RANTES)//2.8e-60:397:78//Hs.155464:AF088219

R-HEMBA1006334//Human occludin mRNA, complete cds//0.72:369:59//Hs.93518:U49184

R-HEMBA1006344//Human plectin (PLEC1) mRNA, complete cds//0.016:217:64//Hs.79706:U53204

R-HEMBA1006347//ESTs, Highly similar to HYPOTHETICAL 97.6 KD PROTEIN IN SHP1-SEC17 INTERGENIC REGION [Saccharomyces cerevisiae]//3.6e-119:582:97//Hs.42343:AI417075

R-HEMBA1006349//ESTs//5.2e-57:305:94//Hs.6338:AA411382

R-HEMBA1006359//ESTs//8.2e-90:426:99//Hs.100873:AA678008

R-HEMBA1006364//ESTs//2.2e-98:582:91//Hs.23837:AA541787

R-HEMBA1006377//EST//0.0097:145:62//Hs.133027:AI049830

R-HEMBA1006380//Homo sapiens mRNA for KIAA0594 protein, partial cds//1.0e-41:349:79//Hs.154872:AB011166

R-HEMBA1006381//ESTs//5.1e-46:320:85//Hs.37573:H59651

R-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-87:582:84//Hs.23094:M19503

R-HEMBA1006416//ESTs//1.5e-17:251:73//Hs.33950:AI218923

R-HEMBA1006419//EST//8.5e-65:353:94//Hs.141309:H72778

R-HEMBA1006421//Oxytocin receptor//1.2e-12:249:68//Hs.2820:X64878

R-HEMBA1006424//ESTs, Weakly similar to pot. ORF II [H.sapiens]//6.3e-13:263:66//Hs.43127:AA258004

R-HEMBA1006426//ESTs//6.5e-84:401:99//Hs.37303:C16964

R-HEMBA1006438//EST//0.87:266:57//Hs.99456:AA457380

R-HEMBA1006445//ESTs//2.0e-81:414:96//Hs.58153:W72033

R-HEMBA1006446//Homo sapiens mRNA for cadherin-6, complete cds//1.6e-05:487:58//Hs.32963:D31784

R-HEMBA1006461//ESTs//5.1e-78:393:97//Hs.142677:R95895

R-HEMBA1006467//ESTs, Weakly similar to putative p150 [H.sapiens]//3.0e-17:342:63//Hs.111730:AA604403

R-HEMBA1006471//ESTs//3.8e-66:370:92//Hs.14063:T77441

R-HEMBA1006474

R-HEMBA1006483//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.2e-40:365:78//Hs.46468:U45984

R-HEMBA1006485//H.sapiens mRNA for aminopeptidase//2.5e-92:517:91//Hs.132243:Y07701

R-HEMBA1006486//EST//7.0e-47:240:76//Hs.161917:AA483223

R-HEMBA1006489//ESTs//2.1e-93:440:99//Hs.125264:AA873350

R-HEMBA1006492//ESTs//0.00034:52:90//Hs.163219:AA810720

R-HEMBA1006494//EST//1.8e-06:192:67//Hs.141401:H93387

R-HEMBA1006497//ESTs//6.2e-45:232:97//Hs.118015:N33117

R-HEMBA1006502//Complement component 5 receptor 1 (C5a ligand)//8.7e-16:135:72//Hs.2161:M62505

R-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//3.9e-117:570:96//Hs.153858:AB014566

R-HEMBA1006521//ESTs//9.9e-99:496:96//Hs.64906:AA677300

R-HEMBA1006530//ESTs//0.18:260:60//Hs.24970:AI057628

R-HEMBA1006535//GS1 PROTEIN//0.52:267:62//Hs.78991:M86934

R-HEMBA1006540//EST//0.016:143:66//Hs.148189:AA897331

R-HEMBA1006546//Homo sapiens mRNA for KIAA0582 protein, partial cds//2.2e-48:287:91//Hs.79507:AB011154

R-HEMBA1006559//ESTs, Moderately similar to neurodegeneration-associated protein 1 [R.norvegicus]//1.8e-109:547:96//Hs.21122:AA191594

R-HEMBA1006562//EST//1.1e-13:327:63//Hs.149641:AI283064

R-HEMBA1006566//ESTs//2.6e-59:311:97//Hs.146014:R51876

R-HEMBA1006569//ESTs//4.7e-89:458:96//Hs.42861:W74725

R-HEMBA1006579//ESTs//2.9e-19:110:99//Hs.126191:AA873876

R-HEMBA1006583//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//9.5e-29:276:76//Hs.144563:AF057280

R-HEMBA1006595//ESTs//1.3e-96:487:96//Hs.43228:N67390

R-HEMBA1006597//Small inducible cytokine A5 (RANTES)//9.8e-44:291:85//Hs.155464:AF088219

R-HEMBA1006612

R-HEMBA1006617//ESTs//1.2e-25:225:80//Hs.138852:AA284247

R-HEMBA1006624//ESTs//1.9e-93:454:98//Hs.72531:AA773630

R-HEMBA1006631//Human mRNA for KIAA0033 gene, partial cds//7.5e-60:286:90//Hs.22271:D26067

R-HEMBA1006635//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//2.7e-91:426:100//Hs.139469:AI299889

R-HEMBA1006639//ESTs, Highly similar to POLYADENYLATE-BINDING PROTEIN [Homo sapiens]//3.4e-37:186:100//Hs.109818:AA411185

R-HEMBA1006643//ESTs//1.8e-35:189:97//Hs.139640:AA846777

R-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds//8.1e-108:567:94//Hs.6196:U40282

R-HEMBA1006652//ESTs//7.6e-100:536:93//Hs.142613:AA129427

R-HEMBA1006653//ESTs//2.0e-33:181:87//Hs.153599:AI282511

R-HEMBA1006665//EST//1.2e-13:141:72//Hs.145596:AI263102

R-HEMBA1006674//ESTs//3.1e-32:212:83//Hs.95115:AA206594

R-HEMBA1006676//ESTs//2.6e-95:510:93//Hs.39140:AI041842

R-HEMBA1006682//EST//1.4e-05:277:62//Hs.145762:AI269435

R-HEMBA1006695//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.9e-32:261:79//Hs.77579:AF013263

R-HEMBA1006696//ESTs//4.5e-95:448:99//Hs.155694:AI032695

R-HEMBA1006708//ESTs, Weakly similar to Miller-Dieker lissencephaly gene [H.sapiens]//1.1e-92:483:94//Hs.6525:AI205313

R-HEMBA1006709//ESTs//3.4e-25:207:80//Hs.88617:AA872062

R-HEMBA1006717
 R-HEMBA1006737//EST//5.9e-30:317:75//Hs.140568:AA826002
 R-HEMBA1006744//Interleukin 10//3.7e-41:419:74//Hs.2180:M57627
 R-HEMBA1006754//ESTs//1.2e-46:276:83//Hs.141254:AI334099
 R-HEMBA1006758//ESTs//0.00043:48:100//Hs.157265:AA489646
 R-HEMBA1006767//EST//0.094:120:65//Hs.159873:R92763
 R-HEMBA1006779//EST//9.3e-45:298:85//Hs.149580:AI281881
 R-HEMBA1006780//ESTs//1.6e-46:423:77//Hs.141602:N63562
 R-HEMBA1006789//ESTs//7.6e-55:245:95//Hs.6459:AI092936
 R-HEMBA1006795//ESTs//8.6e-47:315:78//Hs.140491:W52705
 R-HEMBA1006796//ESTs//0.26:175:65//Hs.103280:AI334978
 R-HEMBA1006807//Homo sapiens DEC-205 mRNA, complete cds//5.7e-47:461:75/
 /Hs.153563:AF011333
 R-HEMBA1006821//ESTs//3.5e-12:222:68//Hs.150439:AI016305
 R-HEMBA1006824//Homo sapiens mRNA, clone:RES4-16//6.7e-51:298:90//Hs.121
 493:D25272
 R-HEMBA1006832//ESTs//0.0050:108:70//Hs.12853:T65556
 R-HEMBA1006849//Human mRNA for KIAA0118 gene, partial cds//2.1e-49:367:8
 3//Hs.154326:D42087
 R-HEMBA1006865//ESTs//0.85:112:63//Hs.116430:AA644665
 R-HEMBA1006877//Homo sapiens mRNA for KIAA0772 protein, complete cds//1.
 8e-67:611:74//Hs.15519:AB018315
 R-HEMBA1006885//ESTs//2.4e-66:347:96//Hs.100624:N95453
 R-HEMBA1006900//ESTs//2.7e-91:466:96//Hs.32984:R89739
 R-HEMBA1006921//ESTs//2.2e-33:170:100//Hs.152277:AA593117
 R-HEMBA1006926//ESTs, Weakly similar to ZK1053.6 [C.elegans]//2.9e-28:21
 3:84//Hs.9096:AA029400
 R-HEMBA1006929//ESTs//4.0e-13:210:66//Hs.100895:AA479308
 R-HEMBA1006936//ESTs//3.9e-05:60:93//Hs.8737:W22712

R-HEMBA1006938//EST//0.0021:244:62//Hs.144237:W52382
 R-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein/
 /6.5e-77:371:98//Hs.42644:AJ010841
 R-HEMBA1006949//ESTs//1.2e-67:335:98//Hs.25780:R51321
 R-HEMBA1006973//ESTs//0.029:242:61//Hs.146074:N34457
 R-HEMBA1006976//EST//0.70:206:61//Hs.147092:AI189827
 R-HEMBA1006993//Human mRNA for KIAA0327 protein, complete cds//2.6e-47:3
 68:80//Hs.149323:AB002325
 R-HEMBA1006996//ESTs//0.027:326:58//Hs.105008:AA451679
 R-HEMBA1007002//ESTs//0.13:116:66//Hs.26928:Z41440
 R-HEMBA1007017//ESTs//4.3e-47:208:87//Hs.155243:N70293
 R-HEMBA1007018//ESTs, Moderately similar to LIC-2 [R.norvegicus]//2.8e-1
 12:558:96//Hs.107905:AI248363
 R-HEMBA1007045
 R-HEMBA1007051//ESTs//2.5e-39:321:80//Hs.146811:AA410788
 R-HEMBA1007052//EST//3.4e-41:377:74//Hs.44634:N34839
 R-HEMBA1007062//ESTs//1.2e-92:439:99//Hs.162882:AA807140
 R-HEMBA1007066//ESTs//0.85:204:61//Hs.22795:AI208272
 R-HEMBA1007073//ESTs//6.6e-52:362:85//Hs.30821:AI096866
 R-HEMBA1007078//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING
 ENTRY !!!! [H.sapiens]//7.2e-40:163:83//Hs.152369:AA504818
 R-HEMBA1007085//ESTs//8.1e-103:519:96//Hs.90638:AI348087
 R-HEMBA1007087//ESTs//3.1e-51:354:86//Hs.6449:W95025
 R-HEMBA1007112//EST//0.090:328:59//Hs.136623:AA633597
 R-HEMBA1007113//Homo sapiens mRNA, clone:RES4-16//1.1e-47:427:76//Hs.121
 493:D25272
 R-HEMBA1007129//ESTs//6.1e-13:314:65//Hs.137538:AA769438
 R-HEMBA1007147
 R-HEMBA1007149//ESTs//9.7e-103:540:94//Hs.127240:AA149818

R-HEMBA1007151//ESTs//8.2e-102:505:96//Hs.24948:AA977674
 R-HEMBA1007174//Homo sapiens epsin 2b mRNA, complete cds//1.6e-104:529:9
 4//Hs.22396:AF062085
 R-HEMBA1007178//ESTs//2.2e-57:366:90//Hs.21648:AI302954
 R-HEMBA1007194//ESTs//9.0e-68:336:98//Hs.49760:AA741051
 R-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.
 7e-62:332:95//Hs.3363:D86987
 R-HEMBA1007206//Human c-yes-1 mRNA//4.5e-49:390:80//Hs.75680:M15990
 R-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//7.4
 e-98:471:97//Hs.27197:AB018340
 R-HEMBA1007251//ESTs//1.6e-78:377:99//Hs.98912:AA436864
 R-HEMBA1007256//ESTs//3.5e-20:127:79//Hs.137352:AA024934
 R-HEMBA1007267//Homo sapiens KIAA0395 mRNA, partial cds//8.8e-48:343:83/
 /Hs.43681:AL022394
 R-HEMBA1007273//ESTs//1.0e-98:472:98//Hs.122610:AA807062
 R-HEMBA1007279//ESTs//3.3e-107:558:94//Hs.126480:AI221207
 R-HEMBA1007281//EST//0.074:244:63//Hs.29304:R73543
 R-HEMBA1007288//EST//9.4e-43:344:81//Hs.162112:AA524804
 R-HEMBA1007300//ESTs//0.096:371:57//Hs.102680:N52990
 R-HEMBA1007301
 R-HEMBA1007319//ESTs//7.7e-113:570:96//Hs.29263:AI337917
 R-HEMBA1007320//ESTs, Moderately similar to hypothetical protein 2 [H.sa
 piens]//5.5e-15:311:64//Hs.142764:AA205569
 R-HEMBA1007322//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//
 5.7e-49:383:83//Hs.139107:K00629
 R-HEMBA1007327//Human melanoma antigen recognized by T-cells (MART-1) mR
 NA//1.9e-42:371:79//Hs.154069:U06452
 R-HEMBA1007341//EST//3.0e-17:291:68//Hs.150788:AI301848
 R-HEMBA1007342//EST//2.7e-11:263:67//Hs.145259:AI218684

R-HEMBA1007347//Homo sapiens DEC-205 mRNA, complete cds//9.7e-47:368:82/
/Hs.153563:AF011333

R-HEMBB1000005//ESTs, Weakly similar to putative p150 [H.sapiens]//3.3e-
44:341:71//Hs.111730:AA604403

R-HEMBB1000008//Homo sapiens tumor necrosis factor superfamily member LI
GHT mRNA, complete cds//3.2e-40:292:83//Hs.129708:AF064090

R-HEMBB1000018//H.sapiens mRNA for urea transporter//5.0e-49:311:87//Hs.
66710:X96969

R-HEMBB1000024//ESTs//7.5e-21:234:76//Hs.157049:AI345418

R-HEMBB1000025//ESTs//2.2e-36:371:78//Hs.56562:AA056332

R-HEMBB1000030//ESTs//3.2e-76:373:97//Hs.140190:AA701449

R-HEMBB1000036//ESTs, Highly similar to HYPOTHETICAL 43.2 KD PROTEIN C3
4E10.1 IN CHROMOSOME III [Caenorhabditis elegans]//6.0e-92:477:95//Hs.48
77:AA418465

R-HEMBB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, c
omplete cds//2.5e-92:467:97//Hs.20815:AF084928

R-HEMBB1000039//ESTs//1.8e-43:361:71//Hs.108206:N64702

R-HEMBB1000044//EST//7.6e-70:367:95//Hs.140860:R42954

R-HEMBB1000048//EST//1.5e-45:262:91//Hs.157627:AI357802

R-HEMBB1000050//ESTs//0.039:91:74//Hs.163189:AA236903

R-HEMBB1000054//ESTs//3.0e-104:550:94//Hs.152395:AA533107

R-HEMBB1000055//ESTs, Moderately similar to UBIQUINOL-CYTOCHROME C REDUC
TASE COMPLEX SUBUNIT VI REQUIRING PROTEIN [H.sapiens]//1.1e-72:350:99//H
s.116490:AA659584

R-HEMBB1000059//ESTs//1.7e-10:200:70//Hs.163954:N57939

R-HEMBB1000083//Homo sapiens mRNA for GCP170, complete cds//6.0e-41:337:
80//Hs.4953:D63997

R-HEMBB1000089//Human mRNA for KIAA0355 gene, complete cds//3.5e-39:487:
70//Hs.153014:AB002353

R-HEM BB1000099//ESTs//5.7e-37:353:75//Hs.22910:W18193
 R-HEM BB1000103//Homo sapiens mRNA for KIAA0640 protein, partial cds//6.5
 e-18:298:69//Hs.153026:AB014540
 R-HEM BB1000113//EST//8.2e-94:437:100//Hs.136893:AA805239
 R-HEM BB1000119//Homo sapiens ASMTL gene//1.2e-84:428:95//Hs.6315:Y15521
 R-HEM BB1000136//ESTs//0.043:262:59//Hs.61304:AA025692
 R-HEM BB1000141//ESTs//5.0e-38:254:79//Hs.141658:N77915
 R-HEM BB1000144//ESTs//9.6e-05:235:60//Hs.61700:AA033951
 R-HEM BB1000173//EST//9.6e-44:258:76//Hs.161917:AA483223
 R-HEM BB1000175//ESTs//4.8e-98:475:97//Hs.149740:AI199558
 R-HEM BB1000198//ESTs//1.0:123:62//Hs.116602:AA665965
 R-HEM BB1000215//Human mRNA for KIAA0355 gene, complete cds//2.2e-46:302:
 86//Hs.153014:AB002353
 R-HEM BB1000217//ESTs//2.2e-105:496:99//Hs.65973:AI339364
 R-HEM BB1000218//Homo sapiens DNA fragmentation factor 40 kDa subunit (DF
 F40) mRNA, complete cds//1.1e-48:292:79//Hs.133089:AF064019
 R-HEM BB1000226//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B04
 95.8 IN CHROMOSOME II [C.elegans]//5.1e-73:449:89//Hs.16803:AA843214
 R-HEM BB1000240//ESTs//1.1e-109:536:97//Hs.13528:AA523106
 R-HEM BB1000244//Small inducible cytokine A5 (RANTES)//9.5e-42:323:83//Hs
 .155464:AF088219
 R-HEM BB1000250//EST//8.8e-12:284:64//Hs.145960:AI276783
 R-HEM BB1000258//EST//4.5e-14:315:66//Hs.162551:AA584782
 R-HEM BB1000264
 R-HEM BB1000266//ESTs, Weakly similar to similar to the beta transducin f
 amily [C.elegans]//2.7e-102:556:93//Hs.16079:AA083522
 R-HEM BB1000272//ESTs//4.3e-91:480:94//Hs.107467:H11385
 R-HEM BB1000274//Homo sapiens mRNA for KIAA0557 protein, partial cds//7.9
 e-24:198:72//Hs.101414:AB011129

R-HEM BB1000284//ESTs//4.8e-64:389:91//Hs.118043:N50458
 R-HEM BB1000307//Human mRNA for KIAA0355 gene, complete cds//3.6e-43:288:
 87//Hs.153014:AB002353
 R-HEM BB1000312//ESTs//6.0e-23:272:73//Hs.121354:AA758601
 R-HEM BB1000317//ESTs//7.5e-90:424:99//Hs.150042:AI298034
 R-HEM BB1000318//Small inducible cytokine A5 (RANTES)//3.3e-41:318:80//Hs
 .155464:AF088219
 R-HEM BB1000335//ESTs//3.7e-15:324:65//Hs.85077:AA968576
 R-HEM BB1000336//ESTs//6.4e-76:402:95//Hs.17207:H92480
 R-HEM BB1000337//ESTs//2.1e-80:391:97//Hs.118990:AI378084
 R-HEM BB1000338//Small inducible cytokine A5 (RANTES)//4.0e-39:274:85//Hs
 .155464:AF088219
 R-HEM BB1000339//EST//5.8e-41:336:79//Hs.151873:AA205736
 R-HEM BB1000341//ESTs//3.8e-19:310:68//Hs.37573:H59651
 R-HEM BB1000343//EST//1.1e-77:396:95//Hs.162664:AA605020
 R-HEM BB1000354//Human mRNA for KIAA0186 gene, complete cds//1.7e-15:293:
 65//Hs.36232:D80008
 R-HEM BB1000369//ESTs//1.6e-21:234:73//Hs.111583:AA463590
 R-HEM BB1000374//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
 0487//2.3e-56:335:77//Hs.92381:AB007956
 R-HEM BB1000376//H.sapiens mRNA for urea transporter//2.7e-50:525:74//Hs.
 66710:X96969
 R-HEM BB1000391//ESTs//6.6e-50:316:88//Hs.142259:AA828840
 R-HEM BB1000399//Homo sapiens mRNA for cell cycle checkpoint protein//3.8
 e-109:531:97//Hs.16184:AJ001642
 R-HEM BB1000402//H.sapiens mRNA for MACH-alpha-2 protein//2.7e-35:369:72/
 /Hs.19949:X98173
 R-HEM BB1000404//ESTs//0.088:298:59//Hs.61607:AA032026
 R-HEM BB1000420//EST//2.2e-78:376:98//Hs.160787:AI336591

R-HEMBB1000434//Human mRNA for KIAA0118 gene, partial cds//3.9e-50:302:89//Hs.154326:D42087

R-HEMBB1000438//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !
!!! [H.sapiens]//0.30:214:63//Hs.142209:AA873303

R-HEMBB1000441//Human c-yes-1 mRNA//2.2e-46:280:90//Hs.75680:M15990

R-HEMBB1000449//ESTs//7.8e-59:332:92//Hs.87013:AA130221

R-HEMBB1000455//EST//4.8e-14:421:65//Hs.68832:AA088438

R-HEMBB1000472//ESTs//1.1e-104:505:98//Hs.132824:AI033396

R-HEMBB1000480//Human mRNA for KIAA0392 gene, partial cds//2.5e-49:295:90//Hs.40100:AB002390

R-HEMBB1000487//EST//0.78:87:68//Hs.134601:AI081506

R-HEMBB1000490//Small inducible cytokine A5 (RANTES)//4.0e-39:320:80//Hs.155464:AF088219

R-HEMBB1000491//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.7e-50:312:76//Hs.113283:AF018080

R-HEMBB1000493//ESTs//7.1e-18:150:82//Hs.142068:AA176125

R-HEMBB1000510//EST//1.4e-45:139:97//Hs.152260:AA489703

R-HEMBB1000518//Human mRNA for KIAA0118 gene, partial cds//4.8e-50:415:78//Hs.154326:D42087

R-HEMBB1000523//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.7e-57:497:78//Hs.113283:AF018080

R-HEMBB1000530//ESTs//2.7e-73:425:90//Hs.141254:AI334099

R-HEMBB1000550//EST//2.9e-11:113:79//Hs.161503:N68662

R-HEMBB1000554//Human huntingtin interacting protein (HIP1) mRNA, complete cds//8.2e-13:92:81//Hs.97206:AF052288

R-HEMBB1000556//ESTs//1.1e-94:529:92//Hs.33476:N36986

R-HEMBB1000564//ESTs//1.3e-19:128:91//Hs.142058:N34258

R-HEMBB1000573//ESTs//1.6e-86:494:90//Hs.120979:AI160709

R-HEMBB1000575//ESTs//1.6e-45:232:74//Hs.141019:AA287618

R-HEMBB1000586//ESTs//5.1e-42:281:83//Hs.138852:AA284247
R-HEMBB1000589//ESTs//1.0e-10:184:71//Hs.142677:R95895
R-HEMBB1000591//ESTs//3.2e-40:406:75//Hs.138787:H73704
R-HEMBB1000592//ESTs//1.8e-97:455:99//Hs.94229:W65391
R-HEMBB1000598//Human antisecretory factor-1 mRNA, complete cds//1.8e-46
:305:85//Hs.148495:AF050199
R-HEMBB1000623//ESTs//8.3e-47:277:92//Hs.6045:W67125
R-HEMBB1000630//ESTs//5.1e-106:538:96//Hs.13422:AI082249
R-HEMBB1000631//ESTs//5.1e-100:508:96//Hs.110379:N58152
R-HEMBB1000632//ESTs//6.2e-44:371:80//Hs.132722:AA618531
R-HEMBB1000637//Human mRNA for KIAA0080 gene, partial cds//6.4e-49:254:8
6//Hs.74554:D38522
R-HEMBB1000638//EST//2.2e-38:371:76//Hs.162236:AA551582
R-HEMBB1000643//ESTs//0.0049:191:62//Hs.55445:W31963
R-HEMBB1000649//ESTs, Moderately similar to hTAFII68 [H.sapiens]//4.0e-7
6:399:95//Hs.124106:AA948100
R-HEMBB1000652//ESTs//1.5e-14:271:64//Hs.163954:N57939
R-HEMBB1000665//ESTs//4.2e-12:109:87//Hs.41407:W94988
R-HEMBB1000671//ESTs//2.8e-68:439:87//Hs.140491:W52705
R-HEMBB1000673//EST//0.58:46:82//Hs.142286:AA338293
R-HEMBB1000684//ESTs//8.5e-20:307:72//Hs.122825:AA765454
R-HEMBB1000693//Homo sapiens neuroan1 mRNA, complete cds//6.5e-52:287:93
//Hs.158300:AF040723
R-HEMBB1000705//Small inducible cytokine A5 (RANTES)//4.6e-24:165:78//Hs
.155464:AF088219
R-HEMBB1000706//EST//1.2e-10:211:65//Hs.105524:AA521412
R-HEMBB1000709//ESTs, Weakly similar to putative p150 [H.sapiens]//3.9e-
50:245:99//Hs.111730:AA604403
R-HEMBB1000725//Human mRNA for KIAA0308 gene, partial cds//0.11:350:59//

Hs.10351:AB002306

R-HEM BB1000726//EST//5.3e-49:303:88//Hs.149580:AI281881

R-HEM BB1000738//Homo sapiens mRNA, clone:RES4-16//2.5e-49:302:89//Hs.121
493:D25272

R-HEM BB1000749//ESTs//1.6e-49:331:86//Hs.152788:AA630925

R-HEM BB1000763//ESTs//9.7e-104:474:95//Hs.77480:AA100522

R-HEM BB1000770//EST//1.0e-75:359:99//Hs.136564:AA642445

R-HEM BB1000781//ESTs//5.3e-66:317:99//Hs.28827:AI125541

R-HEM BB1000789//ESTs//5.9e-83:394:99//Hs.120842:AA435771

R-HEM BB1000790//PLATELET GLYCOPROTEIN V PRECURSOR//1.3e-37:193:75//Hs.73
734:Z23091

R-HEM BB1000794//ESTs//7.1e-98:490:96//Hs.105743:AA532718

R-HEM BB1000807//ESTs//2.6e-22:145:92//Hs.53913:AA908961

R-HEM BB1000810//Small inducible cytokine A5 (RANTES)//1.8e-34:206:79//Hs
.155464:AF088219

R-HEM BB1000821//ESTs//2.4e-90:425:99//Hs.118659:AI052447

R-HEM BB1000822//ESTs//1.7e-45:288:89//Hs.24130:R27124

R-HEM BB1000826//Small inducible cytokine A5 (RANTES)//2.9e-51:245:82//Hs
.155464:AF088219

R-HEM BB1000827//EST//2.8e-40:295:84//Hs.149580:AI281881

R-HEM BB1000831//ESTs//4.0e-59:291:98//Hs.62675:AA044176

R-HEM BB1000835//ESTs//7.3e-21:124:82//Hs.102671:N52545

R-HEM BB1000840//ATPase, Na+/K+ transporting, beta 2 polypeptide//1.3e-43
:163:84//Hs.78854:AF007876

R-HEM BB1000848//Homo sapiens mRNA for KIAA0565 protein, complete cds//9.
5e-41:367:78//Hs.129740:AB011137

R-HEM BB1000852//EST//1.2e-09:188:70//Hs.127869:AA968599

R-HEM BB1000870//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//1
.0e-41:483:73//Hs.2379:U23942

R-HEMBB1000876//EST//0.0022:211:63//Hs.125552:AA884141
 R-HEMBB1000883//ESTs//1.4e-65:343:95//Hs.98269:H27247
 R-HEMBB1000887//ESTs//4.0e-22:212:79//Hs.138965:AI004740
 R-HEMBB1000888//EST//8.2e-07:196:64//Hs.118276:W15258
 R-HEMBB1000890//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.1e-46:327:83//Hs.
 51048:X68830
 R-HEMBB1000893//EST//4.7e-34:242:85//Hs.149580:AI281881
 R-HEMBB1000908//EST//0.95:27:100//Hs.142568:AA285066
 R-HEMBB1000910//ESTs//1.9e-36:318:78//Hs.141140:AA715983
 R-HEMBB1000913//Human mRNA for KIAA0327 protein, complete cds//2.5e-33:3
 67:73//Hs.149323:AB002325
 R-HEMBB1000915//ESTs//0.00018:188:61//Hs.144847:AI222742
 R-HEMBB1000917//Homo sapiens KIAA0414 mRNA, partial cds//3.7e-41:228:84/
 /Hs.127649:AB007874
 R-HEMBB1000927//ESTs//2.2e-62:307:98//Hs.97044:AA365784
 R-HEMBB1000947//ESTs, Weakly similar to F26E4.13 [C.elegans]//3.3e-60:35
 0:91//Hs.49163:AA532881
 R-HEMBB1000959//Human Line-1 repeat mRNA with 2 open reading frames//8.1
 e-84:546:86//Hs.23094:M19503
 R-HEMBB1000973//ESTs//6.8e-95:445:99//Hs.105859:AI419354
 R-HEMBB1000975//ESTs//1.2e-39:197:100//Hs.26176:AI032007
 R-HEMBB1000981//EST//7.7e-58:284:98//Hs.60179:AA007242
 R-HEMBB1000985//ESTs//1.2e-103:524:95//Hs.43102:AA131369
 R-HEMBB1000991//EST//0.99:58:72//Hs.100246:T23625
 R-HEMBB1000996//Homo sapiens LIM protein mRNA, complete cds//1.3e-41:482
 :70//Hs.154103:AF061258
 R-HEMBB1001004//ESTs//5.7e-70:362:95//Hs.6434:W27112
 R-HEMBB1001008//ESTs, Weakly similar to hypothetical L1 protein [H.sapie
 ns]//2.3e-25:339:71//Hs.129992:H58762

R-HEMBB1001011//ESTs//4.0e-53:325:92//Hs.33268:AI191214
 R-HEMBB1001014//ESTs//1.3e-46:323:83//Hs.163980:AA715814
 R-HEMBB1001020//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.0e-46:30
 5:76//Hs.113283:AF018080
 R-HEMBB1001024//ESTs//8.5e-47:374:80//Hs.141602:N63562
 R-HEMBB1001037//ESTs//2.6e-47:282:91//Hs.155384:Z78385
 R-HEMBB1001047//EST//6.2e-33:232:74//Hs.160146:AI049975
 R-HEMBB1001051//ESTs//3.7e-79:385:98//Hs.95290:AA046107
 R-HEMBB1001056//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.
 1e-87:497:91//Hs.15832:AB014518
 R-HEMBB1001058//Homo sapiens mRNA for KIAA0475 protein, complete cds//2.
 2e-26:125:81//Hs.5737:AB007944
 R-HEMBB1001060//ESTs//1.9e-37:541:69//Hs.141534:N64785
 R-HEMBB1001063//ESTs//4.7e-42:269:88//Hs.55855:AA621381
 R-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds//9.1e-107:51
 2:97//Hs.12953:AF034803
 R-HEMBB1001096//Human HsLIM15 mRNA for HsLim15, complete cds//1.2e-20:23
 3:70//Hs.37181:D64108
 R-HEMBB1001102//Human mRNA for KIAA0355 gene, complete cds//9.1e-40:299:
 82//Hs.153014:AB002353
 R-HEMBB1001105//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.8e-46:29
 6:87//Hs.113283:AF018080
 R-HEMBB1001114//ESTs//6.2e-44:293:86//Hs.70279:AA757426
 R-HEMBB1001117//ESTs//1.1e-80:471:90//Hs.61935:T75092
 R-HEMBB1001119//ESTs//4.0e-38:213:84//Hs.109140:AI289942
 R-HEMBB1001126
 R-HEMBB1001133//Human SS-A/Ro ribonucleoprotein autoantigen 60 kd subuni
 t mRNA, complete cds//1.6e-24:285:73//Hs.554:M25077
 R-HEMBB1001137//ESTs//4.6e-10:66:100//Hs.74924:AI332962

R-HEMBB1001142//EST//6.4e-48:315:85//Hs.149580:AI281881
R-HEMBB1001151
R-HEMBB1001153//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING
ENTRY !!!! [H.sapiens]//1.3e-65:331:96//Hs.154179:AA579197
R-HEMBB1001169//Oxytocin receptor//1.5e-25:165:73//Hs.2820:X64878
R-HEMBB1001175//ESTs//3.5e-41:233:93//Hs.129218:AA991162
R-HEMBB1001177
R-HEMBB1001182//ESTs//1.9e-86:455:95//Hs.6937:AA524349
R-HEMBB1001199
R-HEMBB1001208//ESTs//3.3e-43:216:99//Hs.121806:N71183
R-HEMBB1001209//ESTs//6.7e-80:409:96//Hs.141185:R99549
R-HEMBB1001210//ESTs//2.2e-46:290:88//Hs.103329:D11573
R-HEMBB1001218//Kangai 1 (suppression of tumorigenicity 6, prostate; CD8
2 antigen (R2 leukocyte antigen, antigen detected by monoclonal and anti
body IA4))//3.1e-44:298:87//Hs.103458:X53795
R-HEMBB1001221//ESTs//9.4e-75:353:100//Hs.151504:AA550817
R-HEMBB1001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [G
allus gallus]//3.8e-80:400:96//Hs.71873:AA148213
R-HEMBB1001242//ESTs//1.6e-63:404:87//Hs.25534:AA149560
R-HEMBB1001249//ESTs//3.8e-34:360:70//Hs.150727:AI292236
R-HEMBB1001253//EST//0.0011:84:77//Hs.124579:AA853987
R-HEMBB1001254//ESTs//4.5e-95:444:99//Hs.161059:AI431268
R-HEMBB1001267//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0501//1.3e-50:524:73//Hs.159897:AB007970
R-HEMBB1001271//Human mRNA for KIAA0118 gene, partial cds//4.0e-45:323:8
4//Hs.154326:D42087
R-HEMBB1001282//EST//2.9e-78:401:96//Hs.72871:AA169412
R-HEMBB1001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK
353.7 IN CHROMOSOME III [Caenorhabditis elegans]//2.6e-104:515:97//Hs.16

606:W81021

R-HEMBB1001289//ESTs//7.8e-45:440:75//Hs.44702:AI148840

R-HEMBB1001294//ESTs//1.9e-100:476:99//Hs.109017:AI057112

R-HEMBB1001302

R-HEMBB1001304//ESTs//4.0e-92:431:99//Hs.113750:AI091154

R-HEMBB1001314//Interleukin 10//6.3e-41:334:79//Hs.2180:M57627

R-HEMBB1001315//Interleukin 10//1.9e-43:285:87//Hs.2180:M57627

R-HEMBB1001317//Human cytochrome P450-IIB (hIIB3) mRNA, complete cds//8.4e-45:357:81//Hs.110194:M29873

R-HEMBB1001326//ESTs//0.85:174:62//Hs.133487:AI393754

R-HEMBB1001331//ESTs, Weakly similar to DFS70 [H.sapiens]//6.5e-61:313:96//Hs.43071:AA206222

R-HEMBB1001335//EST//5.2e-80:381:99//Hs.116769:AA630365

R-HEMBB1001337//ESTs//2.7e-84:404:99//Hs.148966:AI242639

R-HEMBB1001339//ESTs//2.1e-97:485:96//Hs.88357:AA262470

R-HEMBB1001346

R-HEMBB1001348//ESTs//1.1e-43:295:85//Hs.163604:R94354

R-HEMBB1001356//EST//6.0e-11:89:88//Hs.152366:AA486721

R-HEMBB1001364//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.0e-12:129:79//Hs.9792:AA027055

R-HEMBB1001366//Human mRNA for KIAA0118 gene, partial cds//1.2e-50:550:72//Hs.154326:D42087

R-HEMBB1001367//ESTs//1.2e-19:165:82//Hs.146314:R99617

R-HEMBB1001369//Small inducible cytokine A5 (RANTES)//1.9e-25:217:80//Hs.155464:AF088219

R-HEMBB1001380//ESTs//4.0e-08:216:63//Hs.143763:AI174205

R-HEMBB1001384//ESTs//6.6e-110:547:96//Hs.6671:AI341699

R-HEMBB1001387//ESTs//1.1e-104:497:98//Hs.87654:AA853970

R-HEMBB1001394//ESTs//6.4e-73:428:89//Hs.139922:AA281350

R-HEMBB1001410//Alcohol dehydrogenase 7 sigma subunit (class IV)//0.88:3
65:58//Hs.389:X76342

R-HEMBB1001424//ESTs//1.3e-88:466:94//Hs.42174:AA194644

R-HEMBB1001426//ESTs//2.2e-45:337:82//Hs.37573:H59651

R-HEMBB1001429//EST//3.8e-59:543:76//Hs.158803:AI376846

R-HEMBB1001436//ESTs//3.7e-69:332:99//Hs.156518:AA724317

R-HEMBB1001443//ESTs//4.8e-54:270:98//Hs.21898:AI088201

R-HEMBB1001449//ESTs//3.2e-43:170:84//Hs.150727:AI292236

R-HEMBB1001454//ESTs//9.1e-46:304:86//Hs.139190:N55515

R-HEMBB1001458//ESTs//3.2e-98:478:97//Hs.50144:N67293

R-HEMBB1001463//Homo sapiens KIAA0421 mRNA, partial cds//4.3e-50:440:78/
/Hs.41742:AB007881

R-HEMBB1001464//ESTs, Weakly similar to K01H12.1 [C.elegans]//0.25:222:6
1//Hs.13275:AI341468

R-HEMBB1001482//ESTs, Moderately similar to zinc finger protein [R.norve
gicus]//0.80:53:83//Hs.26799:W74481

R-HEMBB1001500//EST//1.4e-13:310:67//Hs.162663:AA604515

R-HEMBB1001521//Homo sapiens mRNA for KIAA0737 protein, complete cds//2.
5e-29:186:92//Hs.17630:AB018280

R-HEMBB1001527//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1
098.3 IN CHROMOSOME III [Caenorhabditis elegans]//4.7e-51:404:81//Hs.141
429:AA631915

R-HEMBB1001531//ESTs//3.3e-13:250:67//Hs.139158:AA226159

R-HEMBB1001535//H.sapiens mRNA for sigma 3B protein//1.9e-39:291:82//Hs.
154782:X99459

R-HEMBB1001536//Human mRNA for KIAA0355 gene, complete cds//5.0e-44:318:
83//Hs.153014:AB002353

R-HEMBB1001537//Homo sapiens KIAA0409 mRNA, partial cds//3.2e-47:318:80/
/Hs.5158:AB007869

R-HEMBB1001555//ESTs//2.6e-13:182:71//Hs.112671:AI377274
 R-HEMBB1001562//ESTs//1.7e-43:316:83//Hs.151365:AA643962
 R-HEMBB1001564//EST//1.3e-35:141:81//Hs.162197:AA535216
 R-HEMBB1001565//Human mRNA for KIAA0331 gene, complete cds//5.1e-18:152:
 85//Hs.146395:AB002329
 R-HEMBB1001585//ESTs//1.1e-32:190:84//Hs.33354:AA179944
 R-HEMBB1001586//ESTs//4.9e-94:447:99//Hs.124084:AA843219
 R-HEMBB1001588//EST//8.3e-27:363:69//Hs.141603:N66015
 R-HEMBB1001603//ESTs//1.2e-101:482:99//Hs.12403:AI090184
 R-HEMBB1001618//ESTs//5.8e-35:437:70//Hs.136868:AA805044
 R-HEMBB1001619//EST//1.7e-38:476:70//Hs.139093:AA166888
 R-HEMBB1001630//Homo sapiens mRNA, clone:RES4-16//5.7e-41:193:90//Hs.121
 493:D25272
 R-HEMBB1001635//ESTs//9.5e-34:304:82//Hs.140444:AI002082
 R-HEMBB1001637//ESTs//1.0e-42:443:74//Hs.21978:AA009633
 R-HEMBB1001641//EST//2.4e-06:67:86//Hs.162398:AA572813
 R-HEMBB1001653//ESTs//4.8e-80:381:99//Hs.140502:AA806438
 R-HEMBB1001665//ESTs//2.3e-44:372:79//Hs.132818:AI038577
 R-HEMBB1001668//ESTs//0.73:212:62//Hs.8928:N32572
 R-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//5.
 9e-117:573:97//Hs.24439:AB014546
 R-HEMBB1001684//ESTs, Moderately similar to Tbc1 [M.musculus]//5.4e-106:
 523:97//Hs.26939:AA804534
 R-HEMBB1001685//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING
 ENTRY !!!! [H.sapiens]//1.9e-43:292:86//Hs.96337:AA225358
 R-HEMBB1001695//ESTs//3.7e-101:539:94//Hs.78289:R60867
 R-HEMBB1001704//EST//0.96:248:57//Hs.163025:AA703038
 R-HEMBB1001706//ESTs//1.3e-39:308:81//Hs.141318:N71080
 R-HEMBB1001707//ESTs, Moderately similar to hypothetical protein 2 [H.sa

piens] //4.9e-32:277:73//Hs.142764:AA205569
R-HEM BB1001717//ESTs//1.6e-34:225:87//Hs.57883:AA218645
R-HEM BB1001735//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HO
MOLOG [Homo sapiens] //8.6e-11:158:71//Hs.141263:H64113
R-HEM BB1001736//ESTs//0.0035:223:60//Hs.21354:AA203403
R-HEM BB1001747//EST//9.9e-55:293:81//Hs.112866:AA620488
R-HEM BB1001749//ESTs//2.5e-13:95:91//Hs.139888:N25287
R-HEM BB1001753//ESTs//2.6e-07:141:70//Hs.144604:AI052059
R-HEM BB1001756//EST//2.6e-06:165:64//Hs.121195:AA757211
R-HEM BB1001760//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//1.3e-24:264:
74//Hs.70008:L00352
R-HEM BB1001762//ESTs//2.1e-81:447:93//Hs.152766:AA211369
R-HEM BB1001785//ESTs//0.040:390:58//Hs.116651:AA993406
R-HEM BB1001797//ESTs//2.1e-90:428:99//Hs.8958:AA169253
R-HEM BB1001802//Desmin//9.9e-95:497:93//Hs.119104:M63391
R-HEM BB1001812//ESTs//1.2e-12:91:78//Hs.138852:AA284247
R-HEM BB1001816//Human Line-1 repeat mRNA with 2 open reading frames//5.9
e-13:143:76//Hs.23094:M19503
R-HEM BB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCI
P1) mRNA, complete cds//5.5e-106:498:98//Hs.159396:AF056209
R-HEM BB1001836//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0488//9.6e-39:288:73//Hs.67619:AB007957
R-HEM BB1001839
R-HEM BB1001850//EST//0.020:119:68//Hs.32767:H38125
R-HEM BB1001863//ESTs//4.5e-17:226:72//Hs.157253:AI357539
R-HEM BB1001867//ESTs//2.3e-16:254:68//Hs.123664:AA806106
R-HEM BB1001868//EST//9.8e-30:155:100//Hs.160572:AA888397
R-HEM BB1001869//ESTs//2.8e-42:376:78//Hs.141973:N21434
R-HEM BB1001872//EST//0.85:156:64//Hs.119501:AA487980

R-HEMBB1001874//EST//0.64:107:70//Hs.147482:AI215572
R-HEMBB1001875//EST//0.079:199:59//Hs.121810:AA775240
R-HEMBB1001880//Thromboxane A2 receptor//9.0e-47:297:88//Hs.89887:D38081
R-HEMBB1001899//ESTs//6.3e-68:323:100//Hs.121538:AA609310
R-HEMBB1001905//ESTs//4.4e-19:227:73//Hs.146173:AA906191
R-HEMBB1001906//ESTs//1.6e-90:463:95//Hs.28266:H46725
R-HEMBB1001908//Homo sapiens EVI5 homolog mRNA, complete cds//3.7e-27:55
7:64//Hs.26929:AF008915
R-HEMBB1001910//EST//6.0e-37:308:78//Hs.162197:AA535216
R-HEMBB1001911//Homo sapiens tapasin (NGS-17) mRNA, complete cds//8.0e-5
8:367:79//Hs.5247:AF029750
R-HEMBB1001915//ESTs//3.1e-73:395:93//Hs.17054:AI139897
R-HEMBB1001921//Human mRNA for KIAA0392 gene, partial cds//2.7e-50:323:8
8//Hs.40100:AB002390
R-HEMBB1001922//H.sapiens mRNA for novel member of serine-arginine domain
protein, SRrp129//7.4e-38:531:70//Hs.153086:Y11251
R-HEMBB1001925//Human mRNA for KIAA0327 protein, complete cds//9.5e-19:1
99:77//Hs.149323:AB002325
R-HEMBB1001930//EST//1.9e-18:136:78//Hs.132635:AI032875
R-HEMBB1001944//EST//0.034:228:57//Hs.93664:N23366
R-HEMBB1001945//ESTs//1.8e-83:439:95//Hs.7341:N57875
R-HEMBB1001947//ESTs//5.6e-109:533:97//Hs.48855:AA134589
R-HEMBB1001950//ESTs//1.5e-107:583:93//Hs.8033:N94998
R-HEMBB1001952//ESTs//3.1e-40:283:85//Hs.146811:AA410788
R-HEMBB1001953//Human mRNA for KIAA0080 gene, partial cds//6.2e-50:284:8
3//Hs.74554:D38522
R-HEMBB1001957//EST//4.8e-50:382:81//Hs.149580:AI281881
R-HEMBB1001962//ESTs//1.5e-20:143:88//Hs.11924:W26972
R-HEMBB1001967//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.

3e-61:296:88//Hs.153468:AB011147
 R-HEMBB1001973//ESTs//1.4e-48:303:88//Hs.132722:AA618531
 R-HEMBB1001983//ESTs//2.6e-72:374:95//Hs.141022:H06475
 R-HEMBB1001988//ESTs//2.0e-31:204:88//Hs.142531:N91572
 R-HEMBB1001990//ESTs//9.4e-115:574:96//Hs.44426:AA173223
 R-HEMBB1001996
 R-HEMBB1001997//ESTs//7.6e-78:380:98//Hs.32682:H37798
 R-HEMBB1002002//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//
 3.0e-18:222:71//Hs.103948:K00627
 R-HEMBB1002005//EST//2.2e-41:339:80//Hs.160833:AI345334
 R-HEMBB1002009//EST//2.9e-44:245:94//Hs.28788:R66896
 R-HEMBB1002015//EST//0.0027:198:63//Hs.160868:AI359052
 R-HEMBB1002042//ESTs//1.1e-75:529:84//Hs.106919:AA523900
 R-HEMBB1002043//ESTs//7.9e-40:292:83//Hs.70279:AA757426
 R-HEMBB1002044//ESTs//2.1e-92:460:94//Hs.115897:AA156638
 R-HEMBB1002045//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.6e-75:30
 1:85//Hs.113283:AF018080
 R-HEMBB1002049//ESTs//3.8e-77:409:94//Hs.122624:R82638
 R-HEMBB1002050//ESTs//8.7e-45:330:82//Hs.44702:AI148840
 R-HEMBB1002068//ESTs//8.3e-70:333:99//Hs.134807:AI090671
 R-HEMBB1002069//Homo sapiens neuronal thread protein AD7c-NTP mRNA, comp
 lete cds//1.5e-75:486:81//Hs.129735:AF010144
 R-HEMBB1002092//ESTs//6.5e-46:331:83//Hs.22910:W18193
 R-HEMBB1002094//EST//3.6e-45:280:88//Hs.149580:AI281881
 R-HEMBB1002115
 R-HEMBB1002139//ESTs//4.2e-45:318:85//Hs.107657:AA126814
 R-HEMBB1002142//Homo sapiens haemopoietic progenitor homeobox HPX42B (HP
 X42B) mRNA, complete cds//1.4e-45:281:88//Hs.125231:AF068006
 R-HEMBB1002152//EST//4.3e-39:250:89//Hs.156552:AA833553

R-HEMBB1002189//H.sapiens mRNA for translin associated protein X//1.4e-4
 7:328:85//Hs.96247:X95073
 R-HEMBB1002190//ESTs//8.3e-05:122:70//Hs.41974:AF039185
 R-HEMBB1002193//Human sky mRNA for Sky, complete cds//8.9e-24:398:69//Hs
 .301:U18934
 R-HEMBB1002217//EST//6.6e-50:303:89//Hs.149580:AI281881
 R-HEMBB1002218//ESTs//2.3e-19:150:86//Hs.136031:W95841
 R-HEMBB1002232//ESTs//8.9e-47:445:77//Hs.163971:N27584
 R-HEMBB1002247//EST//6.6e-09:236:65//Hs.130578:AI004631
 R-HEMBB1002249//ESTs//5.2e-16:325:64//Hs.156253:AI334807
 R-HEMBB1002254//Human Line-1 repeat mRNA with 2 open reading frames//3.8
 e-99:590:88//Hs.23094:M19503
 R-HEMBB1002255//Human mRNA for KIAA0365 gene, partial cds//5.6e-45:342:8
 3//Hs.84123:AB002363
 R-HEMBB1002266//ESTs//4.4e-98:472:98//Hs.65366:AI189112
 R-HEMBB1002280//EST//2.9e-41:247:90//Hs.161917:AA483223
 R-HEMBB1002300//ESTs//8.4e-19:229:75//Hs.138463:N72305
 R-HEMBB1002306//Homo sapiens KIAA0432 mRNA, complete cds//0.0021:138:67/
 /Hs.155174:AB007892
 R-HEMBB1002327//EST//0.042:249:61//Hs.121097:AA714637
 R-HEMBB1002329//ESTs//1.7e-94:453:99//Hs.7114:R24312
 R-HEMBB1002340//ESTs//5.8e-15:163:77//Hs.26378:H10228
 R-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein/
 /0.85:46:84//Hs.42644:AJ010841
 R-HEMBB1002358//ESTs//2.0e-52:319:81//Hs.140255:AA708322
 R-HEMBB1002359//ESTs//2.7e-106:517:97//Hs.13634:AI051613
 R-HEMBB1002364//Human mRNA for KIAA0080 gene, partial cds//5.3e-37:360:6
 5//Hs.74554:D38522
 R-HEMBB1002371//Catalase//3.3e-22:235:77//Hs.76359:X04085

R-HEM BB1002381//Homo sapiens (JH8) mRNA, partial cds//1.0e-08:120:78//Hs.142296:AF072467

R-HEM BB1002383//ESTs//3.5e-108:520:98//Hs.45140:D80055

R-HEM BB1002387

R-HEM BB1002415//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.3e-23:168:77//Hs.133526:N21103

R-HEM BB1002425//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//3.2e-57:304:90//Hs.144563:AF057280

R-HEM BB1002442//ESTs//2.7e-48:289:87//Hs.155243:N70293

R-HEM BB1002453//Human mRNA for KIAA0355 gene, complete cds//6.2e-45:292:87//Hs.153014:AB002353

R-HEM BB1002457//Human mRNA for KIAA0118 gene, partial cds//2.7e-46:546:71//Hs.154326:D42087

R-HEM BB1002458//EST//1.8e-72:343:100//Hs.162006:AA508089

R-HEM BB1002477//ESTs//1.6e-38:215:93//Hs.18240:AA460083

R-HEM BB1002489//ESTs//1.2e-101:534:94//Hs.7981:H15176

R-HEM BB1002492//ESTs//5.0e-14:350:62//Hs.99205:AA204969

R-HEM BB1002495//ESTs//2.1e-19:147:86//Hs.163747:AA174017

R-HEM BB1002502//ESTs, Weakly similar to p40 [H.sapiens]//1.2e-68:336:98//Hs.141515:T41142

R-HEM BB1002509//ESTs//2.7e-97:459:99//Hs.127638:AI014615

R-HEM BB1002510//ESTs, Weakly similar to located at OATL1 [H.sapiens]//2.2e-48:265:95//Hs.48827:AA873278

R-HEM BB1002520//EST//7.2e-40:198:84//Hs.140493:AA804538

R-HEM BB1002522//Human putative transmembrane receptor IL-1Rrp mRNA, complete cds//0.50:142:69//Hs.159301:U43672

R-HEM BB1002531//EST//0.024:147:61//Hs.148305:AA909605

R-HEM BB1002534//EST//3.1e-22:168:84//Hs.146794:AI149478

R-HEM BB1002545//ESTs//9.2e-90:421:99//Hs.118317:AI033259

R-HEM BB1002550//ESTs, Weakly similar to similar to *S. cerevisiae* LAG1 [*C. elegans*] //5.1e-22:210:81//Hs.11896:T68813

R-HEM BB1002556//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.9e-45:344:82//Hs.51048:X68830

R-HEM BB1002579//ESTs//4.6e-47:326:85//Hs.155184:AA573189

R-HEM BB1002582//ESTs//0.00036:91:76//Hs.140039:AA047045

R-HEM BB1002590//ESTs//1.0e-37:210:84//Hs.36658:N91138

R-HEM BB1002596//Human mRNA for KIAA0118 gene, partial cds//2.2e-46:297:87//Hs.154326:D42087

R-HEM BB1002600//EST//2.5e-17:147:84//Hs.121918:AA777424

R-HEM BB1002601//ESTs//7.8e-68:358:95//Hs.101489:R66923

R-HEM BB1002603//EST//1.1e-47:281:90//Hs.149580:AI281881

R-HEM BB1002607//ESTs//5.4e-75:379:97//Hs.29438:H42896

R-HEM BB1002610//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [*H.sapiens*] //6.2e-07:140:70//Hs.155456:AA707265

R-HEM BB1002613//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//8.5e-47:278:83//Hs.159187:AB007977

R-HEM BB1002614//ESTs//3.4e-81:383:99//Hs.13012:AI094150

R-HEM BB1002617//Homo sapiens protease-activated receptor 4 mRNA, complete cds//7.4e-19:151:80//Hs.137574:AF055917

R-HEM BB1002623//ESTs//1.6e-45:288:87//Hs.138852:AA284247

R-HEM BB1002635//Small inducible cytokine A5 (RANTES)//5.5e-39:278:81//Hs.155464:AF088219

R-HEM BB1002664//EST//8.9e-49:315:87//Hs.149580:AI281881

R-HEM BB1002677//ESTs//0.65:159:62//Hs.163517:AI419775

R-HEM BB1002683//H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase //8.6e-54:543:75//Hs.2638:Z28339

R-HEM BB1002684//ESTs//3.0e-18:148:87//Hs.158270:AA776646

R-HEM BB1002686//ESTs//6.1e-80:419:96//Hs.103002:W02753

R-HEMBB1002692//ESTs//3.3e-58:451:82//Hs.141254:AI334099
 R-HEMBB1002697//ESTs//6.2e-86:423:98//Hs.129812:AA769487
 R-HEMBB1002699//EST//5.6e-46:322:84//Hs.140231:AI054398
 R-HEMBB1002702//ESTs//5.6e-36:412:72//Hs.154993:AA142842
 R-HEMBB1002705//POLYPOSIS LOCUS PROTEIN 1//0.024:412:58//Hs.74648:M73547
 R-HEMBB1002712//ESTs//9.0e-96:451:99//Hs.136806:AA805682
 R-MAMMA1000009//ESTs//3.0e-78:392:96//Hs.163947:AA678701
 R-MAMMA1000019//Small inducible cytokine A5 (RANTES)//1.5e-47:247:87//Hs.
 .155464:AF088219
 R-MAMMA1000020//Zinc finger protein 2 (A1-5)//4.9e-49:384:80//Hs.155533:
 X60152
 R-MAMMA1000025//Homo sapiens KIAA0441 mRNA, complete cds//4.7e-11:154:71
 //Hs.32511:AB007901
 R-MAMMA1000043//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.0
 e-58:277:84//Hs.93121:AB018304
 R-MAMMA1000045//ESTs//1.0e-38:225:92//Hs.142567:AA287165
 R-MAMMA1000055//EST//0.14:91:67//Hs.144061:AA996350
 R-MAMMA1000057//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltrans
 ferase, Bombay phenotype included)//3.8e-77:545:83//Hs.69747:M35531
 R-MAMMA1000069//ESTs//8.0e-108:546:96//Hs.44856:N37065
 R-MAMMA1000084//Homo sapiens clone 23632 mRNA sequence//7.3e-43:313:83//
 Hs.46918:AF052099
 R-MAMMA1000085//ESTs, Highly similar to PUTATIVE CYSTEINYL-TRNA SYNTHET
 ASE C29E6.06C [Schizosaccharomyces pombe]//7.7e-104:546:94//Hs.7779:AA04
 5241
 R-MAMMA1000092//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING
 ENTRY !!!! [H.sapiens]//4.2e-22:287:71//Hs.136063:U51713
 R-MAMMA1000103//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//8.4e-49:334:
 86//Hs.70008:L00352

R-MAMMA1000117//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
RY !!!! [H.sapiens]//3.1e-08:96:80//Hs.115088:AA230172
R-MAMMA1000129//EST//2.8e-64:310:99//Hs.136394:AA523577
R-MAMMA1000133
R-MAMMA1000134//ESTs//1.1e-21:152:87//Hs.163747:AA174017
R-MAMMA1000139//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0501//6.3e-40:288:78//Hs.159897:AB007970
R-MAMMA1000143//EST//5.0e-52:314:89//Hs.149580:AI281881
R-MAMMA1000155//Homo sapiens apoptotic protease activating factor 1 (Apa
f-1) mRNA, complete cds//1.5e-59:562:75//Hs.77579:AF013263
R-MAMMA1000163//ESTs//2.8e-92:457:96//Hs.114413:AA884787
R-MAMMA1000171//Homo sapiens mRNA for putative lipoic acid synthetase, p
artial//2.5e-39:173:83//Hs.53531:AJ224162
R-MAMMA1000173//ESTs, Highly similar to SRC SUBSTRATE P80/85 PROTEINS [
Gallus gallus]//2.4e-07:63:90//Hs.90367:AI357069
R-MAMMA1000175//EST//0.66:217:58//Hs.146444:AI127611
R-MAMMA1000183//ESTs//6.7e-30:341:73//Hs.125254:AA872054
R-MAMMA1000198//EST//2.8e-45:185:88//Hs.149580:AI281881
R-MAMMA1000221//ESTs, Weakly similar to circadian clock protein [M.muscu
lus]//1.4e-41:272:90//Hs.68398:AA421103
R-MAMMA1000227//EST//2.4e-39:388:76//Hs.144175:H70425
R-MAMMA1000241//EST//0.0027:263:61//Hs.37532:H57946
R-MAMMA1000251//Homo sapiens mRNA for KIAA0772 protein, complete cds//5.
3e-47:322:86//Hs.15519:AB018315
R-MAMMA1000254//Homo sapiens tumor necrosis factor superfamily member LI
GHT mRNA, complete cds//2.2e-43:315:83//Hs.129708:AF064090
R-MAMMA1000257//EST//1.6e-62:330:93//Hs.141728:W73041
R-MAMMA1000264//Von Hippel-Lindau syndrome//2.3e-31:141:81//Hs.78160:AF0
10238

R-MAMMA1000266//ESTs//3.4e-34:150:81//Hs.163980:AA715814
R-MAMMA1000270//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0508//2.7e-57:304:78//Hs.159187:AB007977
R-MAMMA1000277//Thiopurine S-methyltransferase//3.7e-27:380:71//Hs.51124
:AF019369
R-MAMMA1000278//ESTs//5.2e-99:504:95//Hs.8494:W72694
R-MAMMA1000279//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0487//3.1e-58:295:83//Hs.92381:AB007956
R-MAMMA1000284//EST//4.1e-10:151:73//Hs.60742:AA017066
R-MAMMA1000287
R-MAMMA1000302//Homo sapiens KIAA0432 mRNA, complete cds//1.0:50:84//Hs.
155174:AB007892
R-MAMMA1000307//Human mRNA for KIAA0033 gene, partial cds//1.8e-48:468:7
6//Hs.22271:D26067
R-MAMMA1000309//ESTs//1.7e-94:491:94//Hs.135106:AI335251
R-MAMMA1000312//ESTs//8.9e-74:377:96//Hs.133163:AI051434
R-MAMMA1000313//EST//8.3e-19:294:62//Hs.127400:AA954491
R-MAMMA1000331//ESTs, Moderately similar to envelope protein [H.sapiens]
//8.6e-54:278:97//Hs.139170:AA662998
R-MAMMA1000339//EST//6.8e-44:169:89//Hs.149580:AI281881
R-MAMMA1000340//Homo sapiens mRNA for KIAA0625 protein, partial cds//0.8
2:204:61//Hs.154919:AB014525
R-MAMMA1000348//ESTs//3.3e-34:320:75//Hs.139158:AA226159
R-MAMMA1000356//ESTs, Highly similar to URIDYLATE KINASE [Saccharomyces
cerevisiae]//0.42:172:61//Hs.11463:AA535912
R-MAMMA1000360//Human mRNA for KIAA0118 gene, partial cds//3.8e-43:212:8
2//Hs.154326:D42087
R-MAMMA1000361//ESTs//3.1e-17:188:68//Hs.164036:AA845659
R-MAMMA1000372//ESTs//1.0e-46:307:85//Hs.145032:AA343523

R-MAMMA1000385//ESTs//8.2e-97:467:98//Hs.152282:AA412065
R-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like facto
r, complete cds//8.6e-14:106:92//Hs.32170:AB015132
R-MAMMA1000395//ESTs//1.9e-57:292:96//Hs.11365:AI301060
R-MAMMA1000402//ESTs, Moderately similar to RETROVIRUS-RELATED POL POLY
PROTEIN [Mus musculus]//9.1e-47:316:81//Hs.138698:N38973
R-MAMMA1000410//Archain//1.8e-40:443:74//Hs.33642:X81198
R-MAMMA1000413//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.
3e-27:304:72//Hs.119387:AB007958
R-MAMMA1000414//ESTs//2.9e-27:181:87//Hs.141254:AI334099
R-MAMMA1000416//Human macrophage-derived chemokine precursor (MDC) mRNA,
complete cds//1.5e-58:282:82//Hs.97203:U83171
R-MAMMA1000421//Thromboxane A2 receptor//4.9e-48:372:80//Hs.89887:D38081
R-MAMMA1000422//ESTs//0.077:240:62//Hs.123136:AA631067
R-MAMMA1000423//Human mRNA for KIAA0392 gene, partial cds//1.3e-48:375:8
1//Hs.40100:AB002390
R-MAMMA1000424//Human melanoma antigen recognized by T-cells (MART-1) mR
NA//1.4e-44:418:75//Hs.154069:U06452
R-MAMMA1000429//ESTs//3.9e-113:565:96//Hs.5076:N53461
R-MAMMA1000431//Human macrophage-derived chemokine precursor (MDC) mRNA,
complete cds//8.6e-68:302:85//Hs.97203:U83171
R-MAMMA1000444//Calcium modulating ligand//5.5e-44:344:81//Hs.13572:AF06
8179
R-MAMMA1000446//ESTs//1.0:236:60//Hs.126958:AI147447
R-MAMMA1000458
R-MAMMA1000468//ESTs//4.4e-51:271:96//Hs.6839:AA055176
R-MAMMA1000472//ESTs//5.4e-39:146:86//Hs.141581:AA315361
R-MAMMA1000478//ESTs//2.3e-74:365:98//Hs.140591:AA828959
R-MAMMA1000483//ESTs//9.9e-23:235:75//Hs.163592:AA280886

R-MAMMA1000490//EST//2.1e-80:500:87//Hs.142137:AA213759
R-MAMMA1000500//Small inducible cytokine A5 (RANTES)//4.7e-43:283:86//Hs
.155464:AF088219
R-MAMMA1000501//ESTs//4.2e-37:250:86//Hs.141323:N80390
R-MAMMA1000516//Human mRNA for KIAA0392 gene, partial cds//5.1e-46:459:7
5//Hs.40100:AB002390
R-MAMMA1000522//ESTs//9.5e-16:226:70//Hs.116673:AA669267
R-MAMMA1000559//ESTs//5.2e-34:244:84//Hs.150727:AI292236
R-MAMMA1000565//EST//2.7e-38:386:76//Hs.162404:AA573131
R-MAMMA1000567//EST//0.33:49:79//Hs.147754:AI220561
R-MAMMA1000576//ESTs//4.9e-57:348:89//Hs.108921:N31211
R-MAMMA1000583//Homo sapiens KIAA0412 mRNA, partial cds//1.3e-52:373:77/
/Hs.6200:AB007872
R-MAMMA1000585//ESTs//5.1e-40:337:78//Hs.130815:AA936548
R-MAMMA1000594//Small inducible cytokine A5 (RANTES)//3.0e-45:225:80//Hs
.155464:AF088219
R-MAMMA1000597//ESTs//2.0e-98:461:99//Hs.43212:AA993042
R-MAMMA1000605//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA,
3429 nt]//1.5e-50:500:73//Hs.116007:S79267
R-MAMMA1000612//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPEATS CO
NTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION [Saccharomyces cerevisi
ae]//8.6e-108:559:94//Hs.29203:AI344105
R-MAMMA1000616//EST//0.071:169:60//Hs.144096:AI032180
R-MAMMA1000621//ESTs//1.0e-90:477:94//Hs.26073:R96361
R-MAMMA1000623
R-MAMMA1000625//ESTs//3.4e-98:556:91//Hs.119482:AI361002
R-MAMMA1000643//EST//4.9e-74:379:96//Hs.137447:AA342203
R-MAMMA1000664//Homo sapiens mRNA for putative lipoic acid synthetase, p
artial//3.2e-43:400:76//Hs.53531:AJ224162

R-MAMMA1000669//EST//6.9e-53:368:84//Hs.149580:AI281881

R-MAMMA1000670//ESTs, Highly similar to HYPOTHETICAL PROTEIN IN TONB 3' REGION [*Klebsiella pneumoniae*]//8.4e-98:464:98//Hs.31431:AI022065

R-MAMMA1000672//ESTs//2.0e-80:382:99//Hs.106747:AI080476

R-MAMMA1000684//ESTs//6.2e-72:357:98//Hs.67896:AA865212

R-MAMMA1000696//Human mRNA for KIAA0345 gene, complete cds//3.3e-52:216:75//Hs.98938:AB002343

R-MAMMA1000707//EST//7.0e-11:195:68//Hs.147002:AI184644

R-MAMMA1000713//Homo sapiens DEC-205 mRNA, complete cds//1.5e-45:485:74//Hs.153563:AF011333

R-MAMMA1000714//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//1.2e-29:158:79//Hs.142764:AA205569

R-MAMMA1000718//ESTs//3.1e-45:264:88//Hs.152413:AA780515

R-MAMMA1000720//ESTs//7.4e-44:244:87//Hs.111742:R39329

R-MAMMA1000723//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//5.6e-52:350:82//Hs.46328:D87942

R-MAMMA1000731//ESTs//1.1e-19:420:66//Hs.35036:H95267

R-MAMMA1000732//EST//2.9e-20:229:74//Hs.135400:AI056893

R-MAMMA1000733//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [*Caenorhabditis elegans*]//1.2e-35:371:74//Hs.141429:AA631915

R-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.1e-58:253:98//Hs.31575:AF100141

R-MAMMA1000738//ESTs, Weakly similar to similar to *Achlya ambisexualis* antheridiol steroid receptor [*C.elegans*]//2.3e-116:557:98//Hs.71472:AA632288

R-MAMMA1000744//ESTs//0.015:143:67//Hs.135382:AI224205

R-MAMMA1000746//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-90:568:86//Hs.23094:M19503

R-MAMMA1000752//Interleukin 10//2.8e-43:339:80//Hs.2180:M57627
 R-MAMMA1000760//EST//5.0e-44:306:86//Hs.162404:AA573131
 R-MAMMA1000761//EST//5.0e-41:187:85//Hs.162335:AA564256
 R-MAMMA1000775//Human mRNA for KIAA0355 gene, complete cds//3.0e-46:465:
 76//Hs.153014:AB002353
 R-MAMMA1000776//ESTs//1.9e-43:429:73//Hs.141742:W22204
 R-MAMMA1000778//ESTs//1.8e-31:445:70//Hs.111723:H57439
 R-MAMMA1000782//EST//0.0019:102:68//Hs.120686:AA747150
 R-MAMMA1000798//ESTs//1.4e-13:267:69//Hs.140156:AA704163
 R-MAMMA1000802//Clathrin, light polypeptide (Lcb)//1.5e-45:358:76//Hs.73
 919:X81637
 R-MAMMA1000831//ESTs//1.3e-104:510:97//Hs.17494:AA572675
 R-MAMMA1000839//EST//2.9e-51:307:89//Hs.149580:AI281881
 R-MAMMA1000841//ESTs//1.3e-34:412:72//Hs.121256:AA757902
 R-MAMMA1000842//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING
 ENTRY !!!! [H.sapiens]//9.4e-44:363:79//Hs.96337:AA225358
 R-MAMMA1000843//ESTs//2.2e-106:525:97//Hs.152016:AA603097
 R-MAMMA1000845//ESTs//1.6e-66:327:98//Hs.156900:AA468955
 R-MAMMA1000851//ESTs//3.7e-14:115:86//Hs.140590:R76251
 R-MAMMA1000855//Human mRNA for KIAA0392 gene, partial cds//5.7e-47:281:9
 1//Hs.40100:AB002390
 R-MAMMA1000856//EST//1.8e-16:150:79//Hs.136811:AA789212
 R-MAMMA1000862//EST//3.2e-05:93:73//Hs.161205:AI419311
 R-MAMMA1000863//ESTs//1.0e-46:446:73//Hs.153432:AA098922
 R-MAMMA1000865//Homo sapiens clone 23632 mRNA sequence//3.0e-39:324:80//
 Hs.46918:AF052099
 R-MAMMA1000867//ESTs//9.8e-16:193:76//Hs.152340:AA521399
 R-MAMMA1000875//EST//3.1e-24:301:72//Hs.132635:AI032875
 R-MAMMA1000876//ESTs//9.9e-48:246:97//Hs.112165:AA621243

R-MAMMA1000877//ESTs//1.4e-38:324:79//Hs.141024:H07128
R-MAMMA1000880//Homo sapiens mRNA for KIAA0594 protein, partial cds//3.2e-40:542:68//Hs.154872:AB011166
R-MAMMA1000883//ESTs//1.0:207:60//Hs.47199:N51107
R-MAMMA1000897//ESTs//2.6e-78:383:97//Hs.41067:AI310215
R-MAMMA1000905//Human mRNA for KIAA0331 gene, complete cds//9.7e-53:307:91//Hs.146395:AB002329
R-MAMMA1000906//ESTs//8.0e-25:206:83//Hs.141825:AA017093
R-MAMMA1000908//ESTs//4.4e-32:176:96//Hs.38559:AA701634
R-MAMMA1000914//ESTs//0.032:150:63//Hs.119162:AA399989
R-MAMMA1000921//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//7.7e-38:269:74//Hs.108966:U48696
R-MAMMA1000931//ESTs//1.2e-80:457:91//Hs.122319:AA782335
R-MAMMA1000940//ESTs//3.3e-43:329:82//Hs.35254:AI133727
R-MAMMA1000941//ESTs//7.5e-55:306:84//Hs.163936:AA632281
R-MAMMA1000942//ESTs//2.5e-83:405:98//Hs.116491:AA650428
R-MAMMA1000943//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//9.3e-79:567:80//Hs.1361:M55053
R-MAMMA1000956//EST//5.7e-53:256:100//Hs.162209:AA536178
R-MAMMA1000957//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))//7.5e-49:340:85//Hs.103458:X53795
R-MAMMA1000962//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.0e-48:216:85//Hs.153468:AB011147
R-MAMMA1000968//EST//6.2e-46:302:86//Hs.149580:AI281881
R-MAMMA1000975//ESTs//1.4e-85:428:96//Hs.141742:W22204
R-MAMMA1000979//Homo sapiens mRNA for KIAA0761 protein, partial cds//8.0e-39:338:79//Hs.93121:AB018304

R-MAMMA1000987//EST//2.8e-41:249:90//Hs.149580:AI281881
R-MAMMA1000998//Homo sapiens apoptotic protease activating factor 1 (Apar-1) mRNA, complete cds//3.9e-50:445:77//Hs.77579:AF013263
R-MAMMA1001003//Sialophorin (gpL115, leukosialin, CD43)//4.1e-51:282:82//Hs.80738:X52075
R-MAMMA1001008//ESTs, Weakly similar to renin [H.sapiens]//1.9e-82:405:97//Hs.25863:AA630313
R-MAMMA1001021//Homo sapiens DEC-205 mRNA, complete cds//3.0e-44:309:86//Hs.153563:AF011333
R-MAMMA1001024//ESTs//6.8e-35:333:78//Hs.107657:AA126814
R-MAMMA1001030//ESTs//1.6e-110:552:96//Hs.59483:AA524536
R-MAMMA1001035//ESTs//1.0e-45:273:85//Hs.138856:H47461
R-MAMMA1001038//Human mRNA for KIAA0392 gene, partial cds//3.0e-50:298:91//Hs.40100:AB002390
R-MAMMA1001041//ESTs//3.6e-86:445:95//Hs.122625:R68650
R-MAMMA1001050//EST//2.2e-54:387:85//Hs.149580:AI281881
R-MAMMA1001059//ESTs, Moderately similar to RNA helicase [M.musculus]//1.7e-13:273:65//Hs.98738:AI015487
R-MAMMA1001067//ESTs//1.3e-38:324:78//Hs.20190:AA525532
R-MAMMA1001073//ESTs//5.2e-106:554:94//Hs.12336:W63748
R-MAMMA1001074//Human mRNA for KIAA0355 gene, complete cds//1.2e-38:544:68//Hs.153014:AB002353
R-MAMMA1001075//ESTs//2.0e-98:463:99//Hs.18341:N38944
R-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-84:556:85//Hs.23094:M19503
R-MAMMA1001082//ESTs//2.4e-71:356:97//Hs.152302:T90222
R-MAMMA1001091//ESTs//4.7e-83:429:95//Hs.154412:AA310926
R-MAMMA1001092//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//6.4e-34:262:82//Hs.129727:AF035587

R-MAMMA1001105//Human putative RNA binding protein RNPL mRNA, complete cds//4.2e-27:232:76//Hs.61840:U28686

R-MAMMA1001110//ESTs//1.6e-17:128:87//Hs.161314:AI421576

R-MAMMA1001126//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//8.8e-53:462:78//Hs.116007:S79267

R-MAMMA1001133//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.8e-59:460:81//Hs.5247:AF029750

R-MAMMA1001139//ESTs//1.3e-62:341:94//Hs.18819:R01029

R-MAMMA1001143//ESTs//3.0e-48:383:80//Hs.152340:AA521399

R-MAMMA1001145//Calcium modulating ligand//5.1e-48:403:79//Hs.13572:AF068179

R-MAMMA1001154//EST//6.8e-35:313:75//Hs.162404:AA573131

R-MAMMA1001161//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.1e-58:409:84//Hs.5247:AF029750

R-MAMMA1001162//ESTs, Highly similar to t-BOP [M.musculus]//2.1e-91:430:99//Hs.129982:AI420970

R-MAMMA1001181//ESTs//5.0e-112:557:96//Hs.118181:W02251

R-MAMMA1001186//ESTs//3.8e-85:410:99//Hs.163811:W44959

R-MAMMA1001191//ESTs//0.018:57:87//Hs.141253:AA226519

R-MAMMA1001198//ESTs, Weakly similar to involved in signaling by the epidermal growth factor receptor [M.musculus]//2.6e-80:358:96//Hs.163827:AA074202

R-MAMMA1001202//ESTs//7.0e-43:230:95//Hs.79788:AA527348

R-MAMMA1001203//Clathrin, light polypeptide (Lcb)//2.8e-65:348:79//Hs.73919:X81637

R-MAMMA1001206//EST//0.098:84:72//Hs.162941:AA635148

R-MAMMA1001215//ESTs//1.3e-43:156:86//Hs.155243:N70293

R-MAMMA1001220//ESTs//8.9e-17:276:68//Hs.116518:AA653202

R-MAMMA1001222//ESTs//0.49:112:66//Hs.24668:AA897315

R-MAMMA1001243//EST//0.99:143:62//Hs.68522:C20701
R-MAMMA1001244//ESTs//2.2e-06:79:83//Hs.123163:AA809619
R-MAMMA1001249//ESTs//4.2e-68:343:97//Hs.147139:AI191307
R-MAMMA1001256//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens] //4.7e-31:221:77//Hs.142764:AA205569
R-MAMMA1001259//ESTs//1.3e-43:266:90//Hs.6193:AA045149
R-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//2.0e-21:226:75//Hs.65238:AB014561
R-MAMMA1001268//H.sapiens HCG II mRNA//2.4e-53:181:85//Hs.146333:X81001
R-MAMMA1001271//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK [Mus musculus] //1.1e-108:546:95//Hs.18999:N30643
R-MAMMA1001274//Homo sapiens mRNA for KIAA0572 protein, partial cds//4.4e-32:188:94//Hs.14409:AB011144
R-MAMMA1001280//EST//0.0015:170:62//Hs.116770:AA630371
R-MAMMA1001292//ESTs//5.6e-102:481:99//Hs.94810:AA811876
R-MAMMA1001296//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.2e-27:348:70//Hs.15731:AB011135
R-MAMMA1001298//ESTs//1.4e-44:375:79//Hs.70279:AA757426
R-MAMMA1001305//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.0e-43:300:85//Hs.46468:U45984
R-MAMMA1001322//Homo sapiens stress-activated protein kinase 4 mRNA, complete cds//8.8e-12:188:70//Hs.55771:AF004709
R-MAMMA1001324//ESTs//5.3e-68:297:88//Hs.121228:AA709471
R-MAMMA1001330//ESTs//1.6e-57:429:83//Hs.70279:AA757426
R-MAMMA1001341//Homo sapiens 4F5S mRNA, complete cds//4.8e-27:285:75//Hs.32567:AF073519
R-MAMMA1001343//ESTs//8.1e-51:273:93//Hs.162208:AA536127
R-MAMMA1001346//ESTs//1.0:122:65//Hs.33028:AA482478
R-MAMMA1001383//ESTs//1.4e-45:377:80//Hs.114671:N39322

R-MAMMA1001388//EST//7.7e-47:361:80//Hs.162197:AA535216
 R-MAMMA1001397//EST//8.7e-48:337:83//Hs.149580:AI281881
 R-MAMMA1001408//EST//1.2e-38:251:87//Hs.162677:AA604831
 R-MAMMA1001411//ESTs//4.3e-93:435:99//Hs.105460:AA780275
 R-MAMMA1001419//Homo sapiens translation initiation factor 4e mRNA, complete cds//1.6e-19:117:96//Hs.19122:AF038957
 R-MAMMA1001420//ESTs//7.3e-96:507:95//Hs.55299:AI335267
 R-MAMMA1001435//ESTs//5.0e-97:459:99//Hs.144843:AI222168
 R-MAMMA1001442//ESTs//7.1e-28:167:83//Hs.141019:AA287618
 R-MAMMA1001446//Homo sapiens KIAA0432 mRNA, complete cds//6.2e-19:328:67
 //Hs.155174:AB007892
 R-MAMMA1001452//EST//5.6e-44:487:75//Hs.161476:N57542
 R-MAMMA1001465
 R-MAMMA1001476//Homo sapiens yolk sac permease-like molecule 3 (YSPL3) mRNA, complete cds//0.79:182:66//Hs.136529:AF058317
 R-MAMMA1001487//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-35:328:78/
 /Hs.43681:AL022394
 R-MAMMA1001501//ESTs//4.6e-100:472:98//Hs.123660:AA813065
 R-MAMMA1001502//Human mRNA for KIAA0080 gene, partial cds//5.6e-15:220:6
 9//Hs.74554:D38522
 R-MAMMA1001510
 R-MAMMA1001522//ESTs//3.2e-16:214:75//Hs.152816:AA634242
 R-MAMMA1001547//H.sapiens mRNA for urea transporter//2.3e-45:282:89//Hs.
 66710:X96969
 R-MAMMA1001551//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.9e-56:489:76//Hs.108966:U486
 96
 R-MAMMA1001575//ESTs//4.3e-92:440:98//Hs.162882:AA807140
 R-MAMMA1001576//ESTs, Highly similar to TUBULIN GAMMA CHAIN [Homo sapie

ns]//1.9e-111:549:96//Hs.21635:AI417305
R-MAMMA1001590//ESTs//1.1e-63:324:96//Hs.142217:AA278441
R-MAMMA1001600//ESTs//5.6e-15:159:78//Hs.138633:H98792
R-MAMMA1001604
R-MAMMA1001606//ESTs, Weakly similar to finger protein kox1 [H.sapiens]//
/1.9e-97:488:96//Hs.143263:AI057616
R-MAMMA1001620//Homo sapiens mRNA, clone:RES4-16//5.4e-43:408:76//Hs.121
493:D25272
R-MAMMA1001627//Homo sapiens mRNA for KIAA0772 protein, complete cds//2.
0e-49:472:76//Hs.15519:AB018315
R-MAMMA1001630//ESTs, Weakly similar to putative p150 [H.sapiens]//6.8e-
15:168:73//Hs.115216:AA291074
R-MAMMA1001633//EST//5.1e-14:228:68//Hs.141456:N36377
R-MAMMA1001635//ESTs//3.4e-37:368:75//Hs.164033:AA769606
R-MAMMA1001649
R-MAMMA1001663//Homo sapiens neuronal thread protein AD7c-NTP mRNA, comp
lete cds//1.7e-54:272:81//Hs.129735:AF010144
R-MAMMA1001670//Small inducible cytokine A5 (RANTES)//5.7e-50:304:89//Hs
.155464:AF088219
R-MAMMA1001671//EST//1.9e-14:312:65//Hs.137153:R46248
R-MAMMA1001679//H.sapiens mRNA for rho GDP-dissociation Inhibitor 1//0.0
66:196:62//Hs.159161:X69550
R-MAMMA1001683//ESTs//4.9e-94:447:98//Hs.134464:AI151081
R-MAMMA1001686//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0488//1.0e-17:246:73//Hs.67619:AB007957
R-MAMMA1001692//Human mRNA for KIAA0063 gene, complete cds//2.1e-47:294:
89//Hs.3094:D31884
R-MAMMA1001711//ESTs//2.4e-86:439:96//Hs.18498:N52088
R-MAMMA1001715//ESTs//1.2e-73:399:93//Hs.124620:AI082338

R-MAMMA1001730//ESTs//1.1e-85:403:99//Hs.125464:AI084596
R-MAMMA1001735//ESTs, Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus] //3.7e-110:552:96//Hs.6923:AI161158
R-MAMMA1001740//ESTs//4.6e-45:342:82//Hs.37573:H59651
R-MAMMA1001743//EST//2.7e-58:412:85//Hs.149742:AI285666
R-MAMMA1001744
R-MAMMA1001745//EST//5.6e-54:374:84//Hs.137041:AA877817
R-MAMMA1001751//EST//3.5e-36:375:73//Hs.139715:N25041
R-MAMMA1001754//EST//0.18:144:66//Hs.71957:AA151413
R-MAMMA1001757//ESTs//1.0e-98:488:96//Hs.45184:C14904
R-MAMMA1001760//ESTs//8.7e-29:206:86//Hs.143310:AI142276
R-MAMMA1001764//ESTs//0.00012:434:58//Hs.120051:AA707847
R-MAMMA1001768//Human mRNA for KIAA0327 protein, complete cds//2.3e-41:299:85//Hs.149323:AB002325
R-MAMMA1001769//EST//1.7e-15:139:81//Hs.162399:AA572825
R-MAMMA1001771//ESTs, Moderately similar to semaphorin B [M.musculus] //7.6e-43:257:91//Hs.7634:AA481246
R-MAMMA1001783//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//5.6e-42:272:86//Hs.73614:U83460
R-MAMMA1001785//ESTs//1.5e-87:431:98//Hs.131065:AA972238
R-MAMMA1001788//EST//0.95:108:62//Hs.145881:AI274644
R-MAMMA1001790//ESTs//4.0e-41:340:80//Hs.158045:AA425744
R-MAMMA1001806//EST//1.4e-40:297:84//Hs.141240:H60313
R-MAMMA1001812//ESTs//2.4e-93:446:98//Hs.129034:AA776892
R-MAMMA1001815//EST//0.00053:371:59//Hs.133255:AI052659
R-MAMMA1001817//Human mRNA for KIAA0226 gene, complete cds//2.1e-46:325:87//Hs.44106:D86979
R-MAMMA1001818
R-MAMMA1001820//EST//1.9e-49:303:89//Hs.149580:AI281881

R-MAMMA1001824//Homo sapiens 4F5S mRNA, complete cds//4.3e-48:438:75//Hs.32567:AF073519

R-MAMMA1001836//ESTs//3.8e-06:128:71//Hs.143611:M78140

R-MAMMA1001837//Homo sapiens KIAA0395 mRNA, partial cds//3.8e-47:339:83//Hs.43681:AL022394

R-MAMMA1001848//ESTs//2.1e-16:125:85//Hs.161662:AA836811

R-MAMMA1001851//ESTs//4.5e-48:344:84//Hs.138856:H47461

R-MAMMA1001854//Small inducible cytokine A5 (RANTES)//2.6e-38:280:83//Hs.155464:AF088219

R-MAMMA1001858//ESTs//1.1e-44:331:83//Hs.44702:AI148840

R-MAMMA1001864//Homo sapiens mRNA for KIAA0475 protein, complete cds//7.8e-31:262:77//Hs.5737:AB007944

R-MAMMA1001868//Homo sapiens antigen NY-CO-16 mRNA, complete cds//9.2e-06:450:58//Hs.132206:AF039694

R-MAMMA1001874//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.9e-46:332:83//Hs.73614:U83460

R-MAMMA1001878//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//1.2e-46:429:78//Hs.2379:U23942

R-MAMMA1001880//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//7.6e-26:230:79//Hs.106008:AA147606

R-MAMMA1001890//ESTs//1.1e-39:338:79//Hs.146811:AA410788

R-MAMMA1001907//Kangai 1 (suppression of tumorigenicity 6, prostate; CD8 2 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))//6.7e-47:283:89//Hs.103458:X53795

R-MAMMA1001908//ESTs//0.043:134:65//Hs.145333:AI251374

R-MAMMA1001931//ESTs//1.8e-75:361:99//Hs.148125:AA693801

R-MAMMA1001956//Homo sapiens mRNA for KIAA0706 protein, complete cds//1.4e-18:174:77//Hs.139648:AB014606

R-MAMMA1001963//ESTs//6.7e-28:206:84//Hs.163254:AA828790

R-MAMMA1001969//ESTs, Weakly similar to hypothetical protein [H.sapiens]
 //6.7e-24:331:71//Hs.140506:AA308018

R-MAMMA1001970//ESTs//8.9e-61:286:84//Hs.141575:AA211734

R-MAMMA1001992//ESTs//4.4e-43:339:82//Hs.155498:W27084

R-MAMMA1002009//Small inducible cytokine A5 (RANTES)//4.6e-24:330:70//Hs
 .155464:AF088219

R-MAMMA1002011//ESTs//9.5e-72:360:97//Hs.13525:R39054

R-MAMMA1002032//Human melanoma antigen recognized by T-cells (MART-1) mR
 NA//3.7e-45:370:80//Hs.154069:U06452

R-MAMMA1002033//EST//4.6e-23:264:74//Hs.161917:AA483223

R-MAMMA1002041//ESTs//3.8e-100:465:100//Hs.141361:AI206412

R-MAMMA1002042//Homo sapiens 4F5S mRNA, complete cds//1.1e-43:407:76//Hs
 .32567:AF073519

R-MAMMA1002047//Homo sapiens mRNA for chemokine LEC precursor, complete
 cds//1.9e-37:316:74//Hs.10458:AF088219

R-MAMMA1002056//EST//1.3e-51:310:90//Hs.149580:AI281881

R-MAMMA1002058//ESTs//5.9e-16:135:84//Hs.95807:AA146979

R-MAMMA1002068//ESTs, Weakly similar to HYPOTHETICAL 43.3 KD PROTEIN IN
 QOXD-VPR INTERGENIC REGION [Bacillus subtilis]//4.0e-45:404:78//Hs.13859
 6:N38806

R-MAMMA1002078//EST//2.2e-15:207:71//Hs.132635:AI032875

R-MAMMA1002082//Homo sapiens mRNA for TSC403 protein, complete cds//1.7e
 -42:314:83//Hs.10887:AB013924

R-MAMMA1002084//Human mRNA for KIAA0392 gene, partial cds//3.7e-46:308:8
 7//Hs.40100:AB002390

R-MAMMA1002093//EST//0.89:213:60//Hs.151201:AI125907

R-MAMMA1002108//ESTs//1.0e-95:515:93//Hs.29002:H11347

R-MAMMA1002118

R-MAMMA1002125//Thromboxane A2 receptor//7.2e-43:335:83//Hs.89887:D38081

R-MAMMA1002132//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.4e-58:396:78//Hs.129735:AF010144

R-MAMMA1002140//Homo sapiens nephrin (NPHS1) mRNA, complete cds//1.4e-37:422:75//Hs.128834:AF035835

R-MAMMA1002143//ESTs//0.050:123:69//Hs.8231:AA152276

R-MAMMA1002145//Homo sapiens KIAA0426 mRNA, complete cds//5.0e-21:371:69//Hs.97476:AB007886

R-MAMMA1002153//ESTs//2.0e-31:159:77//Hs.130815:AA936548

R-MAMMA1002155//Human Line-1 repeat mRNA with 2 open reading frames//8.7e-39:506:69//Hs.23094:M19503

R-MAMMA1002156//Homo sapiens mRNA for putative lipoic acid synthetase, partial//2.9e-44:336:82//Hs.53531:AJ224162

R-MAMMA1002158//ESTs//3.0e-40:313:83//Hs.118273:AA626040

R-MAMMA1002170//Homo sapiens mRNA for TRAF5, complete cds//7.7e-37:370:77//Hs.29736:AB000509

R-MAMMA1002174//ESTs//2.5e-16:186:75//Hs.141203:H52638

R-MAMMA1002198//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//6.2e-51:318:82//Hs.92381:AB007956

R-MAMMA1002209//ESTs//9.2e-34:111:88//Hs.141575:AA211734

R-MAMMA1002215//ESTs//3.6e-101:530:94//Hs.26780:N50038

R-MAMMA1002219//Homo sapiens mRNA for KIAA0640 protein, partial cds//5.2e-45:283:88//Hs.153026:AB014540

R-MAMMA1002230//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//9.1e-50:330:77//Hs.108966:U48696

R-MAMMA1002236

R-MAMMA1002243

R-MAMMA1002250//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.2e-44:299:87//Hs.113283:AF018080

R-MAMMA1002267//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0487//1.6e-54:207:81//Hs.92381:AB007956

R-MAMMA1002268//ESTs//2.9e-94:439:100//Hs.68061:AI042283

R-MAMMA1002269//ESTs//7.4e-05:170:65//Hs.140466:AA766772

R-MAMMA1002282//ESTs//7.8e-09:69:78//Hs.159502:AA225141

R-MAMMA1002292//ESTs//5.3e-64:334:94//Hs.113606:AI138751

R-MAMMA1002293//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//
1.7e-39:203:81//Hs.154257:AI275982

R-MAMMA1002294//EST//8.1e-43:326:82//Hs.149580:AI281881

R-MAMMA1002297//ESTs//6.5e-45:323:83//Hs.155475:AA761454

R-MAMMA1002298//ESTs//1.7e-68:355:96//Hs.52683:H87153

R-MAMMA1002299//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HO
MOLOG [Homo sapiens]//2.3e-58:346:91//Hs.140385:AA773359

R-MAMMA1002308

R-MAMMA1002310//Human melanoma antigen recognized by T-cells (MART-1) mR
NA//2.2e-44:280:87//Hs.154069:U06452

R-MAMMA1002311//Human Line-1 repeat mRNA with 2 open reading frames//2.3
e-70:503:81//Hs.23094:M19503

R-MAMMA1002312//EST//1.7e-31:144:80//Hs.135936:N36094

R-MAMMA1002317//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//4.
3e-49:457:76//Hs.144563:AF057280

R-MAMMA1002319//ESTs//3.9e-38:297:70//Hs.140326:AA827183

R-MAMMA1002322//ESTs//1.1e-46:301:86//Hs.155498:W27084

R-MAMMA1002329//EST//2.6e-09:146:72//Hs.132366:AI026658

R-MAMMA1002332//Homo sapiens clone 23892 mRNA sequence//2.6e-45:387:70//
Hs.91916:AF035317

R-MAMMA1002333//EST//1.8e-09:139:74//Hs.137800:AA886897

R-MAMMA1002339//ESTs//4.2e-47:310:76//Hs.138865:W57618

R-MAMMA1002347//ESTs//1.5e-44:326:83//Hs.111723:H57439

R-MAMMA1002351//ESTs//3.0e-112:545:97//Hs.26209:AI143127
 R-MAMMA1002352//Homo sapiens mRNA for leukemia associated gene 2//1.5e-5
 8:259:92//Hs.43628:Y15228
 R-MAMMA1002353//Human mRNA for KIAA0392 gene, partial cds//4.5e-40:360:7
 7//Hs.40100:AB002390
 R-MAMMA1002355//ESTs//1.4e-29:307:75//Hs.3769:AI085367
 R-MAMMA1002356//Clathrin, light polypeptide (Lcb)//4.9e-31:217:88//Hs.73
 919:X81637
 R-MAMMA1002359//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-70:48
 3:84//Hs.113283:AF018080
 R-MAMMA1002360//ESTs//3.5e-19:301:69//Hs.124701:AA701475
 R-MAMMA1002361//Homo sapiens X-ray repair cross-complementing protein 2
 (XRCC2) mRNA, complete cds//2.6e-30:244:81//Hs.129727:AF035587
 R-MAMMA1002362//ESTs//2.3e-43:241:88//Hs.150727:AI292236
 R-MAMMA1002380//ESTs//5.1e-36:322:79//Hs.136994:AA843542
 R-MAMMA1002384//Small inducible cytokine A5 (RANTES)//1.8e-42:298:84//Hs
 .155464:AF088219
 R-MAMMA1002385//ESTs//0.57:203:63//Hs.146303:AA579061
 R-MAMMA1002392//Human mRNA for platelet-activating factor acetylhydrolas
 e 2, complete cds//5.8e-41:305:83//Hs.86188:D87845
 R-MAMMA1002411//ESTs//4.4e-68:385:92//Hs.53478:N92294
 R-MAMMA1002413//Homo sapiens mRNA for small GTP-binding protein, complet
 e cds//3.3e-14:138:75//Hs.115325:D84488
 R-MAMMA1002417//ESTs//1.6e-98:475:98//Hs.96345:N22588
 R-MAMMA1002427//ESTs//3.1e-39:274:79//Hs.141130:H28477
 R-MAMMA1002428//ESTs//8.4e-11:215:66//Hs.141022:H06475
 R-MAMMA1002434//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNIN
 G ENTRY !!!! [H.sapiens]//2.5e-106:521:98//Hs.112152:AA487348
 R-MAMMA1002446//ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING EN

TRY !!!! [H.sapiens]//4.7e-37:374:68//Hs.157142:U85996
R-MAMMA1002454//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0485//2.0e-60:323:81//Hs.89121:AB007954
R-MAMMA1002461//ESTs//4.7e-111:548:97//Hs.104281:AA147076
R-MAMMA1002470//ESTs, Highly similar to HYPOTHETICAL 80.7 KD PROTEIN IN
ERG7-NMD2 INTERGENIC REGION [Saccharomyces cerevisiae]//8.5e-104:544:93
//Hs.94570:AI192106
R-MAMMA1002475//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
RY !!!! [H.sapiens]//3.4e-31:263:79//Hs.38687:AA744496
R-MAMMA1002480//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
RY !!!! [H.sapiens]//1.0e-34:159:79//Hs.133526:N21103
R-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds/
/8.9e-116:560:97//Hs.155223:AF055460
R-MAMMA1002494//ESTs//3.2e-47:303:88//Hs.155243:N70293
R-MAMMA1002498//Human novel homeobox mRNA for a DNA binding protein//0.0
043:331:58//Hs.37035:U07664
R-MAMMA1002524//ESTs//0.0039:354:61//Hs.125797:AA806277
R-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gam
ma) mRNA, complete cds//3.9e-103:529:95//Hs.18858:AF065214
R-MAMMA1002545//Homo sapiens mRNA for KIAA0575 protein, complete cds//9.
5e-50:317:88//Hs.153468:AB011147
R-MAMMA1002554//ESTs//2.3e-85:445:95//Hs.139140:AA218851
R-MAMMA1002556//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
RY !!!! [H.sapiens]//1.0e-12:280:65//Hs.12725:T65058
R-MAMMA1002566//ESTs//2.3e-88:421:99//Hs.17602:AA705681
R-MAMMA1002571//ESTs//5.1e-97:456:99//Hs.152834:AA595693
R-MAMMA1002573//ESTs//3.1e-38:258:87//Hs.163989:R74433
R-MAMMA1002585//ESTs//7.8e-96:533:91//Hs.26009:H49371
R-MAMMA1002590//ESTs//0.61:202:62//Hs.161190:AI419258

R-MAMMA1002597//Cytochrome P450, subfamily IIB (phenobarbital-inducible)
 , polypeptide 6//2.9e-21:177:75//Hs.1360:M29874
 R-MAMMA1002598//ESTs//3.4e-113:544:97//Hs.20263:AA573737
 R-MAMMA1002603//Thiopurine S-methyltransferase//7.6e-35:225:80//Hs.51124
 :AF019369
 R-MAMMA1002612//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//4.2e-46:424:75//Hs.1361:M55053
 R-MAMMA1002617//ESTs//1.1e-38:229:92//Hs.96987:W27389
 R-MAMMA1002618//Landsteiner-Wiener blood group glycoprotein//1.3e-27:185
 :73//Hs.108287:L27670
 R-MAMMA1002619//ESTs//1.7e-95:480:96//Hs.54873:AA526306
 R-MAMMA1002622//Thromboxane A2 receptor//3.2e-46:298:87//Hs.89887:D38081
 R-MAMMA1002623//EST//4.3e-49:336:85//Hs.149580:AI281881
 R-MAMMA1002625//ESTs, Moderately similar to ovarian-specific protein [R. norvegicus]//2.3e-35:308:79//Hs.93332:AA811920
 R-MAMMA1002629//Homo sapiens mRNA for small GTP-binding protein, complete cds//9.7e-57:283:86//Hs.115325:D84488
 R-MAMMA1002636//Human mRNA for KIAA0392 gene, partial cds//1.2e-49:303:89//Hs.40100:AB002390
 R-MAMMA1002637//ESTs//1.3e-55:391:85//Hs.95074:AI144421
 R-MAMMA1002646//ESTs//7.4e-36:182:80//Hs.163937:N69915
 R-MAMMA1002650//ESTs//1.6e-102:547:94//Hs.57841:W63776
 R-MAMMA1002655
 R-MAMMA1002662//Homo sapiens KIAA0426 mRNA, complete cds//2.2e-46:462:75
 //Hs.97476:AB007886
 R-MAMMA1002665//Human mRNA for KIAA0118 gene, partial cds//9.1e-51:376:82//Hs.154326:D42087
 R-MAMMA1002671//ESTs, Weakly similar to coded for by C. elegans cDNA yk5
 2e10.5 [C.elegans]//5.3e-108:544:96//Hs.16464:W19606

R-MAMMA1002673//EST//3.3e-35:169:79//Hs.140046:AA668213
R-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds//4.
6e-109:544:96//Hs.3363:D86987
R-MAMMA1002685//EST//1.9e-31:223:86//Hs.112540:AA601385
R-MAMMA1002698//ESTs//5.9e-43:292:85//Hs.144660:AA652675
R-MAMMA1002699//ESTs//3.2e-25:134:100//Hs.126049:F22510
R-MAMMA1002701//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
RY !!!! [H.sapiens]//6.9e-70:353:96//Hs.138404:R70986
R-MAMMA1002708//ESTs//2.1e-76:413:94//Hs.57932:W69234
R-MAMMA1002711//ESTs//1.9e-44:236:96//Hs.138575:H67858
R-MAMMA1002721//Homo sapiens DEC-205 mRNA, complete cds//2.7e-43:273:89/
/Hs.153563:AF011333
R-MAMMA1002727//ESTs//2.9e-84:395:100//Hs.162826:AA679571
R-MAMMA1002728//Small inducible cytokine A5 (RANTES)//3.4e-42:266:88//Hs
.155464:AF088219
R-MAMMA1002744//ESTs//4.2e-18:473:63//Hs.42826:AA846757
R-MAMMA1002746//ESTs//1.8e-100:473:99//Hs.117558:AA779907
R-MAMMA1002748//Human melanoma antigen recognized by T-cells (MART-1) mR
NA//5.8e-40:330:80//Hs.154069:U06452
R-MAMMA1002754//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
RY !!!! [H.sapiens]//4.5e-40:369:77//Hs.105292:AA504776
R-MAMMA1002758
R-MAMMA1002764//ESTs//4.2e-103:486:99//Hs.159909:AI393281
R-MAMMA1002765//ESTs//1.6e-37:338:76//Hs.37573:H59651
R-MAMMA1002769//ESTs//0.72:409:57//Hs.141376:AI301272
R-MAMMA1002780//ESTs//1.6e-52:292:92//Hs.135985:AA342750
R-MAMMA1002782//ESTs//1.0e-31:157:80//Hs.159510:AA297145
R-MAMMA1002796//ESTs//3.8e-49:284:92//Hs.156479:AA513812
R-MAMMA1002807//Archain//1.4e-39:315:80//Hs.33642:X81198